

Rapid Universal Early Screening for Alzheimer's Disease and Related Dementia via Pattern Discovery in Diagnostic History

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SUMMARY

Alzheimer's disease (AD) is a progressive, incurable and ultimately fatal neurodegenerative condition. In this study, we introduce the Zero-burden Co-morbid Risk (ZCoR) score to screen for the future risk of AD and related dementia (ADRD) 1 – 10 years before a clinical diagnosis. Requiring no new bloodwork or cognitive tests, ZCoR leverages uncharted comorbidity patterns, to potentially enable near-instantaneous universal point-of-care screening of entire patient populations. In validation, ZCoR ($n = 729,018$) achieves out-of-sample $AUC > 90\%$ for predicting a diagnosis immediately after screening, an $AUC > 87\%$ for a diagnosis made one year earlier than in current practice, and maintaining over $> 80\%$ AUC for predictions made a decade earlier, irrespective of sex. We achieve high predictability in patients lacking any of the currently suspected risk factors; demonstrating effectiveness in cohorts at higher risk of missed diagnoses. Additionally, ZCoR can target mild cognitive impairment (MCI) with performance at par with questionnaire-based assessments ($AUC 88\text{--}90\%$), maintaining high effectiveness ($AUC \approx 80\%$) for predicting impairment upto 3 years into the future. Powered by stochastic learning algorithms that enhance standard machine learning, ZCoR enables discovery in electronic health record databases, can reduce ADRD and MCI diagnostic delays, and the impact of socio-economic and demographic variables, with immediate impact on patient outcomes.

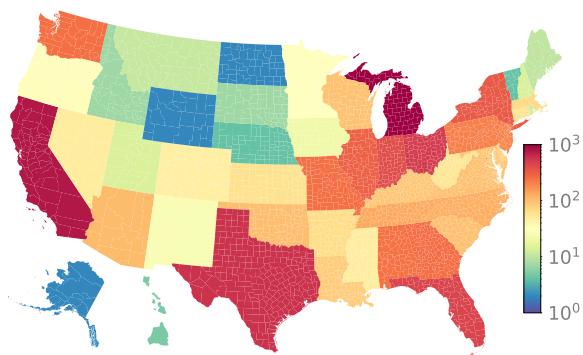
INTRODUCTION

DEMENTIA is an acquired loss of cognition in one or more domains including learning and memory, social cognition, language, executive function, complex attention, and perceptual motor function, severe enough to significantly diminish social or occupational function¹. Affecting approximately 47 million people worldwide¹, including over 5.5 million in the United States^{2,3}; and projected to be over 81 million worldwide by 2040⁴, there is an immediate need to find effective interventions, and screening tools that enable them.

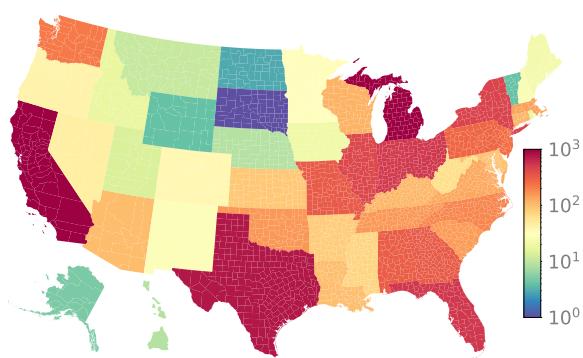
The most common cause of dementia, contributing to 60%–80% of cases, is believed to be Alzheimer's disease (AD), a progressive, fatal, and currently incurable neurodegenerative condition⁵. Based on patient years lived with disability plus years lost to premature mortality, AD ranked as the 6th most burdensome disease or injury in the US in 2016, up from 12th in 1990⁶, and was implicated in over 250,000 deaths in 2018⁵.

AD-related neuropathology appears to progress over years or decades, independently of the clinical course, suggesting lengthy asymptomatic, subclinical, and/or subtly symptomatic periods before a clinical diagnosis⁷.

a. Prevalence in Truven Dataset:
Male



b. Prevalence in Truven Dataset:
Female



C. Cumulative probability of ADRD diagnosis
in Truven dataset

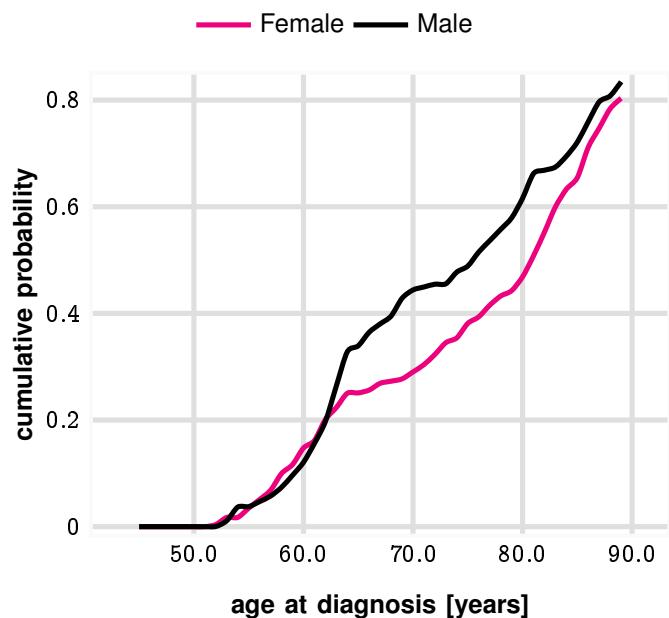


Fig. 1: Descriptive statistics of database. Panels a and b show geographic locations of study participants. Panel c illustrates the distribution of patient ages at documented diagnosis, showing that risk starts increasing from around 60 years, matching known ADRD onset age characteristics³. Also, panel c illustrates that the empirical risk per patient is higher for males in the Truven dataset, although there are more females with ADRD in total (See Tables I and II), and more female patients in general in the database in the relevant age groups. The age-stratified prevalence in the Truven dataset align closely with prevalence numbers reported for the US in 2020²⁰.

Accurate screening for both current and future cases on the Alzheimer's clinical spectrum may be expected to lead to earlier detection of AD biomarkers, neuropathology and incipient cognitive impairment or dementia. In turn, accelerating diagnosis may provide several important benefits for patients, caregivers, healthcare providers, and society^{1–3,8–11}: first, pharmacologic and non-pharmacologic interventions may be applied to slow progression of cognitive impairment, while cognition is relatively preserved. Second, use of tailored education strategies may be facilitated to promote cognitively-impaired patients' adherence to and safe use of complex treatment regimens. Third, patient capacity for financial, legal, and health care decision-making may be optimized when it can occur as early as possible in the syndrome's course⁹. And finally, patient access to clinical trials of drugs targeting cognition and dementia may be fostered, and study samples may be enriched, accelerating progress and decreasing costs of such investigations.

However, accurate screening for ADRD is limited by the current diagnostic/prognostic modalities. Imaging or cerebrospinal fluid testing for evidence of beta-amyloid plaques and neurofibrillary tau deposits, the basis for an AD classification⁷ and predictors of potential cognitive worsening, is expensive, invasive, and sometimes inaccessible. Although measurement of phosphorylated tau in plasma has shown promise as a specific marker and prognostic factor for ADRD^{12–16}, this method is as yet unavailable in everyday practice, entails an invasive blood draw, and if widely used, may in aggregate prove costly. Neuropsychological testing instruments such as the Montreal Cognitive Assessment (MOCA)^{17,18} have good diagnostic accuracy and some prognostic utility in identifying mild cognitive impairment (MCI) and mild AD¹⁹, but their time requirements, even when measured in minutes, may add appreciably to length-of-visit, and hence pose challenges in primary care settings^{9,10}. Moreover, these instruments require validation when used in additional locales or languages, and efficacy in predicting future diagnoses might be suspect.

Analysis of routinely-collected health care data in past medical encounters may offer a passive, non-invasive,

TABLE I: Inclusion/Exclusion, Positive/Control Criteria & Cohort Definitions

	Definitions
Inclusion/Exclusion Criteria	<p>Age 50+ years</p> <p>Has medical history for ≥ 3 yrs</p>
Cohort Definition	<p>Positive Cohort: Patients either with at least one target code for ADRD from Tab. III (Case Dx), or with at least one of the target diagnostic codes or a prescription of an ADRD drug (See Tab. IV, Case Dx/Rx)</p> <p>Control Cohort: Patients lacking any target diagnostic code (Case Dx), or additionally any ADRD related prescription (Case Dx/Rx)</p>

CONSORT Diagram

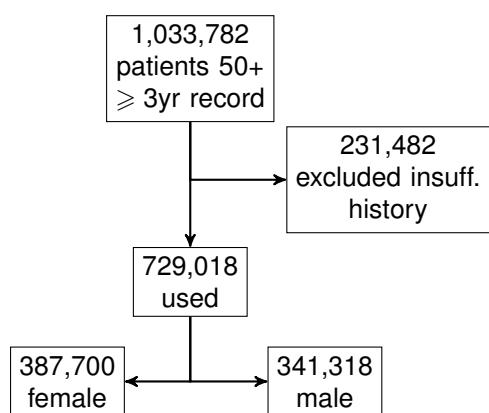


TABLE II: Cohort Sizes

	Male				Female			
	age range	n	n _{positive}	n _{control}	age range	n	n _{positive}	n _{control}
all patients	65-74	45943	1498	44445	65-74	47392	1546	45846
	75-84	16911	2870	14041	75-84	17303	3203	14100
	85+	7837	2383	5454	85+	10727	3753	6974
	total	341318	10397	330921	total	387700	12599	375101
low-risk §	age range	n	n _{positive}	n _{control}	age range	n	n _{positive}	n _{control}
	65-74	3841	108	3733	65-74	5330	101	5229
	75-84	963	170	793	75-84	1165	213	952
	85+	328	106	222	85+	411	170	241
high-risk §	age range	n	n _{positive}	n _{control}	age range	n	n _{positive}	n _{control}
	65-74	42102	1390	40712	65-74	42062	1445	40617
	75-84	15948	2700	13248	75-84	16138	2990	13148
	85+	7509	2277	5232	85+	10316	3583	6733
	total	289819	9600	280219	total	309548	11580	297968

§See Tab. I for cohort definitions, and SI-Table I for diagnostic codes defining the high-risk cohort.

inexpensive, fast and accessible solution, to accurately discover elevated risk of ADRD²¹. The multifactorial etiologies of ADRD imply that numerous risk factors are associated with these syndromes²¹, and administrative claims and hospital databases, due to their large or even vast scope, offer sufficient statistical power to discover exquisitely-detailed algorithms to pinpoint potential cases. Notably, administrative claims and hospital databases may be especially amenable to exploration in heretofore unprecedented depth of associations of ADRD and comorbidities. Observational studies already have suggested that such associations encompass a large number and variety of disorders covering much of the human disease spectrum²²; for example, non-neuropsychiatric chronic conditions such as diabetes, hypertension, hypercholesterolemia, obesity, sleep apnea, thyroid disorders, osteoporosis, and glaucoma have been linked to ADRD^{22,23}. The validated or suspected associations of ADRD with both “intuitive” categories of comorbidity, e.g., neurological, psychiatric, and cardiovascular disorders, and with non-intuitive categories, e.g., metabolic, endocrine, ophthalmologic disorders, and more recently infections^{24,25}, provide rationale for us to seek to leverage comorbid diagnoses to quantify ADRD risk.

Despite extensive documentation of co-morbidities, a reliable risk estimator — purely from ICD code-based comorbidity patterns without any pre-selection of diagnostic codes already known to be a ADRD co-morbidity — is under-explored. The heterogeneity of brain aging processes and ADRD presentation²⁶, make such an endeavor challenging. Here we report the Zero Burden Co-morbid Risk Score (ZCoR) for ADRD, developed and validated using 729,018 unique patients drawn from across the United States, which reliably identifies patients up to 10 years before a contemporary documented clinical diagnosis.

ZCoR is a 701-feature digital signature distilled automatically from past diagnostic code sequences. We make no preselection of codes or ADRD-related risk factors, and require no new blood-work, laboratory tests, familial history or other patient-specific information that might preclude applicability at the point of care. Yet, we achieve an out-of-sample AUC exceeding 87% for either sex (predictions for one year earlier), and $\approx 80\%$ (prediction

made a decade earlier). Importantly, our predictive performance matches the highest AUC achieved by MOCA (92.1%^{19,27}) when making predictions just before a clinical diagnosis ($\geq 91\%$, see Table. IX). Our underlying algorithms are fundamentally novel, designed to learn from sparse, noisy categorical diagnostic sequences, with demonstrable non-trivial performance boost over standard tools used in recent studies.

Additionally, ZCoR for ADRD is sex-stratified, with separate signatures generated for males and females, in line with the growing appreciation of sex as a key contributor to the phenotypic heterogeneity of ADRD^{28,29}. Predictability of eventual dementia in the presence of specific high-risk conditions such as type 2 diabetes has been studied before^{30–32}. However, the complex pathobiology of ADRD implies that “low-risk” patients without any of the known risks, might still develop ADRD. Lacking the known flags, such a low-risk cohort is at a much higher risk of a missed or a delayed diagnosis. We show that ZCoR maintains high predictive performance in such patient groups.

The effectiveness of diverse cognitive assessment tools, often combined with pre-selected risk factors, has been recently surveyed³³, recording AUCs between 55%-89%, sometimes for diagnoses 10 – 20 years into the future^{34,35}. Nevertheless, substantial resource burden - often requiring detailed neurological, cognitive and psychiatric consults - limits applicability of such tools at the point-of-care, which were never conceived of for universal screening. Similarly, recent advances with machine learning²⁶ have often focused on classification of brain imaging data, which, while effective, and backed by well-understood mechanistic models, do not mitigate the barrier to universal adoption.

Thus, our key contribution in this study is to potentially alleviate obstacles to universal testing of the older population. The necessity of such universal screening tools has been well-recognized^{36,37}, with recent attempts at developing electronic health record (EHR)-based digital signatures to assess future ADRD risk. While two other digital signatures^{36,37} have, to our knowledge, been reported since 2020, ZCoR demonstrates significantly better performance. More importantly, Boustani *et al.* used both structured and unstructured data including clinical notes processed for specific AD related keywords, and Park *et al.* makes use of laboratory test results (e.g. blood hemoglobin) which might not be available for every patient at the point-of-care; in contrast, ZCoR exclusively uses data already present in patient records, which would typically vary from one patient to another, with no *a priori* fixed “demand” on any specific item of clinical, familial, demographic or lifestyle information. Thus, ZCoR can be applied almost universally, passively, and nearly instantaneously at the point-of-care.

EHR-based screening has also been explored to a limited extent for MCI³⁸, leveraging patterns extracted from clinical notes. When retrained to detect MCI, ZCoR-MCI is demonstrated to perform significantly better compared to reported results (both at both at the time of screening, and for predictions made years into the future), while, as before, using only ICD codes from past encounters.

RESULTS

Patient Selection

Our patient data comes from the IBM MarketScan® Commercial Claims and Encounters Database for the years 2003-2018³⁹ (previously Truven Health Analytics, and referred to as the “Truven dataset”). This US national database merges data contributed by over 150 insurance carriers and large self-insurance companies, and comprises over seven billion time-stamped diagnosis codes. The database tracks over 87 million patients for 1 to 15 years, reflecting a substantial cross-section of the US population. We select our cohort(s) in accordance with the inclusion/exclusion criteria described in Table I, ensuring that selected patients have at least three years of medical history recorded in the dataset. The geographical distribution of the patients in our selected cohort(s) is illustrated in Fig. 1a-b. Fig. 1c illustrates the age distribution at the time of ADRD diagnosis, which is consistent with the reported onset age characteristics for ADRD (mid-sixties³). Notably, the cumulative risk of onset (number of ADRD cases normalized by the total number of patients in the given age category) increases with age, as shown in Fig. 1c.

Predicting future ADRD diagnosis is modeled as a binary classification problem: we classify time-stamped sequences of diagnostic codes into positive and control categories, where the “positive” category refers to patients diagnosed with ADRD at 1 year from the point of screening, as identified by one or more ICD codes from Table III appearing in record (referred to as the Dx problem definition in Fig. 2 and Tables VII and VIII) or the prescription of AD-related medication^{37,40} (Table IV, donepezil, galantamine, memantine or rivastigmine, referred to as the “Dx/Rx problem definition” in Table VII and VIII). The breakdown of diagnostic codes used for different sex and problem-definition combinations are shown in Table V.

We also consider screening up to M years before the actual diagnosis, considering values of $M = 0, \dots, 10$,

TABLE III: ADRD ICD diagnostic codes

ICD code	description
290.0	Senile dementia uncomplicated
290.1	Presenile dementia
290.11	Presenile dementia w delirium
290.12	Presenile dementia w delusion
290.13	Presenile dementia w depression
290.2	Senile dementia w delusion
290.21	Senile dementia w depressive
290.3	Senile dementia w delirium
290.8	Senile psychosis NEC
290.9	Senile psychot condition NOS
293.9	Transient mental disease NOS
294.2	Demen NOS w/o behavior dstrb
294.21	Demen NOS w behavior dstrb
294.8	Mental disorder NEC other disease
294.9	Mental disorder NOS other disease
331.0	Alzheimer's disease
F00 F00.0	Dementia in Alzheimer's disease
F00.1 F00.2	
F00.2 F00.9	
F03.9	Unspecified dementia without behavioral disturbance
F03.90	Unspecified dementia without behavioral disturbance
F03.91	Unspecified dementia with behavioral disturbance
F05	Delirium due to known physiological condition
F06.8	Other specified mental disorders due to known physiological condition
G30	Alzheimer's disease with early onset
G30.0	Alzheimer's disease with early onset
G30.1	Alzheimer's disease with late onset
G30.8	Other Alzheimer's disease
G30.9	Alzheimer's disease unspecified

TABLE IV: ADRD common prescriptions active ingredients

Drugs
Donepezil Hydrochloride
Galantamine Hydrobromide
Memantine Hydrochloride
Rivastigmine
Rivastigmine Tartrate

TABLE V: Number of diagnostic codes used

target case	gender	Number of codes	Number of unique codes
Dx	Male	6729970	18895
Dx	Female	9693456	19998
Dx/Rx	Male	6721267	18887
Dx/Rx	Female	9682339	19988

i.e., which relate to predicting ADRD immediately before a clinical diagnosis to up to a decade in the future. The control cohort comprises patients who never develop ADRD, i.e., do not have target codes, and are never prescribed related medication. Due to our requirement of minimum 3 years of medical history of record implies the absence of a diagnosis for at least $M + 2$ years in the future from the time of screening. We base our predictions on the past 2 years of diagnostic history. Overall we analyze $n = 729,018$ patients, with 22,996 patients in the positive group and 706,022 patients in the control group (See CONSORT diagram in Fig. 2c), considering approximately 42 million diagnostic codes, with altogether over 46K unique codes for both sexes.

We do not pre-select any diagnostic code based on its suspected comorbidity with ADRD. To investigate if our performance changes substantially for “high-risk” patients identified based on known co-morbidities including obesity, type II diabetes mellitus, hypertension, atherosclerosis, atrial fibrillation, dyslipidemia, depression, alcohol abuse, and pneumonia, we separately test our performance in high-risk and low-risk sub-cohorts. The high-risk sub-cohort comprises patients with one or more of the diagnoses enumerated in SI-Table I, which identify the top known co-morbidities^{22,41}. The low-risk sub-cohort comprises patients who are not at high-risk as specified by the previous condition. Results in the low-risk sub-cohort is of particular significance; these patients are at a higher risk of missed or delayed diagnosis.

Determining the optimal set of target codes for making clinically useful predictions is challenging; too wide a definition makes predictions non-specific, while selecting too few erodes statistical power. The selection of target codes in Table III closely follows Park *et al.*³⁷ to enable a direct performance comparison. We also consider an expanded set of targets, including vascular dementia, frontotemporal dementia, vascular cognitive impairment, dementia with Lewy Bodies, and major neurocognitive disorder, with no significant performance variation (See Results).

The EHR codeset we use to ascertain ADRD-related disorders is intentionally broad, and not meant to diagnose a specific pathology, but predict risk of general dementia. This comports with our aim of developing a universal

TABLE VI: Feature Definitions (Total number of features used: 701)

feature name	explanation	n _{features}
feature-phenotype scores relative to phenotype score	Mean p-score of feature-phenotype codes within sequence divided by general p-score of feature-phenotype	45
feature-phenotype scores relative to whole score	Mean p-score of feature-phenotype codes within sequence divided by mean p-score of all codes in the record	45
aggregation score	aggregation of the p-scores in the record	13
high scores proportion	proportion of codes with very high p-scores among all codes in the record	1
low scores proportion	proportion of codes with very low p-scores among all codes in the record	1
dynamics of mean score	mean p-score of second half of the record divided by mean p-score of first half of the record	1
dynamics of geometric mean score	geometric mean p-score of second half of the record divided by mean p-score of first half of the record	1
dynamics of st.dev score	standard deviation of p-scores of second half of the record divided by standard deviation of p-scores of first half of the record	1
dynamics of score range	range of p-scores of second half of the record divided by range of p-scores of first half of the record	1
dynamics of score skew	skew of p-scores of second half of the record divided by skew of p-scores of first half of the record	1
aggregation relative to phn score	aggregation of all feature-phenotype 's mean scores divided by corresponding general p-score of feature-phenotype	9
aggregation relative to whole score	aggregation of all feature-phenotype 's mean scores divided by mean p-score of all codes in the record	9
feature-phenotype proportion	Ratio of number of weeks with the codes of a given phenotype to the total number of weeks in sequence	45
feature-phenotype prevalence	Ratio of number of weeks with the codes of a given phenotype to the number of weeks with any diagnosis code recorded	45
feature-phenotype first incident	Time interval from observation date to the first phenotype code, normalized by record length	45
feature-phenotype last incident	Time interval from observation date to the last phenotype code, normalized by record length	45
feature-phenotype mean position	Mean time position of phenotype codes in the record, normalized by record length	45
feature-phenotype streak	Length of the longest uninterrupted subsequence of weeks with the codes of a given phenotype recorded	45
feature-phenotype code prevalence	Ratio of number of codes of a given phenotype to the total number of codes in sequence	45
feature-phenotype code density	Ratio of number of codes of a given phenotype to the total number of weeks in sequence	45
Max/Mean/Std/Range intermission	Maximum/Mean/Standard Deviation/Range of the lengths of subsequences of consequent weeks with codes	4
Max/Mean/Std cluster	Maximum/Mean/Standard Deviation of the lengths of subsequences of consequent weeks without codes	3
Max/Std/Range prevalence	Maximum/Standard Deviation/Range of the phenotype prevalences	3
Max/Std/Range code prevalence	Maximum/Standard Deviation/Range of the Ratio of number of codes of a given phenotype to the total number of codes in sequence	3
Max/Std/Range code density	Maximum/Standard Deviation/Range of the Ratio of number of codes of a given phenotype to the total number of weeks in sequence	3
Density of DX Record	Proportion of weeks in a record observed where at least one DX code was recorded	1
feature-phenotype	Sequence Likelihood Defect for a given phenotype	45
feature-phenotype neg log-likelihood	negative log-likelihood score for a given phenotype	45
feature-phenotype pos log-likelihood	positive log-likelihood score for a given phenotype	45
feature-phenotype log-likelihood ratio	Ratio of positive to negative log-likelihood score for a given phenotype	45
Mean Δ^{\ddagger}	Mean negative Sequence Likelihood Defect	1
Geometric Mean Δ^{\ddagger}	Geometric Mean negative Sequence Likelihood Defect	1
Range Δ^{\ddagger}	Range of Sequence Likelihood Defect	1
Std. deviation Δ^{\ddagger}	Standard Deviation of Sequence Likelihood Defect	1
Mean neg log-likelihood	Mean negative log-likelihood score	1
Geometric Mean pos log-likelihood	Geometric Mean negative log-likelihood score	1
Range neg log-likelihood	Range of negative log-likelihood score	1
Std. deviation neg log-likelihood	Standard Deviation of negative log-likelihood score	1
Mean pos log-likelihood	Mean positive log-likelihood score	1
Geometric Mean pos log-likelihood	Geometric Mean positive log-likelihood score	1
Range pos log-likelihood	Range of positive log-likelihood score	1
Std. deviation pos log-likelihood	Standard Deviation of positive log-likelihood score	1
Mean log-likelihood ratio	Mean log-likelihood score ratio	1
Geometric Mean log-likelihood ratio	Geometric Mean log-likelihood score ratio	1
Range log-likelihood ratio	Range of log-likelihood score ratio	1
Std. deviation log-likelihood ratio	Standard Deviation of log-likelihood score ratio	1

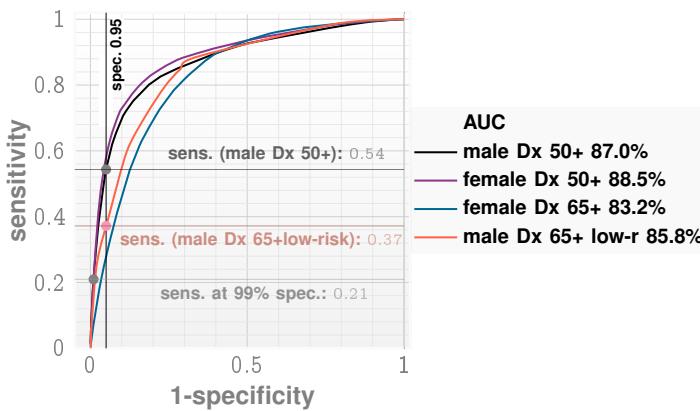
*feature: ICD disease categories, or sets of diagnostic codes tracked

† Δ : Sequence Likelihood Defect (See Methods)

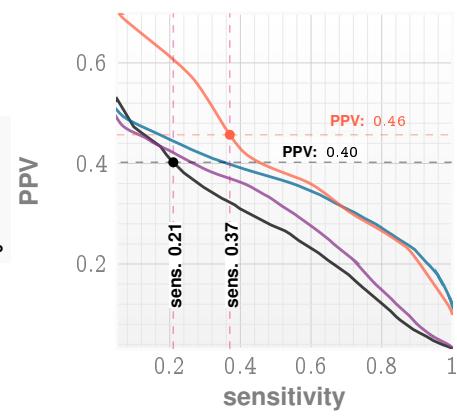
‡ neg log-likelihood: log-likelihood of observed sequence generated by model inferred from control (See Methods)

pos log-likelihood: log-likelihood of observed sequence generated by model inferred from positive (See Methods)

a. Receiver Operator Characteristic curves



b. Precision-Recall curves



c. Feature importances for broad categories of co-morbidities



Fig. 2: Predictive performance of ZCoR for ADRD diagnosis 1 year in the future. Panels a and b show the out-of-sample ROC and precision-recall curves for diagnosis 1 year from the point of screening. We achieve AUCs > 88% for male and > 86% for females in the age group 50+, for the diagnostic criteria based on ICD codes (See description of diagnostic criteria considered in Table I), with sensitivities at 58% (females) and 54% (females) at 95% specificity. See Tables VII and VIII for performance within 65+ cohort, and within the low-risk and high-risk cohorts in each age strata. Panel c shows the top 20 comorbidity categories sorted in the order of inferred importance in estimating risk, where categories for mental and cognitive disorders have been removed to highlight the role of other physiological co-morbidities. Importantly, the comorbidities modulate risk differentially by sex, although the patterns are broadly similar, e.g., metabolic, cardiovascular, ophthalmological, ischemic categories appear in both males and females, with slightly altered ranking. Infections and immunologic disorders appear with high importance.

screening tool, as opposed to a diagnostic instrument, that triggers more detailed neurological assessment.

In addition to ADRD, we also investigate the ability of our basic approach to predict MCI (both at the time of screening, and as a prediction of a future diagnosis), identified by the appearance of ICD codes 331.83 (ICD9) and G31.84 (ICD10). We evaluate the performance of ZCoR-MCI with a retrained pipeline, which, in out-of-sample validation, shows significant improvement over reported literature.

Feature Importance & Comorbidity Spectra

The aggregate importance of the ZCoR features (See Fig. 2c), estimated as the mean change in the raw risk via random perturbations in the feature values, illustrates that metabolic and cardiovascular disorders are the most important diagnostic category modulating risk.

Additionally, we compute the statistically significant log-odds ratio of specific ICD codes occurring in the true positive vs the true negative patient sets. We call these the “comorbidity spectra” (See Figs. 3 and 4). These spectra are based on individual codes, as opposed to the aggregated feature importances shown in Fig. 2c. Clearly, every disorder listed in the co-morbid spectra does not all appear in a single patient; the codes with high log-odds ratio are significantly more likely in the positive cohort. The comorbidity spectra, so named because of disease category-specific color coding, offers unique insight into the predictive co-morbidity burden of ADRD.

Outcomes

In this study we demonstrate the following key results: 1) high out-of-sample predictive performance for identifying a ADRD diagnosis 1 year into future via leveraging subtle comorbidity patterns recorded in the medical history of individual patients (Tables VII-VIII), 2) high predictive performance for diagnosis up to 10 years into the future with sufficiently slow loss of predictive performance to remain clinically useful (Table IX), significantly outperforming recent results (Tables X-XI), 3) effective performance for both low-risk and high-risk cohorts (Tables VII-VIII, see relevant rows). Here, the high-risk cohort comprises patients with commonly surveilled for ADRD co-morbidities. Additionally, 4) maintain high performance for expanded target definitions which include vascular dementia, frontotemporal dementia, vascular cognitive impairment, dementia with Lewy Bodies, and major neurocognitive disorders (Table XII). And finally, 5) high predictive performance to screen for MCI for current and future diagnosis (Table XIII).

Pertaining to our main prediction results for 1-3, Fig. 2a-b illustrate the ROC and the precision-recall curves respectively (for screening one year before current diagnosis), shown separately for males and females. As noted in the panel legends, our out-of-sample predictive performance is $> 88\%$ AUC for females (age 50+) and $> 86\%$ for males (age 50+), with $> 50\%$ sensitivity at 95% specificity (53% for males and 57% for females). At 99% specificity, we obtain a PPV of 42% for females (50+) and 40 – 41% for males (50+) respectively. At these values we obtain an accuracy of $\approx 96 - 97\%$ (Table VII), which indicates the overall fraction of correct predictions. The PPV achieved by ZCoR at maximum accuracy is 54 – 55% for females (50+) and 51 – 53% for males (50+), with a corresponding NPV of 97%. The corresponding results for age 65+ are tabulated in Table VIII.

Thus, to summarize: our predictive pipeline detects about 53-57 out of every 100 patients who get a diagnosis in 1 year, if we operate at 95% specificity. If we wish to operate at the higher specificity of 99%, then out of 100 positive flags, we have about 41-42 true positives. The accuracy metric indicates that we correctly identify the risk status (positive or control) for 96-97 out of 100 patients, irrespective of sex, highlighting the potentially high clinical significance of ZCoR, as a universal screening tool to identify patients for diagnostic workup and/or intensified surveillance.

From the inferred relative importance of the co-morbidity categories (See Fig. 2d-e), we conclude, that metabolic and ischemic diseases, cardiovascular abnormalities, sleep disorders, nervous system disorders, and diseases of the eye are important modulators of risk. Infections also feature in the top 20 co-morbidities shown in these panels. Importantly while there are sex differences, the overall pattern of the relative importance ranking remains substantially sex-invariant. With some exceptions, many of these patterns are not particularly surprising; the contribution of this study is to bring them together systematically to realize an accurate risk estimate via the ZCoR score.

As expected, our predictive performance degrades as we predict earlier (See Table IX, and inset). Importantly, the degradation is slow enough that we can use ZCoR with acceptable reliability up to 10 years into the future, and significantly outperform reported results.

Understanding the seat of this predictive power is important. The feature importances discussed earlier (Fig. 2c) identify the relative impact of broad disease categories. Importantly, to evaluate the feature importance of a specific diagnostic category, we sum the importance of all features based on that category, not just the presence or absence of individual diagnoses. The latter aspect, i.e., the risk burden from the presence of specific codes, is investigated via the co-morbidity spectra for out-of-sample patients, shown separately in Figs. 3 and 4 for males and females, and the two target definitions (Dx and Dx/Rx). We find that the important co-morbidities are diverse, vary with the sex of the patients, but are clearly dominated by mental disorders, circulatory disorders, injuries, and a range of disorders categorized broadly as “ill-defined symptoms” in the ICD framework. Again,

TABLE VII: Detailed ZCoR performance for patients aged 50+, predictions made 1 year before diagnosis

sex	definition	cohort	sens.	PPV	acc	PPV [†]	NPV [†]	spec.	auc
Female	Dx/Rx	all patients	0.57	0.29	0.94	0.55	0.97	95%	0.884 ± 0.008
	Dx	all patients	0.58	0.29	0.94	0.54	0.97	95%	0.885 ± 0.004
	Dx/Rx	all patients	0.22	0.42	0.96	0.55	0.97	99%	0.884 ± 0.008
	Dx	all patients	0.21	0.42	0.96	0.54	0.97	99%	0.885 ± 0.004
Male	Dx/Rx	all patients	0.53	0.25	0.94	0.51	0.97	95%	0.866 ± 0.006
	Dx	all patients	0.54	0.27	0.94	0.53	0.97	95%	0.870 ± 0.011
	Dx/Rx	all patients	0.21	0.41	0.97	0.51	0.97	99%	0.866 ± 0.006
	Dx	all patients	0.21	0.40	0.97	0.53	0.97	99%	0.870 ± 0.011
Female	Dx/Rx	high-risk	0.55	0.28	0.94	0.54	0.97	95%	0.883 ± 0.008
	Dx	high-risk	0.55	0.28	0.94	0.50	0.97	95%	0.883 ± 0.005
	Dx/Rx	high-risk	0.20	0.41	0.96	0.54	0.97	99%	0.883 ± 0.008
	Dx	high-risk	0.19	0.40	0.96	0.50	0.97	99%	0.883 ± 0.005
Male	Dx/Rx	high-risk	0.52	0.25	0.94	0.58	0.97	95%	0.867 ± 0.008
	Dx	high-risk	0.53	0.25	0.94	0.50	0.97	95%	0.871 ± 0.011
	Dx/Rx	high-risk	0.21	0.40	0.97	0.58	0.97	99%	0.867 ± 0.008
	Dx	high-risk	0.20	0.39	0.97	0.50	0.97	99%	0.871 ± 0.011
Female	Dx/Rx	low-risk	0.59	0.28	0.94	0.64	0.98	95%	0.830 ± 0.039
	Dx	low-risk	0.54	0.28	0.94	0.62	0.98	95%	0.833 ± 0.039
	Dx/Rx	low-risk	0.41	0.58	0.97	0.64	0.98	99%	0.830 ± 0.039
	Dx	low-risk	0.37	0.56	0.97	0.62	0.98	99%	0.833 ± 0.039
Male	Dx/Rx	low-risk	0.54	0.26	0.94	0.56	0.97	95%	0.816 ± 0.039
	Dx	low-risk	0.59	0.28	0.94	0.68	0.97	95%	0.826 ± 0.029
	Dx/Rx	low-risk	0.28	0.48	0.97	0.56	0.97	99%	0.816 ± 0.039
	Dx	low-risk	0.31	0.51	0.97	0.68	0.97	99%	0.826 ± 0.029

*Calculated at 95% specificity

†Maximum PPV at observed prevalence, and NPV at maximum PPV

TABLE VIII: Detailed ZCoR performance for patients aged 65+, predictions made 1 year before diagnosis

sex	definition	cohort	sens.	PPV	acc	PPV [†]	NPV [†]	spec.	auc
Female	Dx/Rx	all patients	0.29	0.43	0.87	0.56	0.89	95%	0.836 ± 0.007
	Dx	all patients	0.28	0.42	0.87	0.54	0.89	95%	0.832 ± 0.010
	Dx/Rx	all patients	0.09	0.54	0.89	0.56	0.89	99%	0.836 ± 0.007
	Dx	all patients	0.07	0.49	0.88	0.54	0.89	99%	0.832 ± 0.010
Male	Dx/Rx	all patients	0.31	0.41	0.89	0.54	0.91	95%	0.827 ± 0.011
	Dx	all patients	0.31	0.40	0.89	0.54	0.91	95%	0.829 ± 0.013
	Dx/Rx	all patients	0.10	0.53	0.90	0.54	0.91	99%	0.827 ± 0.011
	Dx	all patients	0.09	0.51	0.90	0.54	0.91	99%	0.829 ± 0.013
Female	Dx/Rx	high-risk	0.26	0.43	0.87	0.57	0.89	95%	0.831 ± 0.007
	Dx	high-risk	0.27	0.42	0.87	0.57	0.89	95%	0.827 ± 0.009
	Dx/Rx	high-risk	0.09	0.54	0.88	0.57	0.89	99%	0.831 ± 0.007
	Dx	high-risk	0.07	0.48	0.88	0.57	0.89	99%	0.827 ± 0.009
Male	Dx/Rx	high-risk	0.31	0.41	0.89	0.53	0.91	95%	0.824 ± 0.013
	Dx	high-risk	0.30	0.40	0.89	0.52	0.91	95%	0.827 ± 0.014
	Dx/Rx	high-risk	0.10	0.53	0.90	0.53	0.91	99%	0.824 ± 0.013
	Dx	high-risk	0.09	0.51	0.90	0.52	0.91	99%	0.827 ± 0.014
Female	Dx/Rx	low-risk	0.52	0.58	0.90	0.64	0.92	95%	0.888 ± 0.025
	Dx	low-risk	0.45	0.54	0.89	0.55	0.93	95%	0.869 ± 0.033
	Dx/Rx	low-risk	0.17	0.71	0.89	0.64	0.92	99%	0.888 ± 0.025
	Dx	low-risk	0.10	0.90	0.89	0.55	0.93	99%	0.869 ± 0.033
Male	Dx/Rx	low-risk	0.41	0.48	0.90	0.61	0.92	95%	0.866 ± 0.050
	Dx	low-risk	0.37	0.46	0.89	0.57	0.92	95%	0.858 ± 0.037
	Dx/Rx	low-risk	0.15	0.62	0.91	0.61	0.92	99%	0.866 ± 0.050
	Dx	low-risk	0.14	0.64	0.91	0.57	0.92	99%	0.858 ± 0.037

*Calculated at 95% specificity

†Maximum PPV at observed prevalence, and NPV at maximum PPV

while many of these patterns are known at the population level, design of the personalized ZCoR score is not immediately obvious.

We include predictive performance in conventional high-risk (defined in SI-Table I) and low-risk cohorts in Table VII and VIII, showing that our performance in the high-risk sub-cohort is comparable with that in the full cohort. The AUCs in the low-risk cohort are somewhat lower (> 81% for males 50+ and > 83% for females 50+ respectively), albeit high enough to be clinically effective: we have a maximum PPV of 62 – 68%, and a sensitivity of 54 – 59% at specificity of 95% for 50+ patients who get diagnosed 1 year in the future (See

TABLE IX: Long-range ZCoR AUC estimates (95% confidence bounds) for target set listed in Table III

years to diagnosis	AUC Female	AUC Male	AUC Female Dx/Rx*	AUC Male Dx/Rx
0	0.912 ± 0.015	0.913 ± 0.015	0.909 ± 0.015	0.918 ± 0.015
1	0.885 ± 0.015	0.871 ± 0.015	0.875 ± 0.015	0.867 ± 0.015
2	0.872 ± 0.017	0.858 ± 0.017	0.867 ± 0.017	0.858 ± 0.017
3	0.858 ± 0.019	0.850 ± 0.018	0.852 ± 0.019	0.855 ± 0.019
4	0.863 ± 0.021	0.842 ± 0.020	0.843 ± 0.021	0.860 ± 0.021
5	0.850 ± 0.023	0.841 ± 0.022	0.840 ± 0.024	0.846 ± 0.023
6	0.840 ± 0.026	0.831 ± 0.025	0.832 ± 0.027	0.835 ± 0.025
7	0.830 ± 0.031	0.810 ± 0.028	0.839 ± 0.031	0.835 ± 0.028
8	0.815 ± 0.036	0.815 ± 0.033	0.828 ± 0.037	0.823 ± 0.034
9	0.799 ± 0.046	0.809 ± 0.041	0.811 ± 0.049	0.807 ± 0.042
10	0.841 ± 0.059	0.784 ± 0.049	0.834 ± 0.062	0.810 ± 0.058

* Dx/Rx refers to diagnosis inferred from either codes or AD-related prescriptions

INSET. ZCoR AUC over time

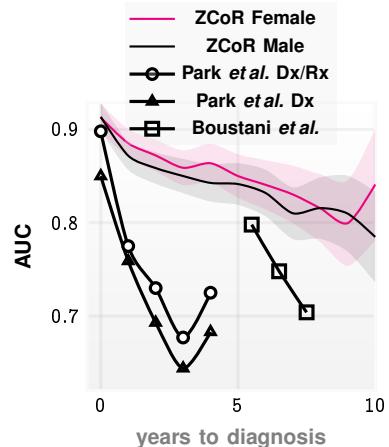


TABLE X: Comparison of AUC achieved in out-of-sample data between ZCoR and Park *et al.*³⁷

Year to diagnosis	Park <i>et al.</i> (Dx/Rx)	Park <i>et al.</i> (Dx)	ZCoR (Dx)	ZCoR (Dx/Rx)	$\Delta(Dx)\%^{\ddagger}$	$\Delta(Dx/Rx)\%^{\dagger}$
0	0.90	0.85	0.91	0.92	7.4726	2.3315
1	0.78	0.76	0.89	0.88	16.621	12.933
2	0.73	0.69	0.87	0.87	25.851	18.793
3	0.68	0.64	0.86	0.86	33.373	26.404
4	0.72	0.68	0.86	0.86	26.467	18.639

TABLE XI: Comparison of AUC achieved in out-of-sample data between ZCoR and Boustani *et al.*³⁶

year to diagnosis	Boustani <i>et al.</i> (Dx)	ZCoR (Dx)	$\Delta(Dx)\%^{\ddagger}$
1-10	0.80	0.85	6.48
3-10	0.75	0.84	11.9
5-10	0.70	0.83	17.8

[‡] Percentage outperformance of ZCoR with the Dx target definition

[†] Percentage outperformance of ZCoR with the Dx/Rx target definition

Tables VII and VIII).

Additionally, Table XII shows that an expanded target definition (described in Methods) yields no significant change in predictive performance. Finally, our results on MCI prediction are shown in Table XIII (carried out with a retrained pipeline targeting MCI), which illustrates an average AUC between 88-90% at the point of screening, degrading to under ≈ 80% for predictions made 3 years into the future. Notably, the performance at the point of screening is at par with MOCA (0.9 – 0.91 ± 0.015 vs .921¹⁹), while being significantly superior to a recently published EHR-based approach using standard machine learning algorithms⁴².

DISCUSSION

We report the development and validation of the ZCoR automated universal screening tool for ADRD, leveraging previously-uncharted co-morbidity patterns discovered from individual longitudinal diagnostic history. Across sexes, ZCoR accurately preempts ADRD cases up to 10 years before a clinical diagnosis is first documented. The broad co-morbidity categories that we infer to be important (Fig. 2c) include metabolic, cardiovascular, ischemic, ophthalmological, and sleep disorders. Diseases of the nervous system, unrelated to ADRD, infections, and immunologic disorders also appear in the list of top risk-modulating co-morbidities. Importantly, the co-morbidities modulate risk differentially by sex (Fig. 2c), although the patterns are broadly similar, with slightly altered ranking.

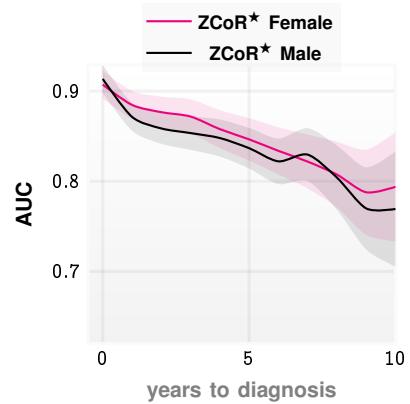
TABLE XII: Long-range ZCoR[★] AUC estimates (95% confidence bounds) for expanded target set (adding vascular dementia, frontotemporal dementia, vascular cognitive impairment, dementia with Lewy Bodies, and major neurocognitive disorder to Table III).

years to diagnosis	AUC Female	AUC Male
0	0.907 ± 0.155	0.913 ± 0.155
1	0.884 ± 0.155	0.871 ± 0.155
2	0.876 ± 0.173	0.858 ± 0.170
3	0.871 ± 0.191	0.853 ± 0.187
4	0.857 ± 0.210	0.847 ± 0.206
5	0.846 ± 0.236	0.836 ± 0.226
6	0.833 ± 0.262	0.822 ± 0.253
7	0.821 ± 0.299	0.829 ± 0.294
8	0.807 ± 0.365	0.804 ± 0.358
9	0.787 ± 0.473	0.769 ± 0.456
10	0.793 ± 0.606	0.769 ± 0.640

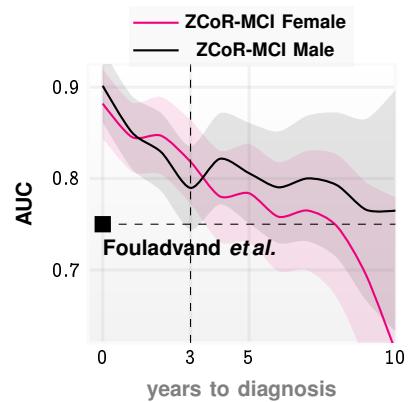
TABLE XIII: Long-range ZCoR-MCI AUC estimates (95% confidence bounds) with MCI identified via ICD codes 331.83 (ICD9) and G31.84 (ICD10).

years to diagnosis	AUC Female	AUC Male
0	0.882 ± 0.038	0.901 ± 0.040
1	0.845 ± 0.038	0.850 ± 0.040
2	0.846 ± 0.042	0.828 ± 0.043
3	0.818 ± 0.046	0.789 ± 0.046
4	0.780 ± 0.050	0.821 ± 0.050
5	0.783 ± 0.054	0.805 ± 0.055
6	0.758 ± 0.060	0.790 ± 0.061
7	0.764 ± 0.066	0.800 ± 0.069
8	0.747 ± 0.079	0.792 ± 0.080
9	0.694 ± 0.102	0.765 ± 0.100
10	0.611 ± 0.168	0.764 ± 0.132

INSET. ZCoR[★] AUC over time



INSET. ZCoR-MCI AUC over time

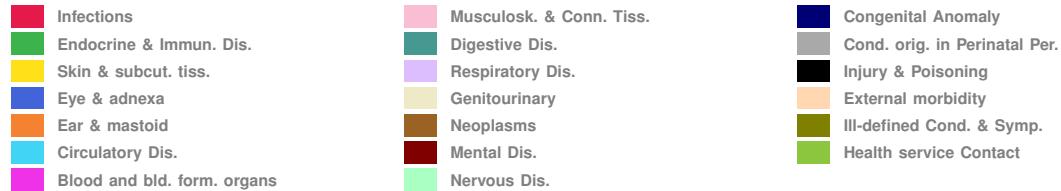


Focusing on the presence/absence of individual diagnostic codes modulating ADRD risk in the co-morbidity spectra (Figs. 3 and 4), we find circulatory disorders are generally over-represented, along with injuries, and conditions related to age-related cognitive decline. Many of these patterns are unsurprising: AD is a amnestic syndrome, injuries might indicate neuropathies from known AD co-morbidities such as diabetes or stroke, and cerebrovascular diseases might signal vascular dementia. Other prominent codes such as ataxia and psychiatric signs were recently associated with specific biomarkers implicated in autosomal dominant early-onset Alzheimer's disease^{43,44}. Appearance of other codes are more surprising, e.g. dysphagia or swallowing impairment is usually noted in the late stages of AD. However, recent studies have documented changes in cortical control of swallowing beginning before dysphagia becomes apparent in dementia patients^{45,46}. Thus, the important illness categories that we find to be associated with ADRD in either sex align with suspected or documented links in statistical^{29,36,37} and observational studies^{22,23}, lending credence to ZCoR rationale and accuracy. Also lending such credence is the score's incorporation, via sex-stratification, of differences between males and females in ADRD risk factors, natural history, and symptoms^{28,29,47–51}.

We find that with increasing patient age, it becomes more difficult to distinguish age related cognitive decline from ADRD (SI-Fig. 1), suggesting that ADRD comorbidities have confounding overlaps with conditions that arise more frequently as patients get older.

To our knowledge, ZCoR is one of three digital signatures for ADRD reported since 2020, joining those of Boustani *et al.*, developed utilizing data from the Indiana Network for Patient Care³⁶, and of Park *et al.*, developed utilizing data from the Korean National Health Insurance Service³⁷. Although the respective reported prognostic time-frames are not fully comparable, our digital signature appeared to achieve the best performance of the three (Table IX inset, and Tables X and XI). Notably, the AUC of ZCoR for ADRD at 10 years before documented diagnosis surpassed the AUCs of the Boustani *et al.*³⁶ signature for the 1-10 year, 3-10 year, or 5-10 year before diagnosis time-frames by 6.5%, 11.9%, and 17.8% respectively, while leveraging diagnostic histories of 1,400% more patients ($\approx 50K$ vs $\approx 700K$ for ZCoR). Also for each prediction time-point made 0 through 4 years before documented diagnosis, the AUCs of ZCoR exceeded those of the Park *et al.*³⁷ signature by 2-7% (0

ICD Class



a. Male Alzheimer's Dis.

518.5	Ac resp flr fol trma/srg
I66.9	Occlusion stenosis
S88.1	Traumatic amput knee ankle lower leg
N32.9	Bladder dis non-sp
R26.0	Ataxic gait
C34.1	Malig neopl up lobe non-sp bronchus lung
N32.3	Diverticulum bladder
Z91.8	Hisry falling
780.6	Fever nos
D51.0	Vitamin b12 deficiency anemia intrinsic fact deficiency
596.8	Inf cyssmy
I44.3	Non-sp atrioventricular block
I63.3	Cerebral infarction thrombosis
173.0	Malig neopl skin lip nos
173.6	Mal neo skin up limb nos
599.7	Hematuria nos
N31.9	Neuromuscular dysfunction bladder non-sp
I44.2	Atrioventricular block complete
I95.1	Orthostatic hypotension
I44.1	Atrioventricular block second
I63.4	Cerebral infarction embolism
S41.0	Wound rt shoulder
I62.0	Nontraumatic subdural hemorrhage non-sp
I69.9	Nonsp sequelae cerebrovascular dis
I67.8	Ac cerebrovascular insufficiency
I63.5	Cerebral infarction non-sp occlusion stenosis
R47.0	Aphasia
I67.1	Cerebral aneurysm nonruptured
F06.3	Mood dis known physcondition non-sp
I95.2	Hypotension drugs
C67.8	Malig neopl overlappings bladder
D41.4	Neoplasm uncertain behavi bladder
D30.3	30-39pc bdy brn/30-39pc 3d
R40.4	Transient alteration awareness
R27.0	Ataxia non-sp
173.2	Malig neo skin ear nos
I61.9	Nontraum intracerebral hem non-sp
R41.8	Age-related cognitive decline
787.2	Dysphagia, oral phase
F29	Non-sp psychosis
R41.3	Amnesia
F05	Delirium known physcondition

2.00 2.50 3.00
log odds ratio of normalized prevalence

b. Female Alzheimer's Dis.

R26.0	Ataxic gait
Z99.8	Dependence on supplemental oxygen
S59.1	Non-sp physeal fracture up end radius rt arm
S22.0	Wedge compression fracture non-sp thoracic vertebra
S42.0	Fracture non-sp part rt clavicle
Z45.0	Checking testing cardiac pacemaker pulse generat [battery]
S30.0	Contusion lower back pelvis
H35.3	Non-sp macular degeneration
787.2	Dysphagia, oral phase
I50.1	Left ventricular failure non-sp
C19	Malig neopl recsigmoid junction
D04.3	Carcinoma in situ skin non-sp part face
S70.0	Contusion non-sp hip
S09.9	Non-sp inj head
R40.0	Somnolence
I50.9	Heart failure non-sp
I74.3	Embolism thrombosis arteries lower extremities
I95.1	Orthostatic hypotension
I69.9	Nonsp sequelae cerebrovascular dis
S42.3	Non-sp fracture shaft humerus rt arm
814.0	Fx navicular wrist-clos
S39.8	Sp injuries abdomen
173.9	Malig neo skin nos
R63.0	Anorexia
J82	Chronic eosinophilic pneumonia
S02.2	Fracture nasal bones
I48.9	Non-sp atrial fibrillation
L97.9	Non-pressure chronic ulcer non-sp lower leg
K26.9	Duodenal ulcer non-sp acute chronic wo hemorrhage perf
J80	Ac respiratory distress syndrome
I80.3	Phlebitis thrombophlebitis lower extremities non-sp
I67.2	Cerebral atherosclerosis
S29.0	Fracture nos-closed
S01.0	Wound scalp
I45.9	Conduction dis non-sp
I49.5	Sick sinus syndrome
S01.8	Wound other part head
N36.2	Urethral caruncle
I69.8	Non-sp sequelae cerebrovascular dis
I65.8	Occlusion stenosis other precerbral arteries
Z95.0	Presence cardiac pacemaker
S32.0	Wedge compression fracture non-sp lumbar vertebra
I44.2	Atrioventricular block complete
173.3	Mal neo skin face nec/nos
I67.9	Cerebrovascular disease non-sp
J69.0	Pneumonitis inhalation food vomit
J81.1	Chronic pulmonary edema
813.8	Fx radius nos-closed
453.8	Ac embl suprfcl up ext
S79.8	Sp injuries rt hip
M80.0	Age-related osteoporosis
R27.0	Ataxia non-sp
R41.8	Age-related cognitive decline
I50.4	Non-sp congestive heart failure
H02.1	Non-sp ectropion rt up eyelid
F29	Non-sp psychosis
R40.4	Transient alteration awareness
I63.5	Cerebral infarction non-sp occlusion stenosis
I67.8	Ac cerebrovascular insufficiency
820.0	Fx up femur epiphy-clos
R41.3	Amnesia
820.8	Fx neck femur nos-cl

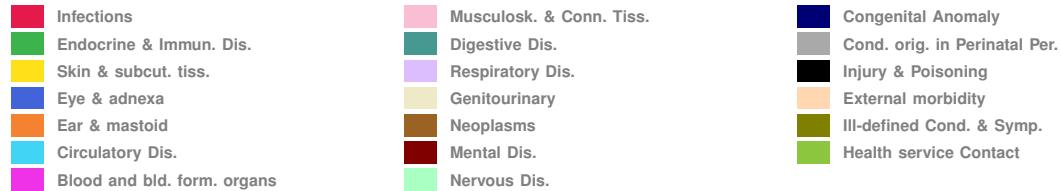
2.00 2.50 3.00
log odds ratio of normalized prevalence

Fig. 3: Co-morbidity Spectrum for the Dx/Rx case. Disorders that increase the odds of the patient being a “true positive” vs a “true negative”, where diagnosis is determined using either ICD codes (See Table III) or ADRD-related medications (See Table IV) in history. Such disorders (ranked according to the log-odds ratio) are more likely to be found in patients who are in the positive cohort. Comparing **panel a** with **panel b**, we note that these odds change from males to females, but as expected the patterns are broadly similar, with over-representation of circulatory disorders.

year), 12.9-16.6% (1 year), 18.8-25.8% (2 years), 26.4-33.3% (3 years) and 18.6-26.5% (4 years), while using 1,750% more patients ($\approx 40K$ vs $\approx 700K$ for ZCoR).

A number of methodological differences contribute to these respective performances. First, ZCoR uses sophisticated pattern discovery on patient history, and is not limited by known risk factors and co-morbidities, allowing for high performance on low-risk and high-risk cohorts alike. More importantly, our new stochastic inference

ICD Class



a. Male Alzheimer's Dis.

N39.4	Urge incontinence
J82	Chronic eosinophilic pneumonia
I73.8	Mal neo skn nec/nos
R32	Non-sp urinary incontinence
599.7	Hematuria nos
780.6	Fever nos
S10.1	Non-sp superficial injuries throat
S09.9	Non-sp inj head
I67.1	Cerebral aneurysm nonruptured
C43.3	Malig melanoma non-sp part face
I67.2	Cerebral atherosclerosis
I66.9	Occlusion stenosis
I69.9	Nonsp sequelae cerebrovascular dis
I95.1	Orthostatic hypotension
S10.9	Non-sp superficial inj non-sp part neck
D32.0	Benign neopl cerebral meninges
I97.7	Intraoperative cardiac arrest
S70.0	Contusion non-sp hip
J18.0	Bronchopneumonia non-sp organism
596.8	Inf cysmy
I63.4	Cerebral infarction embolism
173.2	Malig neo skin ear nos
Q24.5	Malformation coronary vessels
S60.8	Abrasion rt wrist
173.7	Mal neo skn low limb nos
820.8	Fx neck femur nos-cl
787.2	Dysphagia, oral phase
I67.8	Ac cerebrovascular insufficiency
K56.4	Fecal impaction
R40.4	Transient alteration awareness
Z95.3	Presence xenogenic heart valve
I63.5	Cerebral infarction non-sp occlusion stenosis
R40.0	Somnolence
I62.0	Nontraumatic subdural hemorrhage non-sp
S41.0	Wound rt shoulder
S01.0	Wound scalp
I69.8	Non-sp sequelae cerebrovascular dis
S01.9	Wound non-sp part head
I61.9	Nontraum intracerebral hem non-sp
R41.8	Age-related cognitive decline
S06.5	Traumatic subdural hem wo loss conc
F29	Non-sp psychosis
I63.3	Cerebral infarction thrombosis
S06.8	Injury carotid artery intracranial wo loss conc
R41.3	Amnesia

2.00 2.50 3.00 3.50

log odds ratio of normalized prevalence

b. Female Alzheimer's Dis.

R26.0	Ataxic gait
I21.4	Non-st elevation (nSTEMI) myocar infarc
S22.3	Fracture one rib rt side
M62.5	Muscle wasting atrophy non-sp
S01.8	Wound other part head
829.0	Fracture nos-closed
R63.4	Abnormal weight loss
I44.2	Atrioventricular block complete
I69.9	Nonsp sequelae cerebrovascular dis
I67.9	Cerebrovascular disease non-sp
S30.0	Contusion lower back pelvis
L97.4	Non-pressure chronic ulcer heel midfoot
822.0	Fracture patella-closed
787.2	Dysphagia, oral phase
S10.9	Non-sp superficial inj non-sp part neck
S42.0	Fracture non-sp part rt clavicle
S32.0	Wedge compression fracture non-sp lumbar vertebra
173.9	Malig neo skin nos
I77.1	Stricture artery
453.8	Ac embl suprfl up ext
R47.0	Aphasia
L97.5	Non-pressure chronic ulcer foot
S02.2	Fracture nasal bones
R56.9	Non-sp convulsions
I50.4	Non-sp congestive heart failure
D50.1	Sideropenic dysphagia
I63.5	Cerebral infarction non-sp occlusion stenosis
I50.9	Heart failure non-sp
I67.2	Cerebral atherosclerosis
L97.9	Non-pressure chronic ulcer non-sp lower leg
M80.0	Age-related osteoporosis
J81.1	Chronic pulmonary edema
I49.5	Sick sinus syndrome
L97.3	Non-pressure chronic ulcer non-sp ankle
J82	Chronic eosinophilic pneumonia
Z45.0	Checking testing cardiac pacemaker pulse generat [battery]
I50.1	Left ventricular failure non-sp
Z95.0	Presence cardiac pacemaker
I67.8	Ac cerebrovascular insufficiency
R41.8	Age-related cognitive decline
173.6	Mal neo skin up limb nos
821.0	Fx femur shaft-closed
I21.0	Myocar infarc main coronary artery
173.4	Mal neo sclp/skn nck nos
R40.4	Transient alteration awareness
820.8	Fx neck femur nos-cl
F29	Non-sp psychosis
S06.5	Traumatic subdural hem wo loss conc
R41.3	Amnesia

2.00 2.50 3.00

log odds ratio of normalized prevalence

Fig. 4: Co-morbidity Spectrum for the Dx case. Disorders that increase the odds of the patient being a “true positive” vs a “true negative”, where diagnosis is determined using ICD codes (See Table III). Such disorders (ranked according to the log-odds ratio) are more likely to be found in patients who are in the positive cohort. Comparing **panel a** with **panel b**, we note that these odds change from males to females, but as expected the patterns are broadly similar, with over-representation of circulatory disorders.

algorithms are designed to leverage longitudinal patterns, and are not limited to using indicator variables, i.e., simply the presence or absence of specific historical codes. Thus we are able to substantially leverage the emergent dependencies and temporal ordering of patterns emergent across the human disease spectrum.

Additionally, ZCoR for ADRD is stratified by sex. Sex-stratification of AD risk has recently found support in the literature²⁹. Finally, our algorithm is derived using a cohort roughly 10-18-fold larger than those of Boustani

et al. or Park *et al.* (729,018 versus 40,736 and 71,466 respectively), allowing our algorithms to capitalize on significantly larger quantities of data.

Beyond predictive performance, ZCoR addresses the barrier to universal testing. With no specific data demands (we use what we have on the individual patient file), and designed to operate on existing electronic healthcare architectures, the digital signature operates non-invasively, inexpensively, and nearly instantaneously, and is potentially very widely, if not universally accessible at least in developed countries using EHR. Unlike that of Boustani *et al.*, (but like that of Park *et al.*) who use expert opinion-generated variables in the first phase of their digital signature development, our algorithm is completely data-driven. Also, unlike Boustani *et al.* (but like Park *et al.*), we considered only structured data, i.e., ICD codes, and not clinical notes. While clinical notes might reveal substantially more information, such insights most relevant to ADRD might not be available before a neurology consult. And unlike Park *et al.*, we do not use laboratory tests such as hemoglobin levels, which might not be available for every patient in primary care.

We envision three main potential applications of ZCoR. First, the score can serve in primary care or specialist settings (e.g., neurology, gerontology) as a screening tool for future incident overt cases, with the potential diagnostic, therapeutic, psychosocial, caregiver-related, and research benefits noted in the introduction to this paper. ZCoR could, for example, be routinely deployed, alone or along with a brief, validated neuropsychological instrument, as recommended by the American Academy of Neurology⁵², in the cognitive screening mandated since 2011 as part of the Medicare annual wellness visit³. Alternatively, especially given the variable clinical natural history of such patients⁵³, ZCoR could be employed in individuals with subjective memory decline but largely-intact cognition and function, or in those with incipient MCI, e.g., worsening but still personally-appropriate serial neuropsychological test scores, who have not undergone biofluid or imaging assessment for ADRD-related or other dementia-related pathology. Notably, from pharmacoeconomic, practical, and psychosocial standpoints, use of ZCoR for “long-range” clinical prognostication may be compatible with the up-to-decades-long, pre-clinical progression of beta-amyloid and tau neuropathology in AD: even 10 years before overt cognitive impairment, biofluid testing or imaging performed due to ZCoR high-risk status is likely to be informative⁷, and the ZCoR classification, actionable. A second potential ZCoR application could be screening for undiagnosed prevalent cases of ADRD in primary care settings. Considering the estimated 45%–80% of dementia cases in older adults that go undiagnosed in the US⁵⁴, availability of a non-invasive, inexpensive, near-instantaneous, and almost universally-accessible tool could revolutionize detection of such patients. Third, ZCoR could be applied in scientific research regarding ADRD natural history and prevention. Beyond enrichment of trials of prophylactic interventions against cognitive impairment, ZCoR opens intriguing avenues of investigation, e.g., examination of the roles of previously-underrecognized comorbidity classes with important associations with ADRD, e.g., musculoskeletal disorders in males, respiratory infections in females, reproductive or ophthalmological disorders in both sexes. More precise understanding of the particular diseases that indeed are associated with ADRD will facilitate assessment of intriguing hypotheses such as inflammation serving as a key link between comorbidities and ADRD genetic features and phenotype⁵⁵.

Limitations & Conclusion

Our key limitations arise from potential diagnostic mis-codings, and the current imprecision in Alzheimer’s-related nomenclature⁷. Coupled with the high prevalence of undiagnosed dementia, mis-coding could lead to our ADRD signature deriving from data of only a fraction, albeit a substantial fraction, of our true cases. This situation might pose a particular peril under our Dx target definition, which considers only diagnostic codes. Mitigating this concern is the vast size of our control groups (n=375,101 females, n=330,921 males), implying that “non-signal” from large numbers of “true controls” is likely to overwhelm “buried ADRD signal” from “false controls”. An additional possible concern related to mis-coding would be inclusion of non-ADRD age-related dementia cases among the ADRD group. However, given the “mixed” picture of dementia afflicting many patients with ADRD^{1,7}, tracking the characteristics of patients with non-ADRD cognitive impairment is also pertinent.

The performance of ZCoR might be further enhanced with the inclusion of treatment-related factors, e.g., medications, along with comorbidities. As noted, however, using only diagnostic codes may increase the availability of data inputs for ZCoR in everyday practice, and hence the tool’s scalability to routine settings. Moreover, comorbidity codes may be viewed to at least some extent as surrogates capturing the effects of medications that might influence Alzheimer neuropathology, e.g., statins or anti-diabetic agents.

Predictive screening for ADRD raises some ethical concerns. In particular, early detection of progressive, not-yet-well-manageable brain disorders that have major effects on capacity, autonomy, and healthcare and other resource utilization, poses potential risks stemming from the possibility of stigmatization and discrimination⁸. It will be necessary to further explore these and other potential harms of early recognition of Alzheimer cognitive

impairment, and to seek their amelioration through legal and public health policy changes^{3,8}.

It is important to note that however strong its predictive performance, ZCoR is a screening tool, not a diagnostic tool, and by itself certainly does not establish an ADRD diagnosis. ZCoR prediction of high-risk for ADRD should lead to diagnostic testing, e.g., application of cognitive tests or imaging, and to intensified surveillance, as indicated. ZCoR results also can inform discussion with, and planning by, patients and their significant others.

In conclusion, ZCoR opens potentially new avenues in identification of and intervention against cognitive impairment, in neurocognitive research, and in designing effective caregiver support. Moving forward, we will focus on: 1) prospective validation of ZCoR; 2) assessment of the effects of ZCoR use on patient and caregiver quality-of-life, patient cognition and function, and healthcare utilization; 3) correlation with ADRD clinical and neuropathological biomarkers such as neuropsychological and functional test results and biofluid and imaging findings related to beta-amyloid, tau, and neurodegeneration; 4) comparison of ZCoR prospective performance in different racial groups and ethnicities, including examination of the signature's ability to reduce disparities in the rate of diagnosis. The impact of ZCoR on the accuracy and speed of diagnosis, on health care resource utilization, and eventually, on patient and caregiver outcomes, warrant prospective study.

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AUTHOR CONTRIBUTIONS

DO implemented the algorithm and ran validation tests. DO and IC carried out mathematical modeling, and algorithm design. DO, SS, KR, JM and IC interpreted results. JM and IC guided the research. DO, KR, JM and IC wrote the paper. IC procured funding for the study.

DECLARATION OF INTERESTS

IC is a founder and shareholder of Zero Burden Laboratories, Inc. He has not drawn any salary from the company. IC has received funding from the Alzheimer's Association, United States Department of Defense, the National Institutes of Health, and the Neubauer Collegium for Culture and Society. DO is a founder and shareholder of Zero Burden Laboratories. He has not drawn any salary from the company.

STAR METHODS

Resource Availability

Materials availability

This study did not generate or use new unique reagents.

Data and code availability

- **Data:** The Truven database used in this study is not in the public domain, and may be procured under license from <https://www.ibm.com/watson-health/about/truven-health-analytics>. A small de-identified set of patient diagnostic history is made available for testing purposes, and is publicly available as of the date of publication, as noted in the Key Resources Table. Description of ICD codes are available at <https://www.cdc.gov/nchs/icd/icd10cm.htm>, and <https://www.icd10data.com/>. A comprehensive interface for looking up ICD-10-CM code descriptions is provided by the National Library of Medicine, and may be accessed at <https://clincialtables.nlm.nih.gov/apidoc/icd10cm/v3/doc.html>.
- **Code:** Working modules have been deposited at Zenodo and is publicly available as of the date of publication. DOIs are listed in the key resources table. Complete pseudocode is made available in the Supplementary Information text (Algorithms 1, and 2 in Supplementary Information).
- Any additional information required to reanalyze the data reported in this paper is available from the lead contact upon request.

Lead Contact

Further information and requests for resources and software should be directed to and will be fulfilled by the lead contact, Ishanu Chattopadhyay (ishanu@uchicago.edu).

Method Details

Summary of Modeling Steps

Individual diagnostic histories can have long-term memory⁵⁶, implying that the order, frequency, and comorbid interactions between diseases are important for assessing the future risk of our target phenotype. The large number of possible ICD codes, along with the sparsity of codes per patient (approximately one entry every 100 steps on the diagnostic time series) makes this a difficult learning problem.

Step 1: Partitioning The Human Disease Spectrum

We begin by partitioning the human disease spectrum into 45 non-overlapping categories. Each category is defined by a set of diagnostic codes from the International Classification of Diseases, Ninth Revision (ICD9) (See Table SI-II for description of the categories used in this study).

For this study, we ended up using 6462501 and 9426722 diagnostic codes for males and females respectively (17501 and 18633 unique codes) spanning both ICD9 and ICD10 protocols (using ICD10 General Equivalence Mappings (GEMS)⁵⁷ equivalents where necessary), from a total 729,018 patients. Transforming the diagnostic histories to report only the broad categories reduces the number of distinct codes that the pipeline needs to handle, thus improving statistical power.

Our categories largely align with the top-level ICD9 categories, with small adjustments, e.g. bringing all infections under one category irrespective of the pathogen or the target organ. We do not pre-select the phenotypes; we want our algorithm to seek out the important patterns without any manual curation of the input data.

For each patient, the past medical history is a sequence $(t_1, x_1), \dots, (t_m, x_m)$, where t_i are timestamps and x_i are ICD9 codes diagnosed at time t_i . We map individual patient history to a three-alphabet categorical time series z^k corresponding to the disease category k , as follows. For each week i , we have:

$$z_i^k = \begin{cases} 0 & \text{if no diagnosis codes in week } i \\ 1 & \text{if there exists a diagnosis of category } k \text{ in week } i \\ 2 & \text{otherwise} \end{cases} \quad (1)$$

The time-series z^k is observed in the inference period. Thus, each patient is represented by 43 mapped trinary series.

We refer to these individual diagnostic categories as “phenotypes”, since they are observable characteristics of the patients. Each patient is represented by 45 sparse stochastic time series of events, which are compressed into specialized Hidden Markov Models known as Probabilistic Finite Automata (PFSA)^{58,59}. These models are inferred separately for each phenotype, for each sex, and for the control and the positive cohorts, to identify the distinctive average patterns emerging at the population level. We infer $45 \times 2 \times 2 = 180$ PFSA models in total in this study. Our inference algorithm for these models does not presuppose a fixed structure, and is able to work with non-synchronized and variable-length data streams. Variation of these inferred models between the positive and control groups delineate the estimated risk of an ADRD diagnosis at the population level. Given these models, and the history of a specific patient, we can then quantify the likelihood of this patient’s particular history being generated by the control PFSA models as opposed to the positive models. We refer to this likelihood difference as the sequence likelihood defect (SLD)⁶⁰, which is the one of the key informative features in our approach. The SLD is a novel concept, involving the generalization of the notion of Kullback-Liebler divergence⁶¹ between probability distributions to a generalized divergence between possibly non-iid stochastic processes (See Step 2 below). SLD-based features allow the ZCoR measure to factor in complex longitudinal, i.e., temporal patterns beyond simply the presence/absence of comorbidities.

Inference & Event Periods

We train our predictive pipeline with all diagnostic codes that are recorded in the past 2 years from the point at which a prediction is made. This period from which we use data to train our pipeline is called the “inference window”. Our aim is to make predictions on the occurrence of the target diagnostic codes at 1 year from the end of the inference window. For patients in the control cohort, we make sure that no target code appears for 2 years after the end of the inference window. Additionally, when making predictions further into the future, we always make sure that the control group has no target codes for 1 year after the predicted time of diagnosis,

i.e., if we are making a prediction of a diagnosis m years in future, then control group patients are chosen to have no diagnosis in at least next $m + 1$ years.

Step 2: Model Inference & The Sequence Likelihood Defect Δ

The mapped series, disease-category, and ADRD diagnosis-status are considered to be independent sample paths, and we want to explicitly model these systems as specialized HMMs (PFSA). We model the positive and the control cohorts and each disease category separately, ending up with a total of 86 HMMs at the population level (43 categories, 2 ADRD status categories: positive and control). Each of these inferred models is a PFSA; a directed graph with probability-weighted edges, and acts as an optimal generator of the stochastic process driving the sequential appearance of the three letters (as defined by Eq. (1)) corresponding to disease category, and ADRD status-type (See “**Probabilistic Finite State Automata Inference**” for background on PFSA inference).

To reliably infer the ADRD status-type of a new patient, i.e, the likelihood of a diagnostic sequence being generated by the corresponding ADRD status-type model, we generalize the notion of Kullbeck-Leibler (KL) divergence^{61,62} between probability distributions to a divergence $D_{KL}(G||H)$ between ergodic stationary categorical stochastic processes⁶³ G, H as:

$$D_{KL}(G||H) = \lim_{n \rightarrow \infty} \frac{1}{n} \sum_{x:|x|=n} p_G(x) \log \frac{p_G(x)}{p_H(x)} \quad (2)$$

where $|x|$ is the sequence length, and $p_G(x), p_H(x)$ are the probabilities of sequence x being generated by the processes G, H respectively. Defining the log-likelihood of x being generated by a process G as :

$$L(x, G) = -\frac{1}{|x|} \log p_G(x) \quad (3)$$

The cohort-type for an observed sequence x — which is actually generated by the hidden process G — can be formally inferred from observations based on the following provable relationships (See Theorems 1 and 2):

$$\lim_{|x| \rightarrow \infty} L(x, G) = H(G) \quad (4a)$$

$$\lim_{|x| \rightarrow \infty} L(x, H) = H(G) + D_{KL}(G||H) \quad (4b)$$

where $H(\cdot)$ is the entropy rate of a process⁶¹. Importantly, Eq. (4) shows that the computed likelihood has an additional non-negative contribution from the divergence term when we choose the incorrect generative process. Thus, if a patient is eventually going to be diagnosed with ADRD, then we expect that the disease-specific mapped series corresponding to her diagnostic history be modeled by the PFSA in the positive cohort. Denoting the PFSA corresponding to disease category j for positive and control cohorts as G_+^j, G_0^j respectively, we can compute the *sequence likelihood defect* (SLD, Δ^j) as:

$$\Delta^j \triangleq L(G_0^j, x) - L(G_+^j, x) \rightarrow D_{KL}(G_0^j||G_+^j) \quad (5)$$

With the inferred PFSA models and the individual diagnostic history, we estimate the SLD measure on the right-hand side of Eqn. (5). The higher this likelihood defect, the higher the similarity of diagnosis history to that of women with ADRD.

Step 3: Risk Estimation Pipeline With Semi-supervised & Supervised Learning Modules

The risk estimation pipeline operates on patient specific information limited to the available diagnostic history in the inference period, and produces an estimate of the relative risk of ADRD, with an associated confidence value. To learn the parameters and associated model structures of this pipeline, we transform the patient specific data to a set of engineered features, and the feature vectors realized on the positive and control sets are used to train a gradient-boosting classifier⁶⁴. The complete list of 701 features used is provided in Tab. VI.

We need two training sets: one to infer the models, and one to train the classifier with features derived from the inferred models. Thus, we do a random 3-way split of the set of unique patients into *feature-engineering* (25%), *training* (25%) and *test* (50%) sets. We use the feature-engineering set of ids first to infer our PFSA models (*unsupervised model inference in each category*), which then allows us to train the gradient-boosting classifier using the training set and PFSA models (*classical supervised learning*), and we finally execute out-of-sample validation on the test set. Fig. 2c in the main text shows the top 20 features ranked in order of their relative importance (relative loss in performance when dropped out of the analysis).

In addition to the phenotype specific specialized Markov models, we use a range of engineered features reflecting various aspects of diagnostic histories:

Prevalence scores (p-scores): The p-scores focus on individual diagnostic codes, and we create a dictionary of the ratio of relative prevalence of each code (relative to the set of all codes present) in the positive category (for each sex) to the control category. This is the second hyper-training step. In the later steps of the pipeline,

we use dictionary look ups to map codes to their p-scores, and also their aggregate measures such as mean, median, and variance to train a downstream LGBM.

Rare scores: These scores consist of a subset of p-scores which correspond to codes with particularly high and low relative prevalences (p-score > 2 or $< .5$). Thus, this feature category depends on the p-score dictionary generated in the second hyper-training step.

Sequence scores: Sequence scores are relatively straight-forward statistical measures such as mean, median, variance, time since last occurrence etc.. on the trinary phenotype-specific sex-stratified histories. No hyper-training is required for the generation of the sequence features.

Thus we require three splits of the training dataset. The first split is used to carry out hyper-training of the PFSA models and the p-score dictionary. The second split is used to train the score-category specific LGBMs, one for each feature category. And the third split is used to train the final LGBM that takes inputs from the outputs of the four LGBMs in the previous layer. The network layout is shown in SI-Fig. 2.

Validation

In validation, or actual prediction of patient fate, we use the trinary mapping, generate the features using the PFSA models and the p-score dictionary, and calculate the raw-risk via the trained LGBM network. The relative score is then obtained by a choice of the operating point reflecting the specificity/sensitivity trade-off discussed before.

Data Splits: Training and Validation Hold-out

All eligible patients are randomly split into the Training set ($\approx 75\%$ of data) and the Test set ($\approx 25\%$ of data). The Training set is then split into 3 subsets: 1) The hyper-training set (SI-Fig. 2A) is used to train PFSA models p-score dictionary, 2) the second split (referred to as the pre-aggregation split, SI-Fig. 2B) is used to train the four feature-category specific LGBMs, and 3) the final split (referred to as the aggregation split, SI-Fig. 2C) is used to train the aggregate LGBM which uses outputs from the trained LGBMs in the previous layer. This trained pipeline is then validated on the held out validation split ($\approx 25\%$ of data).

Generating PFSA Models From Set of Input Streams with Variable Input Lengths

Our PFSA reconstruction algorithm⁵⁹ is distinct from standard HMM learning. We do not need to pre-specify structures, or the number of states in the algorithm, and all model parameters are inferred directly from data. Additionally, we can operate either with 1) a single input stream, or 2) a set of input streams of possibly varying lengths which are assumed to be different and independent sample paths from the unknown stochastic generator we are trying to infer. At an intuitive level, we use the input data to infer the length of histories one must remember to estimate the current state, and predict futures for the process being modeled. Thus, we do not step through the symbol streams with a pre-specified model structure, and avoid the need to have equal-length inputs. More details of the algorithm are provided in the next section.

The ability to model a set of input streams of varying lengths is particularly important, since medical histories of different patients are typically of different lengths.

Probabilistic Finite State Automata Inference

Software for PFSA inference is made available at <https://pypi.org/project/zedsuite/>.

Let Σ be a finite alphabet of symbols with size $|\Sigma|$. The set of sequences of length d over Σ is denoted by Σ^d . The set of finite but unbounded sequences over Σ is denoted by Σ^* , the Kleene star operation⁶⁵, i.e. $\Sigma^* = \bigcup_{d=0}^{\infty} \Sigma^d$. We use lower case Greek, for example σ or τ , for symbols in Σ , and lower case Latin, for example x or y , for sequences of symbols, i.e. $x = \sigma_1 \sigma_2 \dots \sigma_n$. We use $|x|$ to denote the length of x . The empty sequence is denoted by λ .

We denote the set of strictly infinite sequences over Σ by Σ^ω , and the set of strictly infinite sequences having x as prefix by $x\Sigma^\omega$. Let $S = \{x\Sigma^\omega : x \in \Sigma^*\} \cup \{\emptyset\}$, we can verify that S is a semiring⁶⁶ over Σ^ω . We use \mathcal{F} to denote the sigma algebra generated by S .

Definition 1 (Stochastic Process over Σ). *A stochastic process over a finite alphabet Σ is a collection of Σ -valued random variables $\{X_t\}_{t \in \mathbb{N}}$ indexed by positive integers⁶⁷.*

We are specifically interested in processes in which the X_t s are not necessarily independently distributed.

Definition 2 (Sequence-Induced Measure and Derivative). *For a process \mathcal{P} , let $\Pr_{\mathcal{P}}(x)$ or simply $\Pr(x)$ denote the probability \mathcal{P} producing a sample path prefixed by x . The measure μ_x induced by a sequence $x \in \Sigma^*$ is the extension⁶⁶ to \mathcal{F} of the premeasure defined on the semiring \mathcal{S} given by*

$$\forall x, y \in \Sigma^*, \mu_x(y\Sigma^\omega) \triangleq \frac{\Pr(xy)}{\Pr(x)}, \text{ if } \Pr(x) > 0 \quad (6)$$

For any $d \in \mathbb{N}$, the d -th order derivative of a sequence x , written as ϕ_x^d , is defined to be the marginal distribution of μ_x on Σ^d , with the entry indexed by y denoted by $\phi_x^d(y)$. The first-order derivative is called the **symbolic derivative** and is denoted by ϕ_x for short.

Definition 3 (Probabilistic Nerode Equivalence and Causal States⁶⁸). *For any pair of sequences $x, y \in \Sigma^*$, x is equivalent to y , written as $x \sim y$, if and only if either $\Pr(x) = \Pr(y) = 0$, or $\mu_x = \mu_y$. The equivalence class of a sequence x is denoted by $[x]$ and is called a **causal state**⁶⁹. The cardinality of the set of causal states is called the **probabilistic Nerode index**, or the Nerode index for simplicity.*

We can see from the definition that causal states captures how the history of a process influences its future. Since the probabilistic Nerode equivalence is right invariant, it gives rise naturally to a automaton structure introduced below.

Definition 4 (Probabilistic Finite-State Automaton (PFSA)). *A PFSA G is defined by a quadruple $(Q, \Sigma, \delta, \tilde{\pi})$, where Q is a finite set, Σ is a finite alphabet, $\delta : Q \times \Sigma \rightarrow \Sigma$ is called the transition map, and $\tilde{\pi} : Q \rightarrow \mathbf{P}_\Sigma$, where \mathbf{P}_Σ is the space of probability distributions over Σ , is called the transition probability. The entry of $\tilde{\pi}(q)$ indexed by σ is denoted by $\tilde{\pi}(q, \sigma)$.*

Definition 5 (Transition and Observation Matrices). *The transition matrix Π is the $|Q| \times |Q|$ matrix with the entry indexed by q, q' , written as $\pi_{q,q'}$, satisfying*

$$\pi_{q,q'} \triangleq \sum_{\{\sigma \in \Sigma | \delta(q, \sigma) = q'\}} \tilde{\pi}(q, \sigma) \quad (7)$$

and the observation matrix $\tilde{\Pi}$ is a $|Q| \times |\Sigma|$ matrix with the entry indexed by q, σ equaling $\tilde{\pi}(q, \sigma)$.

We note that both Π and $\tilde{\Pi}$ are stochastic, i.e. non-negative with rows summing up to 1.

Definition 6 (Extension of δ and $\tilde{\pi}$ to Σ^*). *For any $x = \sigma_1 \dots \sigma_k$, $\delta(q, x)$ is defined recursively by*

$$\delta(q, x) \triangleq \delta(\delta(q, \sigma_1 \dots \sigma_{k-1}), \sigma_k) \quad (8)$$

with $\delta(q, \lambda) = q$, and $\tilde{\pi}(q, x)$ is defined recursively by

$$\tilde{\pi}(q, x) \triangleq \prod_{i=1}^k \tilde{\pi}(\delta(q, \sigma_1 \dots \sigma_{i-1}), \sigma_i) \quad (9)$$

with $\tilde{\pi}(q, \lambda) = 1$.

Definition 7 (Strongly Connected PFSA). *We say a PFSA is strongly connected if the underlying directed graph is strongly connected⁷⁰. More precisely, a PFSA $G = (Q, \Sigma, \delta, \tilde{\pi})$ is strongly connected if for any pair of distinct states q and $q' \in Q$, there is an $x \in \Sigma^*$ such that $\delta(q, x) = q'$.*

We assume all PFSA in the discussions in the sequel are strongly connected if not specified otherwise. For strongly connected PFSA G , there is a unique probability distribution over Q that satisfies $\mathbf{v}^T \Pi = \mathbf{v}^T$. This is the **stationary distribution**^{71,72} of G and is denoted as ϱ_G , or ϱ if G is understood.

Definition 8 (Γ -Expression). *We can encode the information contained in δ and $\tilde{\pi}$ by a set of $|Q| \times |Q|$ matrices $\Gamma = \{\Gamma_\sigma | \sigma \in \Sigma\}$, where*

$$\Gamma_\sigma|_{q,q'} \triangleq \begin{cases} \tilde{\pi}(q, \sigma) & \text{if } \delta(q, \sigma) = q', \\ 0 & \text{if otherwise.} \end{cases} \quad (10)$$

Γ_σ is called **event-specific transition matrix**, with the event being that σ is current the output. Γ_σ can also be extended to arbitrary $x \in \Sigma^*$ by defining $\Gamma_x = \prod_{i=1}^k \Gamma_{\sigma_i}$ with $\Gamma_\lambda = I$.

Definition 9 (Sequence-Induced Distribution on States). *For a PFSA $G = (Q, \Sigma, \delta, \tilde{\pi})$ and a distribution ϱ_0 on Q , the distribution on Q induced by a sequence x is given by $\varrho_{G, \varrho_0}^T(x) = [\varrho_0^T \Gamma_x]$ with $\varrho_{G, \varrho_0}(\lambda) = \varrho_0$. The entry indexed by $q \in Q$ of the vector $\varrho_{G, \varrho_0}(x)$ is written as $\varrho_{G, \varrho_0}(x, q)$. When $\varrho_0 = \varrho_G$, the stationary distribution of G , we write $\varrho_{G, \varrho_0}(x)$ as $\varrho_G(x)$, or simply as $\varrho(x)$, if G is understood.*

Definition 10 (Stochastic Process Generated by a PFSA). *Let $G = (Q, \Sigma, \delta, \tilde{\pi})$ be a PFSA and let ϱ_0 be a distribution on Q , the Σ -valued stochastic process $\{X_t\}_{t \in \Sigma}$ generated by G and ϱ_0 satisfies that X_1 follows the distribution ϱ_0 and X_{t+1} follows the distribution $\varrho_{G, \varrho_0}(X_1 \dots X_t)$ for $t \in \mathbb{N}$.*

For the rest of this paper, we will assume $\varrho_0 = \varrho_G$ if not specified otherwise. We can show that, when initialized with ϱ_G , the process generated by a PFSA G is stationary and ergodic. We also note the, for the process generate by G , we have $\phi_x = \varrho_G(x)^\top \tilde{\Pi}$. Since $\varrho_G(\lambda) = \varrho_G$, the symbolic derivative of the empty sequence ϕ_λ is the stationary distribution on the symbols.

Definition 11 (Synchronizable PFSA and Synchronizing Sequence). A **synchronizing sequence** is a finite sequence that sends an arbitrary state of the PFSA to a fixed state⁷³. To be more precise, let $G = (Q, \Sigma, \delta, \tilde{\Pi})$ be a PFSA, we say a sequence $x \in \Sigma^*$ is a synchronizing sequence to a state $q \in Q$ if $\delta(q', x) = q$ for all $q' \in Q$. A PFSA is **synchronizable** if it has at least one synchronizing sequence. Given a sample path generated by a PFSA, we say the PFSA is **synchronized** if a synchronizing sequence transpires in the sample path.

Definition 12 (Equivalence and Irreducibility). Two PFSA G and H are **equivalent** if they generate the same stochastic process. A PFSA G is said to be **irreducible**, if there is not another PFSA with smaller state set that is equivalent to G .

Definition 13. Consider a PFSA G over state set Q . For a give $\varepsilon > 0$, we say a sequence x is a ε -synchronizing sequence to a state $q \in Q$ if

$$\|\varrho_G(x) - \mathbf{e}_q\|_\infty \leq \varepsilon. \quad (11)$$

While there exists PFSA that is not synchronizable, we can show that an irreducible PFSA always has an ε -synchronizing sequence for some state q for arbitrarily small $\varepsilon > 0$. Moreover, we can show that as length increases, sequences produced by PFSA become uniformly ε -synchronizing. These two are the underpinning properties for the inference algorithm of PFSA (See Alg. 1), because they imply that ϕ_x can be used to approximate $\tilde{\pi}(q)$ if x are properly prefixed and long enough.

Definition 14 (Joint ε -Synchronizing Sequence). Let G and H be two PFSA over state sets Q_G and Q_H , respectively. For a fixed ε , a sequence x is said to be **jointly ε -synchronizing** to $(q, r) \in Q_G \times Q_H$ if x is ε -synchronizing to q and to r simultaneously. We define

$$\Sigma_{\varepsilon, (q, r)}^d \triangleq \{x \in \Sigma^d : x \text{ jointly } \varepsilon\text{-synchronizing to } (q, r)\} \quad (12)$$

Definition 15 (Joint Pair of States). Let G and H be two PFSA over state sets Q_G and Q_H , respectively. Define

$$p_G(q, r) \triangleq \lim_{d \rightarrow \infty} p_G(\Sigma_{\varepsilon, (q, r)}^d) \quad (13)$$

A pair of states $(q, r) \in Q_G \times Q_H$ is called a **G -joint pair** of states if $p_G(q, r) > 0$. We also define

$$Q_c \triangleq \{(q, r) \in Q_G \times Q_H : (q, r) \text{ is a } G\text{-joint pair}\} \quad (14)$$

The inference algorithm for PFSA is called **GenESeSS** for Generator Extraction Using Self-similar Semantics. With an input sequence x and a hyperparameter ε , **GenESeSS** outputs a PFSA in the following three steps: 1) approximate an almost synchronizing sequence; 2) identify the transition structure of the PFSA; 3) calculate the transition probabilities of the PFSA. See Alg. 1⁵⁹ for details.

Theoretical Development of Sequence Likelihood Defect

Definition 16 (Entropy Rate and KL Divergence). By entropy rate of a PFSA, we mean the entropy rate of the stochastic process generated by the PFSA⁷⁴. Similarly, by KL divergence of two PFSA, we mean the KL divergence between the two processes generated by them⁷⁵. More precisely, we have

$$\mathcal{H}(G) = - \lim_{d \rightarrow \infty} \frac{1}{d} \sum_{x \in \Sigma^d} p(x) \log p(x) \quad (15)$$

and the KL divergence

$$\mathcal{D}_{KL}(G \| H) = \lim_{d \rightarrow \infty} \frac{1}{d} \sum_{x \in \Sigma^d} p_G(x) \log \frac{p_G(x)}{p_H(x)} \quad (16)$$

whenever the limits exist.

Theorem 1 (Closed-form Formula for Entropy Rate and KL Divergence). The entropy rate of a PFSA $G = (\Sigma, Q, \delta, \tilde{\Pi})$ is given by

$$\mathcal{H}(G) = \sum_{q \in Q} \varrho_G(q) \cdot h(\tilde{\pi}(q)) \quad (17)$$

where $h(\mathbf{v})$ is the based-2 entropy of the probability vector \mathbf{v} .

Consider two PFSA $G = (Q_G, \Sigma, \delta_G, \tilde{\Pi}_G)$ and $H = (Q_H, \Sigma, \delta_H, \tilde{\Pi}_H)$ with μ_G being absolutely continuous with

respect to μ_H . Let Q_c be the set of G -joint pairs of states, we have

$$\mathcal{D}_{KL}(G \parallel H) = \sum_{(q,r) \in Q_c} p_G(q,r) D_{KL}(\tilde{\pi}_G(q) \parallel \tilde{\pi}_H(r)) \quad (18)$$

Definition 17 (Log-likelihood). Let $x \in \Sigma^d$, the log-likelihood⁷⁴ of a PFSA G generating x is given by

$$L(x, G) = -\frac{1}{d} \log p_G(x) \quad (19)$$

The calculation of log-likelihood is detailed in Alg. 2.

Theorem 2 (Convergence of log-likelihood). Let G and H be two reduced PFSA, and let $x \in \Sigma^d$ be a sequence generated by G . Then we have

$$L(x, H) \rightarrow \mathcal{H}(G) + \mathcal{D}_{KL}(G \parallel H) \quad (20)$$

in probability as $d \rightarrow \infty$.

Proof. We first notice that

$$\sum_{x \in \Sigma^d} p_G(x) \log \frac{p_G(x)}{p_H(x)} = \sum_{x \in \Sigma^{d-1}} \sum_{\sigma \in \Sigma} p_G(x) \varrho_G(x) \tilde{\Pi}_G \Big|_{\sigma} \log \frac{p_G(x) \varrho_G(x) \tilde{\Pi}_G \Big|_{\sigma}}{p_H(x) \varrho_H(x) \tilde{\Pi}_H \Big|_{\sigma}} \quad (21)$$

$$= \sum_{x \in \Sigma^{d-1}} p_G(x) \log \frac{p_G(x)}{p_H(x)} + \underbrace{\sum_{x \in \Sigma^{d-1}} p_G(x) \sum_{\sigma \in \Sigma} \varrho_G(x) \tilde{\Pi}_G \Big|_{\sigma} \log \frac{\varrho_G(x) \tilde{\Pi}_G \Big|_{\sigma}}{\varrho_H(x) \tilde{\Pi}_H \Big|_{\sigma}}}_{D_d} \quad (22)$$

By induction, we have $\mathcal{D}_{KL}(G \parallel H) = \lim_{d \rightarrow \infty} \frac{1}{d} \sum_{i=1}^d D_i$, and hence by Cesàro summation theorem⁷⁶, we have $\mathcal{D}_{KL}(G \parallel H) = \lim_{d \rightarrow \infty} D_d$. Let $x = \sigma_1 \sigma_2 \dots \sigma_n$ be a sequence generated by G . Let $x^{[i-1]}$ is the truncation of x at the $(i-1)$ -th symbols, we have

$$-\frac{1}{n} \sum_{i=1}^n \log \varrho_H(x^{[i-1]}) \tilde{\Pi}_H \Big|_{\sigma_i} = \underbrace{\frac{1}{n} \sum_{i=1}^n \log \frac{\varrho_G(x^{[i-1]}) \tilde{\Pi}_G \Big|_{\sigma_i}}{\varrho_H(x^{[i-1]}) \tilde{\Pi}_H \Big|_{\sigma_i}}}_{A_{x,n}} - \underbrace{\frac{1}{n} \sum_{i=1}^n \log \varrho_G(x^{[i-1]}) \tilde{\Pi}_G \Big|_{\sigma_i}}_{B_{x,n}} \quad (23)$$

Since the stochastic process G generates is ergodic, we have

$$\lim_{n \rightarrow \infty} A_{x,n} = \lim_{d \rightarrow \infty} D_d = \mathcal{D}_{KL}(G \parallel H) \quad (24)$$

and $\lim_{n \rightarrow \infty} B_{x,n} = \mathcal{H}(G)$. \square

Quantification & Statistical Analysis

Raw Risk & Relative Risk

We choose a decision threshold on the raw risk computed by our pipeline to make crisp predictions, i.e., if the raw risk is greater than this calibrated threshold, then the individual patient is predicted to be in the positive category.

Threshold Selection on ROC Curve

In situations where the number of negatives vastly outnumber the number of positives (which is the case in our problem), it is better to base this trade-off on a measure that is independent of the number of true negatives. The two popular measures considered in the literature are accuracy and the F1-score:

$$\text{accuracy} = \frac{t_p + t_n}{t_p + f_p + f_n + t_n} \quad (25)$$

$$F1 = \frac{2t_p}{2t_p + f_p + f_n} \quad (26)$$

The F1-score is the same as accuracy where the number of true negatives is the same as the number of true positives, thus partially correcting for the class imbalance.

The selection of the threshold may also be dictated by the current practice of ensuring high specificities in screening tests. Thus, the most relevant clinically operating point is either the one corresponding to 95% specificity, which is highlighted in Fig. 2a.

Performance Measurement

We measure our performance using standard metrics including the AUC, sensitivity, specificity, the positive predictive value (PPV), and the negative predictive value (NPV). We also report accuracy (acc, See Tables VII and VIII), which is the probability of a correct prediction (positive or control), and variation of AUC for predicting ADRD into the future up to 10 years (See Table IX).

Ninety-five percent confidence intervals (95% CIs) on ROC curves and AUCs were obtained via bootstrapping, and AUC p-vales were obtained using the Mann-Whitney U-test statistic.

Note on Reciever Operating Characteristics (ROC) and Precision-recall Curves

The ROC curve is a plot between the False Positive rate (TPR) and the True Positive Rate (TPR), and the area under the ROC curve (AUC) is often used as a measure of classifier performance. For the same of completeness, we introduce the relevant definitions:

In the following P denotes the total number of positive samples (number of patients who are eventually diagnosed), and N denotes the total number of negative samples (number of patients in the control group).

Definition 18. *True positive rate, true negative rate, false positive rate, positive predictive value (PPV), and prevalence (ρ) are defined as:*

$$\text{sensitivity, or TPR} = \frac{t_p}{P} = \frac{t_p}{t_p + f_n} \quad (27)$$

$$\text{specificity, or TNR} = \frac{t_n}{N} = \frac{t_n}{t_n + f_p} \quad (28)$$

$$FPR = 1 - TNR \quad (29)$$

$$\text{precision, or PPV} = \frac{t_p}{t_p + f_p} \quad (30)$$

$$\rho = \frac{P}{N + P} \quad (31)$$

where as before t_p, t_n, f_p, f_n are true positives, true negatives, false positives, and false negatives respectively.

Denoting sensitivity by s , and specificity by c , it follows that:

$$\text{PPV} = \frac{t_p/P}{t_p/P + (f_p/N)(N/P)} = \frac{\text{TPR}}{\text{TPR} + ((N - t_n)/N)(N/P)} \quad (32)$$

$$\Rightarrow \text{PPV} = \frac{s}{s + (1 - c)(\frac{1}{\rho} - 1)} \quad (33)$$

Thus, we note that for a fixed specificity and sensitivity, the PPV depends on prevalence. Indeed, it is clear from the above argument that PPV decreases with decreasing prevalence, and vice versa.

Effect of Class Imbalance

ROC curves are generally assumed to be robust to class imbalance. Note that if we assume that patient outcomes are independent (which is well-justified in the case of a non-communicable condition, particularly in large databases), then t_p should scale linearly with the total number of positives P, implying:

$$\text{TPR} = \frac{t_p}{P} = \frac{t'_p}{P'} \quad (34)$$

implying that with different sizes of the set of positive samples (or negative samples), the ROC curve remains unchanged. In particular, note that even if the prevalence is very small (say 0.01%), we cannot cheat to boost the AUC by labeling all predictions as negative, or stating that risk is always zero: in that case, our P is very small, but our $t_p = 0$ strictly, implying that our TPR = 0, thus leading to a zero AUC. We can cheat to boost the accuracy (See the previous section), but not the AUC.

Note that while relative class sizes or imbalance does not affect the ROC (under the assumption that true positives and true negatives scale with the number of positives and negatives), very small absolute sample sizes might still result in poor performance of the model.

The precision-recall curves do get affected by class imbalance, or the prevalence, as shown by Eq (33). However, in diagnostic analysis, they are important since we are generally less interested in the number of true negatives; the ratio of false positives to the total number of positive recommendations by the algorithm is much more relevant, i.e., the PPV or the precision.

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Key Resources Table

REAGENT	SOURCE	IDENTIFIER
Deposited data		
Truven Marketscan Database	IBM Watson® (with appropriate licensing)	https://www.ibm.com/watson-health/about/truven-health-analytics
Small Patient Database	Excerpt from University of Chicago Medicine de-identified records between 2012-2021	https://github.com/zeronowledgediscovery/EHRdata https://doi.org/10.5281/zenodo.5348229
Software and algorithms		
PFSA inference algorithm implementation	Laboratory of Zero Knowledge Discovery (zed.uchicago.edu)	https://pypi.org/project/zedsuite/
ZCoR modules	Laboratory of Zero Knowledge Discovery (zed.uchicago.edu)	https://github.com/zeronowledgediscovery/ZCOR-ADRD https://doi.org/10.5281/zenodo.5348219

Supplementary Text: Rapid Universal Early Screening for Alzheimer's Disease and Related Dementia via Pattern Discovery in Diagnostic History

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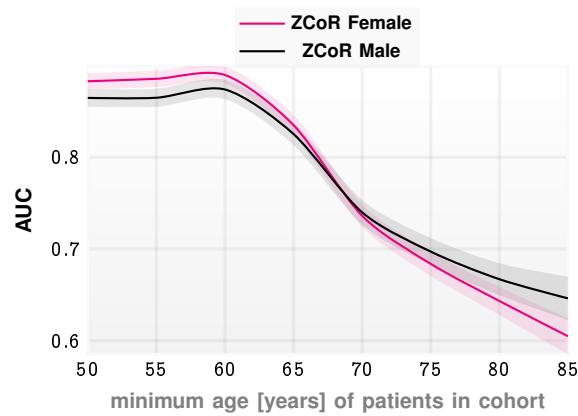
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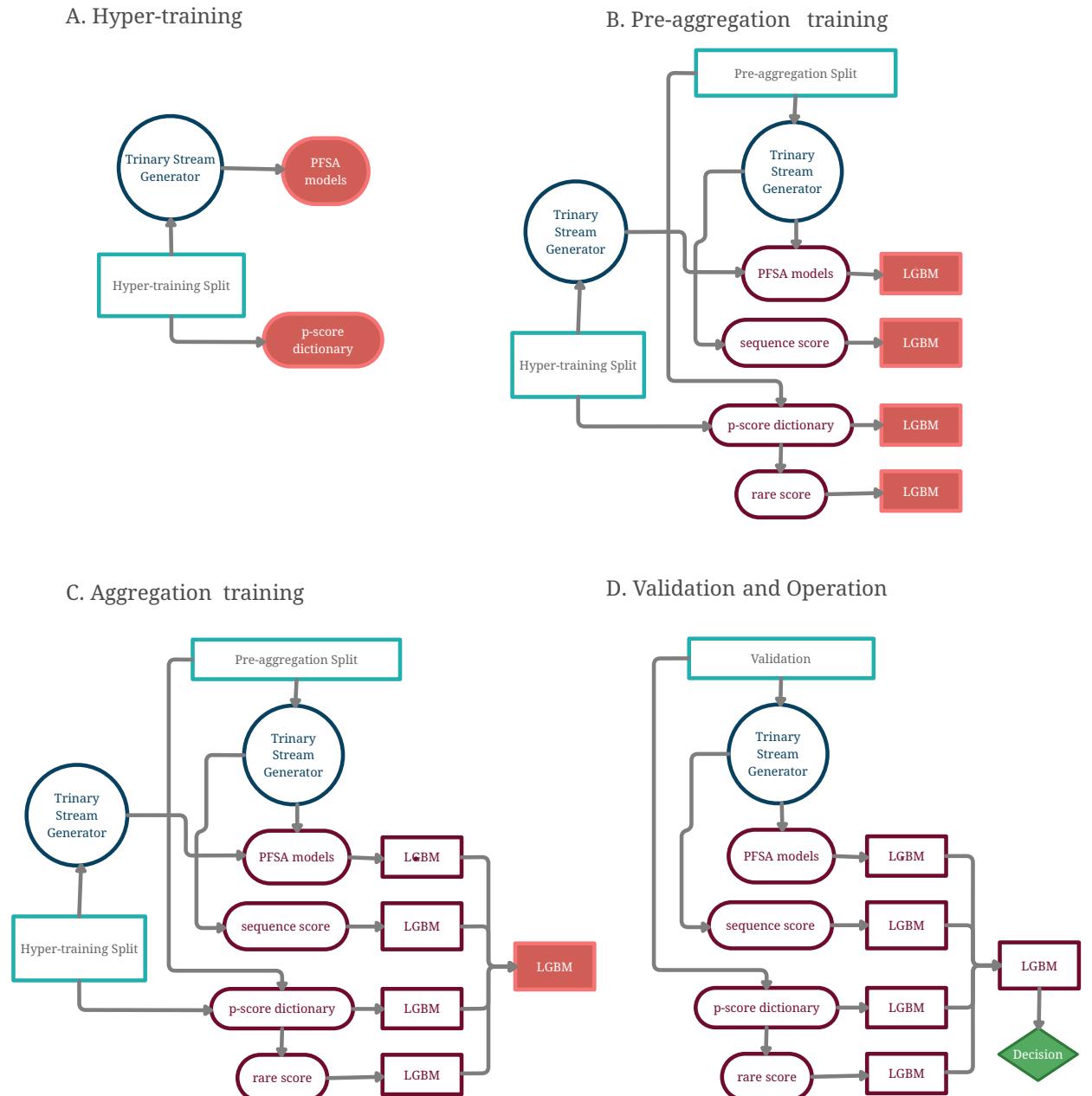
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a. ZCoR AUC over time (95% confidence)

SI-Fig. 1: Degradation of predictive performance with patient age. With increasing patient age it become more difficult to distinguish age related cognitive decline from ADRD. This is reflected in the decreasing AUC with age, suggesting that comorbidity footprints associated with ADRD has confounding overlaps with conditions that arise more frequently as patients get older.



SI-Fig. 2: Schematic of prediction pipeline. Panels A, B and C show the sequential training steps, namely the hyper-training of the PFSA models and the p-score dictionary, the pre-aggregation training of the four LGBM models, and the aggregation training of the final LGBM model respectively. Panel D shows the configuration of the trained pipeline in operation. In the training steps, the filled box represents the component being trained in that step.

SI-Table I: High risk cohort definition based on known comorbidities of AD and related dementia

ICD code	description
250.0	DMII wo cmp nt st uncntr
250.02	DMII wo cmp uncntrld
252.0	Hyperparathyroidism NOS
252.02	Sec hyprprthyrd nonrenal
258.02	Mult endo neop type IIA
272.2	Mixed hyperlipidemia
278.0	Obesity NOS
278.01	Morbid obesity
278.02	Overweight
278.03	Obesity hypovent synd
296.2	Depress psychosis-unspec
296.21	Depress psychosis-mild
296.22	Depressive psychosis-mod
296.23	Depress psychosis-severe
296.24	Depr psychos-sev w psych
296.25	Depr psychos-part remiss
296.26	Depr psychos-full remiss
296.3	Recurr depr psychos-unsp
296.31	Recurr depr psychos-mild
296.32	Recurr depr psychos-mod
296.33	Recur depr psych-severe
296.34	Rec depr psych-psychotic
296.35	Recur depr psyc-part rem
296.36	Recur depr psyc-full rem
303.0	Ac alcohol intox-unspec
303.01	Ac alcohol intox-contin
303.02	Ac alcohol intox-episod
303.03	Ac alcohol intox-remiss
303.9	Alcoh dep NEC/NOS-unspec
303.91	Alcoh dep NEC/NOS-contin
303.92	Alcoh dep NEC/NOS-episod
303.93	Alcoh dep NEC/NOS-remiss
305.0	Alcohol abuse-unspec
305.01	Alcohol abuse-continuous
305.02	Alcohol abuse-episodic
305.03	Alcohol abuse-in remiss
401.0	Malignant hypertension
401.1	Benign hypertension
401.9	Hypertension NOS
402.0	Mal hyp ht dis w/o hf
402.01	Mal hypert hrt dis w hf
402.1	Benign hyp ht dis w/o hf
402.11	Benign hyp ht dis w hf
402.9	Hyp hrt dis NOS w/o hf
402.91	Hyp ht dis NOS w ht fail
403	Hypertensive chronic kidney disease
404	Hypertensive heart and chronic kidney disease
405.01	Mal renovasc hypertens
405.09	Mal second hyperten NEC
405.11	Benign renovasc hyperten
405.19	Benign second hypert NEC
405.91	Renovasc hypertension
405.99	Second hypertension NEC
427.31	Atrial fibrillation
440	Atherosclerosis
E11	Overweight
E66	Type 2 diabetes mellitus
E78	Disorders of lipoprotein metabolism lipidemias
F10.10	Alcohol abuse uncomplicated
F10.159	Alcohol abuse with alcohol-induced psychotic disorder unspecified
F10.20	Alcohol dependence uncomplicated
F10.21	Alcohol dependence in remission
F10.229	Alcohol dependence with intoxication unspecified
F10.231	Alcohol dependence with withdrawal delirium
F10.239	Alcohol dependence with withdrawal unspecified
F10.27	Alcohol dependence with alcohol-induced persisting dementia
F32.0	Major depressive disorder single episode mild
F32.1	Major depressive disorder single episode moderate
F32.2	Major depressive disorder single episode severe without psychotic features
F32.3	Major depressive disorder single episode severe with psychotic features
F32.4	Major depressive disorder single episode in partial remission

Continued on next page

SI-Table I – continued from previous page

ICD code	description
F32.5	Major depressive disorder single episode in full remission
F32.8	Premenstrual dysphoric disorder
F32.9	Major depressive disorder single episode unspecified
F33.0	Major depressive disorder recurrent mild
F33.1	Major depressive disorder recurrent moderate
F33.2	Major depressive disorder recurrent severe without psychotic features
F33.3	Major depressive disorder recurrent severe with psychotic symptoms
F33.41	Major depressive disorder recurrent in partial remission
F33.42	Major depressive disorder recurrent in full remission
F33.9	Major depressive disorder recurrent unspecified
G43.401	Hemiplegic migraine not intractable with status migrainosus
I10	Essential (primary) hypertension
I11.0	Hypertensive heart disease with heart failure
I11.9	Hypertensive heart disease without heart failure
I12.0	Hypertensive chronic kidney disease with stage 5 chronic kidney disease or end stage renal disease
I12.9	Hypertensive chronic kidney disease with stage 1 through stage 4 chronic kidney disease or unspecified chronic kidney disease
I13.0	Hypertensive heart and chronic kidney disease with heart failure and stage 1 through stage 4 chronic kidney disease or unspecified chronic kidney disease
I13.10	Hypertensive heart and chronic kidney disease without heart failure with stage 1 through stage 4 chronic kidney disease or unspecified chronic kidney disease
I13.11	Hypertensive heart and chronic kidney disease without heart failure with stage 5 chronic kidney disease or end stage renal disease
I13.2	Hypertensive heart and chronic kidney disease with heart failure and with stage 5 chronic kidney disease or end stage renal disease
I15.0	Renovascular hypertension
I15.8	Other secondary hypertension
I70.0	Atherosclerosis of aorta
I70.1	Atherosclerosis of renal artery
I70.209	Unspecified atherosclerosis of native arteries of extremities unspecified extremity
I70.219	Atherosclerosis of native arteries of extremities with intermittent claudication unspecified extremity
I70.229	Atherosclerosis of native arteries of extremities with rest pain unspecified extremity
I70.25	Atherosclerosis of native arteries of other extremities with ulceration
I70.269	Atherosclerosis of native arteries of extremities with gangrene unspecified extremity
I70.299	Other atherosclerosis of native arteries of extremities unspecified extremity
I70.399	Other atherosclerosis of unspecified type of bypass graft(s) of the extremities unspecified extremity
I70.499	Other atherosclerosis of autologous vein bypass graft(s) of the extremities unspecified extremity
I70.599	Other atherosclerosis of nonautologous biological bypass graft(s) of the extremities unspecified extremity
I70.8	Atherosclerosis of other arteries
I70.90	Unspecified atherosclerosis
I70.92	Chronic total occlusion of artery of the extremities
J12.0	Adenoviral pneumonia
J12.1	Respiratory syncytial virus pneumonia
J12.2	Parainfluenza virus pneumonia
J12.81	Pneumonia due to SARS-associated coronavirus
J12.89	Other viral pneumonia
J12.9	Viral pneumonia unspecified
J13	Pneumonia due to Streptococcus pneumoniae
J14	Pneumonia due to Hemophilus influenzae
J15.0	Pneumonia due to Klebsiella pneumoniae
J15.1	Pneumonia due to Pseudomonas
J15.20	Pneumonia due to staphylococcus unspecified
J15.211	Pneumonia due to Methicillin susceptible Staphylococcus aureus
J15.212	Pneumonia due to Methicillin resistant Staphylococcus aureus
J15.29	Pneumonia due to other staphylococcus
J15.3	Pneumonia due to streptococcus group B
J15.4	Pneumonia due to other streptococci
J15.5	Pneumonia due to Escherichia coli
J15.6	Pneumonia due to other Gram-negative bacteria
J15.7	Pneumonia due to Mycoplasma pneumoniae
J15.8	Pneumonia due to other specified bacteria
J15.9	Unspecified bacterial pneumonia
J16.0	Chlamydial pneumonia
J16.8	Pneumonia due to other specified infectious organisms
J17	Pneumonia in diseases classified elsewhere
K08.401	Partial loss of teeth unspecified cause class I
K08.402	Partial loss of teeth unspecified cause class II
S02.401A	Maxillary fracture unspecified side initial encounter for closed fracture
S02.401B	Maxillary fracture unspecified side initial encounter for open fracture
Y35.303A	Legal intervention involving unspecified blunt objects suspect injured initial encounter

SI-Table II: Disease Categories With Detailed Set of ICD Codes Used

	Description	Constituent ICD9 Codes
		R89.5 R92.2 R71.0 794.7 R87.620 I20.8 R97.8 R82.5 794.01 R93.9 R87.612 I25.3 I21.11 R85.616 R94.30 R87.611 I25.42 R94.39 R92.8 R88.0 R93.1 R82.2 R85.81 R94.09 I25.10 R82.4 794.6 R87.811 794.31 R87.810 I25.811 R79.1 R80.2 794.4 794.09 I25.2 R87.616 R73.02 R74.8 R87.9 794.14 R83.9 R75 I21.29 794.00 794.10 794.19 R85.612 R93.5 R87.628 I21.4 794.13 R94.112 R78.89 R94.120 R79.81 794.39 R85.615 794.16 R94.31 R73.09 R94.8 R87.624 794.17 R87.623 R89.9 I25.83 R85.82 R93.2 R94.4 R82.99 R87.619 R94.110 R85.613 794.5 R76.8 R80.3 794.2 R86.9 R91.8 I25.9 R94.01 R71.8 R82.3 R97.0 I24.1 I25.41 R87.621 794.11 R87.613 R93.3 R94.113 R94.121 R94.131 R94.5 I24.0 R85.619 R93.4 R97.2 R76.12 R85.614 794.02 R94.111 794.15 R70.0 I21.19 I20.0 R82.0 794.8 I20.1 R79.82 R94.130 R87.820 R87.625 R85.611 R87.622 R78.0 I24.8 794.30 R94.7 R93.0 R89.7 R87.614 I25.89 R74.0 R87.615 R85.9 794.9 I25.810 R90.81 R82.1 R93.7 I21.3 R73.01 R94.2 R97.1 I25.82 R87.610 R94.118 R92.0 R78.81 R91.1 R85.610 R81 I21.09 I25.812 R89.8 R76.11 R93.8 R94.6 794.12
		466.19 466.11 J20.9 I24.8 I25.10 I25.89 I20.8 I25.9 I25.811 I24.1 I25.2 I25.41 I25.810 I25.3 I21.11 466.0 I21.29 I21.3 I24.0 I25.82 I21.4 I25.42 I21.19 I20.0 I20.1 I21.09 I25.812 I25.83
Allergic	Acute-Bronchitis	477.2 493.81 T50.995A J67.2 495.6 T78.03x 372.14 J67 J67.0 M13.89 J30.1 995.63 995.65 558.3 T45.0X1A M13.859 716.27 D29.30 D29.1 L27.2 477.9 495.5 493.22 D69.2 T78.00x 287.33 995.60 J45.31 J45.51 D29.20 J67.7 T78.09xA D29.22 M13.80 J30.9 T78.08x 287.8 H10.45 B44.81 716.20 995.61 T78.05xA 493.92 693.1 493.90 T78.40x J45.20 493.82 J45.40 D69.42 495.7 J67.5 493.20 D69.49 J45.32 287.32 708.0 H65.119 995.64 D69.1 J45.21 D69.6 M13.819 716.23 495.4 995.67 287.1 T78.08xA T78.00x A477.0 493.02 255.65 T78.02xA J67.1 D69.3 T78.04x T78.2xxA D29.4 T78.07xA 716.26 T78.07x A477.0 493.11 716.23 495.3 945.9 495.9 J45.30 493.21 477 495.2 995.62 T78.40x A495.27 287.2 495.8 495.27 5 995.0 493 T78.05xA D29.0 M10.4 493.11 J45.902 D29.0 J45.999 287.9 J45.29 D29.21 J30.0 963.0 495.1 D29.32 L25.9 J44.9 J44.0 477.1 M13.879 493.01 J45.41 T50.995 J45.998 692.9 M13.849 995.66 D69.8 995.66 T78.04xA J30 495.3 M13.869 287.30 J45.991 J44.1 995.3 287.4 J45.52 287.0 381.06 716.21 J45.901 J67.4 287.39 349.93 716.22 373.32 287.31 T78.06x A477.0 493.08 287 K08.55 K52.2 D29.31 J45.50 495.0 J67.6 D69.9 D29.8 T78.02x 716.24 477.8 381.05 D29.493.12 T78.03xA J67.9 716.22 T78.2xx J30.5 999.4 493.00 M13.829 T78.01x T78.06x 493.10 518.6 716.28 J30.2 H01.119 995.68 M13.839 D69.0 T78.09x 381.04 D29.9 T78.01xA 716.29 J30.81 J45.22 J45.42 T45.0X1 J45.909 D69.41 J67.8
Cardiovascular		I35.0 I48.0 I25.728 444.8 P29.38 I94 I63.212 402.00 I70.669 440.30 I89.9 I60.9 I20.1 413.9 I24.1 I80.3 415.1 I77.811 785.9 I69.319 I69.339 I82.5Z9 R04.1 429.6 G43.619 I82.503 I82.611 I70.512 I75.011 I69.834 I70.628 K64.9 I89.0 I20.1 409.42 447.5 442.8 I70.792 454.0 I70.318 I50.83 I70.744 405.0 I426.2 I455.3 I82.2B9 I12 415.433.8 I69.320 I20.7.81 I444.21 I70.735 I82.602 I67.89 I441.4 I425.4 I35.9 I70.693 I69.234 I65.23 427.2 I70.244 I49.02 I82.91 I29.8 P29.9 I69.131 I36.8 I60.8 I60.11 I442.82 I69.852 I75.029 I438.22 I69.120 I70.641 I60.2 426.51 I70.302 I417.9 I63.012 R04.2 R00.2 427.31 I25.718 I05.8 I70.791 I89.426.50 I63.349 I49.49 I444.89 I63.213 I83.12 I70.218 I82.433 I70.532 I97.638 I87.091 I69.999 I07.8 I11.9 I69.390 I445.0 I69.223 I37.2 I87.319 I69.932 I70.208 I82.492 I82.891 I63.233 I70.319 I70.65 I70.012 I80.292 I411.1 I433 I70.532 I97.638 I87.091 I69.999 I07.8 I11.9 I69.390 I445.0 I69.223 I37.2 I87.319 I69.932 I70.208 I82.492 I82.891 I63.233 I70.319 I70.65 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Injuries
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Oth-Joint-disord		
Oth-Urinary		N39.41 599.71 N39.45 N39.42 599.4 I24.8 I25.10 599.69 599.3 I25.89 I20.8 599.5 N39.44 I25.9 599.60 I25.811 N39.8 I24.1 I25.2 N39.46 I25.41 I25.810 I25.3 I21.11 599.70 N39.43 I21.29 I21.3 N39.3 599.9 I24.0 599.0 I25.82 I21.4 599.2 I25.42 N39.490 599.83 599.82 599.72 599.84 I21.19 I20.0 N39.498 599.1 I20.1 I21.09 I25.812 599.89 N39.0 599.81 I25.83
Otic		H66.006 H60.23 H93.249 H62.41 H91.02 388.71 H61.391 H80.20 H93.219 H93.099 381.89 H95.811 H72.10 H73.91 H74.09 H66.21 H70.229 H90.A12 H95.123 384.00 H60.312 H61.302 H95.193 H65.195 H61.011 389.7 H70.009 380.39 H71.31 H69.91 H60.543 H94.01 H66.3X3 H80.91 H75.00 H65.191 H73.822 H68.019 385.8 H65.04 388.0 H68.112 H68.131 H92.20 H60.61 H95.54 H90.2 H74.392 H60.532 H70.211 H65.20 389.17 H69.90 H95.89 H90.3 388.70 H71.33 H74.41 H65.413 H83.12 H90.6 H67.3 H60.8X2 H72.93 H61.323 H80.23 H60.323 H80.92 H72.829 H90.A21 H72.01 H92.21 H93.13 H60.531 H61.103 H74.321 H72.11 H80.01 H70.092 380.5 H95.119 H72.813 381.9 H81.313 388.02 H81.43 H66.10 H70.811 H61.23 386.40 H83.90 H94.03 386.72 H94.80 H72.44 386.32 H83.8X3 H73.811 H75.02 H95.121 H60.539 H73.093 385.13 H66.3X2 H90.A32 H61.003 H60.02 H70.012 H91.380.21 380.30 H95.03 H95.53 H83.386.31 H73.001 H95.111 H60.502 H88.66.005 H65.01 H66.42 H81.12 H60.8X3 H60.42 388.2 389.02 H61.392 380.4 H61.031 H60.43 H91.8X9 H70.099 381.8 H66.009 380.03 H83.3X9 H93.293 H68.012 H62.8X2 H74.42 H72.12 H70.202 380.0 H74.8X3 H60.60 H61.113 H61.819 H93.243 386.48 H65.31 H70.003 380.0 H82.3 H95.88 389.03 H65.06 H79 H60.03 H81.41 H61.393 388.60 H92.13 388.00 H83.3X1 H60.10 389.0 H62.43 H83.19 H95.133 380.50 H61.019 H81.01 H93.071 H73.384.1 H66.23 H71.10 H74.391 H80.03 H72.02 H60.599 H66.91 380.51 380.52 381.62 H60.592 H71.32 H70.011 H74.309 H66.12 H71.93 H68.028 H93.232 H93.8X2 H77.388.11 H72.823 H60.00 H70.093 H65.93 H81.93 H67.2 H93.3X9 389.16 386.5 H60.559 389.08 H73.019 H61.013 H60.521 385.01 H95.113 H70.209 H81.49 H65.21 H74.323 H73.813 H70.012 389.14 H69.62.42 H61.001 H90.A22 386.43 385.23 H61.102 H95.21 H68.129 H83.01 H61.129 H65.196 H72.90 H65.32 H83.2X2 384.8 H73.22 H95.139 H65.90 H74.384 H72.00 H91.20 H83.8X2 H71.23 H88.9X3 H62.8X9 H73.829 H66.11 H71.00 389.11 H65.05 H74.399 H69.03 385.11 384.23 H60.511 H90.72 380.02 H60.391 H81.8X2 386.30 H91.09 H95 H66.003 H75.83 384.25 H83.02 H65.115 H73.10 H65.197 H60.541 H61.81 385.89 H60.331 H81.92 H70.219 385.24 380.9 H61.399 H68.022 384.21 H74.92 380.81 H60.40 H66.93 H92.23 H65.492 H69.02 H70.893 380.8 384.01 H73.821 389.05 H73.93 H91.01 H65.05 H74.393 387.1 H72.13 H81.21 H81.391 H73.013 H70.11 H60.399 H61.123 H69.80 H74.312 H61.93 H74.322 H83.11 H91.91 H75.383.32 H91.93 H74.311 H73.11 381.5 H93.241 H80.83 H90.5 H92.10 385.2 H61.039 380.89 H95.42 H68.133 H80.11 386.34 384.20 H81.11 384.9 H73.819 H93.A9 H80.91 H65.116 H65.193 H73.92 H65.113 H60.542 H70.813 385.21 H90.71 H81.23 386.58 385.12 380.31 381.6 H70.92 H66.22 H65.114 H80.93 H92.03 H65.419 H61.111 H93.223 H93.A2 H94.82 H60.521 H66.012 381.81 380 H93.12 H95.129 H93.H0.11 H74.02 H81.22 385.35 H70.91 H93.239 H69.01 H95.02 386.56 387.58 389.06 H66.014 H70.73.011 H60.333 384.82 H60.20 385.00 H60.392 385.09 H61.032 H74.329 H83.09 388.31 H74.22 H74.03 H93.019 H71.92 388.3 H70.12 H61.311 H93.221 H93.013 389.01 H61.023 H66.019 381.63 H60.529 H71.91 H95.813 H60.549 H75.82 H81.399 H61.119 H91.8X3 H65.22 H93.211 H70.212 H60.92 H71.12 H61.92 H73.21 H80.21 H83.91 H91.22 H73.091 H66.20 H71.11 H72.91 H90.0 H61.121 H70.222 H95.819 H61.301 H70.891 H73.891 H70.009 H66.007 H61.029 H68.113 H71.02 H82.9 H61.813 H70.001 H81.393 H93.8X9 H61.009 H61.109 H94.02 H61.319 H86.41 H80.34 384.20 H81.12 H80.12 H81.312 385.33 H70.812 H74.12 H70.91 H95.132 H93.222 381.52 389.8 H80.80 H66.010 H65.119 H65.111 H93.299 H80.80 H65.195 H68.122 388.01 H95.22 H66.40 H74.13 H95.191 H81.8X9 H60.591 H61.892 H72.2X1 H74.313 H61.329 H65.30 H61.193 H81.13 380.32 387.2 H68.102 H60.523 H66.74.43 H60.501 H83.13 H93.90 387 H91.3 H94.81 H95.52 H66.92 H80.02 H70.13 H73.893 H73.892 H65.00 H90.42 H60.62 H93.92 H60.41 H65.411 H91.11 H91.92 H71.30 389.9 H60.313 H62.8X3 H60.091 H81.392 H73.002 H60.63 H74.20 389.12 385.85 H93.092 H72.68.109 H65.92 H73.90 H80.22 H69.00 H60.322 H66.004 H90 H68.132 H60.503 H71.01 H68.111 H91.13 H74.8X1 H64.388.9 H65.192 H72.821 H81.8X3 388.7 H61.012 H83.3X2 H74.01 H95.131 H66.3X1 H93.11 H83.8X1 386.50 H75.81 386.55 H61.112 H65.33 H60.332 H72.2X3 H81.02 H72.03 388.9 H60.11 380.01 H61.20 389.22 H62.8X1 H95.41 387.9 H73.812 388.8 H60.522 389.2 388.69 H91.8X2 H95.32 H95.812 H92.12 H93.291 H70.10 H70.20 H76.12 H71.22 387.0 H71 H85.72 H72.2X9 H61.321 H65.194 H66.002 H61.91 H92.09 H61.313 H83.2X1 H66.43 H86.8X3 H91.91 H70.002 H89.11 H60.93 H67.1 H69.81 H81.42 H90.11 H71.21 H78 H80.13 H84.388.30 H61.812 H61.021 381.7 H87.4X9 H60.311 H74.90 H90.A31 H60.12 H60.8X8 H69.83 H65.493 H60.551 384.09 H61.893 385.03 H93.3X1 H60.511 H68.123 H72.822 H68.002 H63 H60.397 H91.8X1 H93.011 H61.891 H66.013 H70.899 H60.329 H61.309 H80.82 H62.40 H60.13 H66.016 H75.01 H91.23 H81.09 380.3 386.33 H80 H66.011 381.61 385.3 H93.093 H61.899 H81.91 H93.19 H81.319 H74.21 388 H92.01 H68.021 H83.92 H72.819 H92.02 H71.13 H61.192 H60.321 H62.019 H75.03 H72.811 H66.3X9 H70.203 H81 H68.001 H70.90 H83.03 388 H61.033 H65.491 386.54 H93.3X2 H70.003 H75.80 389.20 H93.A1 389 H68.013 H81.90 H60.01 H75.03 H72.811 H66.3X9 H70.203 H81 381.60 384.22 H95.199 H81.311 H92.389.04 H65.117 H68.101 381.50 H70.93 H73.823 H80.00 H60.519 H83.2X9 H61.122 H74.8X2 H60.509 386.52 385.9 H61.002 H82 385.02 388.32 H95.01 385.10 386.51 H61.191 H60.593 H73.13 H82.1 H95.122 H61.312 389.21 H62.91 H70.11 H73.23 384.81 H68.011 H95.00 H93.8X3 H70.892 H74.11 H80.81 H60.339 H65.02 386.3 H80.8 H65.412 H93.229 H93.231 H66.13 H73.002 H61.199 H67.9 H60.533 380.53 H65 H81.20 H92.11 H81.10 H65.112 H87 H61.21 389.15 H95.51 H93.93 H94.83 H68.003 H83.3X3 H60.21 385.32 H60.319 H61.90 H72.812 384.24 389.1 H74.23 H93.A3 H70.819 388.12 386.4 H60.22 385.19 H65.499 H69.82 H71.03 H74.93 H68.029 H70.013 H91.12 H70.019 H74.91 H70.223 H83.93 H81.392 386.53 H60.552 H61.101 H93.25 H60.91 H67 385.1 H68.103 H71.20 H65.23 388.10 H69.93 H74.19 H66.017 H73.20 H68.90 H41.66 H41.91 H61.03 388.1 H60.552 H65.31 H82.2 386.35 H61.322 H60.90 H81.03 H68.139 385.30 H65.91 389.18 H93.292 H95.112 H94.381 H93.233 386.42 H94.00 389.10 H72.92 H70.221 H72.2X2 H73.899 H93.242 H66.015 385.22 H92.22 384.0 H73.092 H93.91 H76 H69.92 H61.022 384.2 H91.90 381.51 H73.12 385.31 388.61 H83.213 G96.0 H66.90 H61.22 H68.121
PNS		G56.91 G73.3 G81.92 G62.82 355 359.21 P11.5 G81.11 352.5 G57.53 352.4 G82.14 G57.0 354.3 G80.0 354.4 355.3 354.2 353.3 G83.10 G50.0 767.6 R26.9 G56.43 G79.71 G19.1 G60.9 G83.13 350.2 G81.02 G71.13 G81.90 G52.9 G57.32 G56.40 767.7 G81.93 G72.1 G62.89 G65.1 G26.0 356.2 G51.8 G57.92 P14.8 G57.21 G54.4 G72.2 357 G83.30 359.22 358.2 781.94 351.8 G71.11 G54.7 G72.9 G57.22 G83.89 359.81 G65.42 G60.2 G72.41 G82.50 G87. G56.02 359.71 G82.20 359.79 G83.32 G57.10 353.0 781.1 357.7 G57.80 G81.01 359.4 G57.43 354.8 G57.40 G56.00 G59 R26.1 G80.2 G87.61 G56.80 355.2 353.4 G52.2 354.5 G81.14 358.9 G55 G72.89 G83.9 350.9 G57.83 G68 G58 358.8 G82.53 G57.82 G66 781.0 G69 355.0 351.0 R27.8 G54.8 23 352.6 G53.1 G70.89 G52.98 G83.84 G80.4 R29.5 352.1 G70.00 353.6 G61 G56.32 R41.4 R26.2 781.3 G83.4 R29.3 G51.0 G83.23 359.89 G82.52 G54.6 G56 G56.03 G83.20 G56.90 353.5 G60.1 G73 P14.3 G50.8 G60.0 350 358.01 G51.4 G57.02 G50 G61.82 G62 357.9 G43.0 359.3 G57.71 353 352.0 R25.0 G60.8 356.8 355.1 357.89 G54.8 G80.8 G57.90 G71.9 G57.12 G80.3 357.1 781.5 G65 R29. P25.1 G61.81 356.4 357.0 359.29 781.2 G54.1 G70 P14.9 G53 G56.33 G65.0 356.3 G57.73 G56.23 G83.5 353.8 G57.93 781.99 R25.2 G57.13 352.9 G83.24 G54.5 G57.72 359.9 G61.89 355.71 G82.54 355.8 G56.11 G71.8 P14.0 G51.1 351.9 359.24 355.6 G56.93 355.4 G57.50 357.2 G70.01 G76 G73.1 G57.20 359.6 G83.11 351.1 781.8 G56.21 G82 G50.9 G83 R25 G57.63 G65.2 G57.62 G54.0 R25.3 G57.31 G83.82 357.3 355.79 G56.31 G81.00 352.2 G57.91 P11.4 G70.81 G78 R27.9 G62.9 G71 G56.20 358.1 G72.0 G74 P14 767.5 P14.1 G72.3 G83.31 357.81 359 E13.42 G57.70 R27 G57.33 G70.1 G80.1 359.0 356.9 G54 G81.10 P11.3 357.5 G71.12 356.1 781 G51.1 G56.20 350.1 G58.8 G77 355.5 G51 358.00 G81.94 358 G65.22 G83.21 359.23 781.6 G83.34 G67 781.93 G57.41 R29.891 G57.11 G54.3 R29.810 R29.890 359.1 G57.42 352.3 355.9 G52.8 G57.01 353.2 767.4 G57.30 G62.1 P14.2 G54.9 G54.2 G58.7 G52.3 R26.89 G56.12 781.91 G52.7 G70.80 781.7 G70.9 G57.23 356.0 G83.33 R27.0 G52 G61.0 G50.1 G62.2 354.0 359.5 G51.2 R29.0 G60 354.1 356 G62.81 357.6 G83.22 G71.2 354 G61.1 G56.30 G82.21 G73.7 G81.13 G56.41 G56.01 G81.12 G51.3 G83.0 G83.83 R25.9 781.4 G57.51 R29.818 781.92 357.4 G71.3 G57.52 G62.0 R68.3 G57 G63 G83.81 G56.13 G52.1 G57.03 G56.81 G72.81 G81.03 352 G64 353.9 R26 G61.9 G71.14 G72 G83.12 G82.51 G72.49 G60.3 354.9 R26.81 350.8 351 G57.0 351 G57.81 G80.9 G58.9 G75

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	F12.90	F91.8	F12.229	302.3	307.81	F41.3	F32.9	F10.29	F52.1	300.14	313.22	R44.3	F11.21	F13.221	F63.89	F60.81	R40.2440	R48.0	F16.24	F10.230	F15.251	F51.02				
Psychiatric	F35	F40.298	292.84	F42.2	R40.2254	301.4	308.4	F20.2	F14.259	F40.231	F31.4	F40.241	F17.293	296.35	F18.27	F81.89	301.8	312.10	F19.988	F14.94	F42.8	F64.9				
	292.12	F98.5	295.1	F80.0	F1.1	F13.90	F17.299	295.45	F15.250	F10.288	312.2	F13.150	F18.259	F31.0	301.9	F84.3	296.61	F13.939	302.73	293.9	F18.19	F13.232	301.12			
	F41	F10.150	F51.76	F45.21	R40.2240	296.81	F18.988	F19.99	F13.10	F48.1	F1.1	F11.250	313.35	R40.212	F10.94	308.1	291.1	R47.1	299.1	F10.13	288.2	F10.213	295.70			
	F13.99	F11.11	F30.10	F34.9	300.22	F11.14	R40.2231	315.9	307.4	F15.280	R40.2110	293.83	315.4	F19.181	300.01	F99	F80.82	R47.01	F15	F47	296.24	F96	R41.4			
	F12.128	F40.290	307.49	F54.5	R41.0	301.13	295.00	F14.10	307.44	F30.4	F51.4	R37	F17.218	315.31	313.2	F10.920	R40.233	R45.3	F44.7	F25.8	294.0	307.3	R45.2			
	F20.3	F19.920	20.2	F95.43	F15.95	F10.16	20.26	316	291.1	296.90	F6.150	295.63	292.81	296.44	315.3	302.89	R46.2	295.61	301.39	89.43	294.9	315.1	312.30	F83	F15.259	
	F42.3	299	R49.22	F11.90	F15.20	F10.951	F91	F12.222	F45.1	R40.2213	F20.5	F15.11	F19.20	F19.129	302.51	F14.14	298	F31.72	297.75	F14.182	F31.13	295.25	295.20			
	291.82	F94.1	300.00	R40.2212	294.11	F7.07	F18.929	294.10	F46.1	F13.14	R40.214	306.5	F03	295.86	R40.200	2211	R40.2444	295.92	296.36	S9.25	F45.1	F40.2288	F14.980	F15.23		
	291.89	F74	312.01	F30.12	F12.19	29.26	F52.1	F18.24	295.8	F90.0	R40.214	F13.96	R45.28	296.2	F18.04	R40.200	2211	R40.2444	295.92	296.36	S9.25	F45.1	F40.2288	F14.980	F15.23	
	315.5	F10.188	F16.188	F65.5	F13.19	300.20	F41.0	309.2	F10.280	F52.6	F18.42	F19.859	F19.10	F20.26	F16.20	F19.21	F19.14	F65.81	F19.97	F80.2	F13.932	F10.24	F14.21			
	F51.13	307.40	F18.11	F20.0	307.0	296.4	F43.23	290.41	296	R40.2114	R40.2331	298.2	F40.234	F52.32	S1.60	F45.42	F19.980	R46.6	300.9	P6.31	F9.8	F50.02				
	F17.208	F13.151	F13.21	F19.932	F43.29	F45.22	F19.230	R40.2244	F30.11	R40.1	F16.283	F93.0	F43	313.89	F11.10	F14.121	F18.980	F31.32	F15.122	F63	298.4	F98.3				
	313.	F64.1	296.99	F80.1	F0.9	F19.951	F63.0	F18.29	F19.250	F43.9	F10.11	R40.2134	F43.25	F60.5	296.80	297.9	R44.9	F98.1	R40.2413	F31.11	F19.90	F10.20	306.59			
	312.3	F40.2121	291.8	295.73	F11.94	F14.922	F33.1	F25.1	F14.21	F18.140	R49.8	F40.232	296.33	S10.10	R40.225	302.0	F15.920	301.2	297.2	F06.4	F84.8	296.15	F17.211	F32		
	F17.201	F19.96	301.7	R40.2361	F19.122	F65.1	F67.1	R40.2342	R40.2220	296.13	F10.308	300.111	F18.229	F10.231	300.29	F15.982	306.4	F18.120	310.1	302.5	292	F80.4				
	295.35	301	F42	F46	F17.223	F15.129	F31.77	R40.2241	F40.8	R40.2332	F59	F18.221	301.20	290.1	S10.59	F12.920	306.1	F18.129	R45	F14.22	F15.180	295.71				
	F18.150	F10	F18.251	R41.842	F98.29	R40.2142	F43.8	R40.2330	F13.282	R40.2314	F16.129	R40.2341	313.23	302.1	312.2	F1.31	N98.1	F45.8	P50.3	307.23						
	294.20	310.8	F10.96	295.2	306.0	F10.6	F10.982	R40.231	295.22	298.1	F62.295	F9.14	2488	F31.5	F40.233	F64.8	F20.81	F51.11	F60.6	P13.931	F07.81	F13.988	F77	F14.988		
	R40.221	F15.19	F68.8	F11.281	R40.2344	302.9	F16.122	296.3	S0.312	F12.295	F11.1	R43.21	F84	F32.5	F13.94	F63.9	301.16	F14.19	306.2	F18.151	F16.288	F14.251	F15.221			
	F11	F45.0	302.76	F19	F10.988	F51.01	307.47	296.66	F12.259	R40.2424	F49.1	F90.297	F8.1	F10.239	F51.05	300.09	315.8	291.2	307.6	F63.2	F14.181	295.01	302.81	R48		
	F16.99	R40.2421	F22.20	R40.2442	296.13	F11.951	300.1	F31.30	F90.9	295.83	300.6	290.4	F84.5	306.3	F33.40	295.55	F93.5	F50.5	F1.991	F46.3	297.0	F81.81	F28			
	F68.10	F12.950	R40.2141	290.8	295.0	F14.221	F16.251	R40.211	231.34	298.5	F33.64	F29.15	F48	F11.950	293.82	290.42	297	R40.2111	F84.0	F45.4	292.8	F52.31	R43.1			
	302.84	F14.982	R40.2251	F66.34	302.79	F19.939	F19.14	F33.03	F15.20	R40.2360	F29.159	F13.259	296.01	F94.9	R40.2232	F31.74	F14.25	302.4	F43.11	310.9	F42.4					
	F41.9	302.7	R4.7	F90.2	293.89	F11.922	F12.990	R46.7	301.21	296.05	F12.221	F40.240	F44.6	F16.151	F93.8	F17.203	F15.281	F68	F40.210	F13.929	F19.921	F11.20				
	307.48	F13.920	F11.129	296.3	R40.2441	F40.211	F16.180	309.24	F19.80	F11.121	F19.930	F0.51	F1.51	F19.959	F19.17	F87	F19.11	F40.0	315.2	F76	F43	F17.291	312			
	F05	295.91	F15.14	F11.182	F98.0	55.3	306.1	55.1	F48.8	F13.120	295.41	309.3	296.06	F11.188	F19.282	F12.288	F44.89	F18.1	300.81	296.42	R40.2222	F45.20				
	R40.2242	F13.982	R40.2311	F15.21	F51.3	R41.2	314.2	F13.97	300.15	F11.29	F30.1	R4.83	F19.232	F50.81	R45.84	R40.2124	F40.01	F91.1	F1.0	10.95	F99.5	F12.959	R40.222	300.82		
	F10.221	F42.9	F45.5	290.3	F13.27	290.2	292.89	F51.8	F15.959	296.65	F13.959	306.52	F33	F19.16	F11.222	F02.80	F52	F14.29	F31.78	294.8	F31.5	F1.70	315.39			
	F15.921	F33.8	293.1	F16.19	F60.9	R40.2112	293.23	295.34	292.10	2.308	F29.65	30.07	F31.50	296.4	F14.6	F14.16	F1.26	F1.20	F1.00	F10.97	F7.89	F15.92	F1.20			
	F33.41	302.75	315.35	307.80	30.32	12.2	312.2	292.8	295.86	F6.06	F2.4	F66.1	F19.281	F21.1	R4.20	F4.2353	309	F15.188	314.2	F52.0	F19.19	F13.24	295.13	R42.3	308.9	F65.4
	F45.6	309.9	307.3	F45.8	F11.22	F41.1	F30.3	F16.159	F32.89	F34.81	F1.94	F11.31	F10.929	F32.3	299.63	312.34	F16.10	F33.9	F65.51	R40.213	F17.200					
	F17.209	F12.20	F19.180	F10.180	296.26	294.04	F19.950	F31.12	F70	F55.1	F1.5	F10.90	F16.959	300.16	F14.652	F14.250	F34	F17.290	F95.9	F17.221	F19.929					
	300.21	R40.2252	295.7	R40.2324	F95	312.33	F15.10	295.4	314.00	F13.230	F14.159	308.2	F40	F16.120	F94.8	F60.1	295.84	F18.188	F40.243	F68.11	F19.920	F13.950				
	F31.0	F12.150	F51.03	F13.129	F12.122	300.2	F32.20	F16.98	295.93	F60.4	R41.843	F46.296	F31.48	F4.79	F14.221	F31.74	F15.24	F1.20	F1.00	F10.77	F7.89	F15.922	F1.20			
	F19.921	F33.8	293.1	F16.190	R40.2112	293.23	295.34	290.20	296.23	F26.48	F4.80	R40.2420	F30.4	F16.20	F1.46	F1.150	F1.50	F1.31	F1.21	F1.04	F1.37	F1.20	F1.00			
	F17.227	F17.228	R40.2221	F43.0	F31.10	F14.11	R40.2352	F30.9	F14.129	309.0	R40.2253	F14.90	F48.9	294.21	F12.11	R49.21	F14.229	293.81	296.32	F91.3	290					
	296.21	F11.259	F14.222	R40.20	F14.150	F14.92	296.31	307.41	F12.218	F15.121	R49.1	F18	292.9	30.19	F61	G44.209	F11.945	F7.39	S1.81	F1.81	F1.20	280	295.72			
	F40.02	F22.02	F51.04	F30.13	F10.281	292.11	295.4	294	F12.19	F11.22	F1.231	F2.31	R40.2420	F14.950	F14.254	295.6	296.8	F40.230	300.10	F18.94	F16.951	F13.121	F19.159			
	F15.981	F12.10	313.82	296.34	F56.4	F47.81	F81.41	F14.23	F13.159	F1.29	F18.988	29.8	F15.99	30.39	F19.10	F18.151	F55.81	F18.298	F1.20	F1.04	F1.44	F1.20	F1.04			
	F19.982	F80.81	R40.2230	F13.281	R40.2354	F52.21	F34.0	R40.2144	F10.99	302.82	F29	295.10	F11.229	292.85	R40.2423	F12.921	300.5	F48.2	313.21	F10.182	310.81					
	312.56	305.63	313.83	312.32	R48.3	R40.2331	F31.75	F63.1	307.43	304.2	F50.1	F1.20	F1.68	F1.60	F1.64	F1.60	F1.64	F1.60	F1.64	F1.60	F1.64	F1.60	312.00			
	306.53	F61.41	R41.842	F53	R40.2123	313.9	312.2	292.66	60.4	R40.2312	300.0	302.52	R40.2120	307.20	R40.2243	296.9	F15.1	F1.82	R44.8	F1.26	R45.89	F65.3				
	F89	F60.9	F14.929	F60.6	F94.2	R40.2143	F43.8	F18.99	F12.129	F51.9	F37	295.5	F01.50	296.7	R40.243	301.22	F12.280									
Reproductive	764.96	O41.91x	O70.0	628.0	646.03	O31.30x	634.91	608.22	679.10	662.11	O35.0xx0	P24.21	O13.9	656.01	'O34.00	P57.0	649.7	662.00	669.82	656.23	663.60	618.0				
	670.2	O34.529	671.80	O03.32	646.51	771.8	E82.2	668.03	674.80	651.60	661.11	629.9	N82.5	676.32	32	661.21	646.9	73.9	O36.0110	659.90	673.34	649.03	660.33			
	669.0	674.02	666.13	O92.5	675.11	668.65	69.10	674.50	N84.9	O72.4	669.0	662.0	60.2	61.7	602.2	O02.01	O09.1	350.80	N88.0	A48.5	661.30	32	62.0			
	661.2	648.51	62.642	23	666.13	64.308	64.19	60.92	P0.06	N85.4	652.0	618.00	P0.036	61.04	674.32	67.4	T65.89	66.68	N64.89	65.61	67.11	65.61	29.99			
	661.0	674.32	66.687	2.23	666.21	64.303	64.19	60.74	O9.25	674.32	67.4	T65.89	66.68	N64.89	65.61	67.11	65.61	29.99	N64.9	65.61	67.11	65.61	29.99			
	668.50	674.34	66.687	2.23	666.21	64.303	64.19	60.74	O9.25	674.32	67.4	T65.89	66.68	N64.89	65.61	67.11	65.61	29.99	N64.9	65.61	67.11	65.61	29.99			
	668.60	674.35	66.687	2.23	666.21	64.303	64.19	60.74																		

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		J27 J63.0 J12.9 J37.0 P26.0 J39 R05 J69 J15.1 J67.0 516.0 P24.21 J95.859 770.3 502 J09.X9 J34.3 J52 770.81 J03.00 786.9 J95.01 277.09 J20.6 J21.8 J33.8 P28.0 J95.850 J84.848 770.0 J67.7 P28.2 R06.7 J34.89 P27.8 478.30 J01.21 J12.3 518.3 G47.35 495.7 J11.82 J95.71 J64 J82 P28.11 J01.20 J15.8 J45.21 495.4 J39.9 J95.89 P23 P26.9 J95.811 J70.1 J73 J95.862 J66.1 J79 J93.83 J20.9 512 J41.8 J84.112 J03 518 J18.1 J94.9 471.8 J18.1 J34.81 786.7 478.33 J34.2 J93 J32.9 R06 J68.8 J45.30 519.9 327.29 J20.0 J63.8 J84.03 P91.63 770.15 R06.81 495 P19.0 J01.10 770.7 J95.863 J09.X1 J02.0 J34.9 J84.02 J15.212 J81.0 J94.0 478.3 J23 J10.81 J84.116 J49.5.1 507.0 J05.10 P26.1 J11.00 J06.0 J96.91 J33 R06.6 J45.991 516.32 770.12 J49 J32.0 768.4 J87 768.70 J01.00 R06.01 J94.1 512.1 786.51 786.6 J38.02 J95.830 J38.01 478.79 770.84 J68.3 J10.08 J84.115 J25 J01.41 M34.81 P27.0 J07 512.8 R06.00 J11.08 J46 R09.3 J49 J70.5 J95.4 J05.0 J95.02 J31.0 J95.821 P24.80 J91.8 768.71 J30.5 J38 J70.2 J63.4 J86 478.4 J10.00 J84.9 J96.20 J21 J30.2 J31 J01.01 J29 R07.9 J75 15.7 327.22 J61 J93.11 J02.9 478.75 P28.5 491.2 J45.22 J96.11 J67.8 J85.0 J35.0 J96.21 J11.1 J35.01 505 491.1 P28.10 J15.3 J38.0 J67 492.8 R06.2 770.88 770.86 J15.20 J38.5 R07 J30.1 J95.62 J20.1 J22 512.0 G47.30 768.1 P23.0 J35.3 J95.88 P91.60 J95.860 J81 J43.8 J00 J68.0 J83 478.34 J18.9 J94.2 J70.8 J35.9 J33.0 R07.1 770.501.0 J43.2 478.74 J45.20 470 J45.40 786.06 327.23 P28.89 R06.9 J39.0 J98.9 J47.0 J98.3 P22.1 J39.8 R06.83 J65 P24.10 R07.0 J37 R07.89 517 503 786.52 J10 J91.40 J20.95.72 J28 J09.X3 J70 P23.3 J01.80 J97 J12.89 J18.8 516 J67.3 495.9 J40 P24.01 E84.9 J10.01 500.0 J11.2 519 501 J93.0 J98.01 P22 495.8 J08 G47.31 518.8 327.20 J20.5 786.01 786.50 P24.00 J41 770.2 J84.83 J93.81 515.0 J95.03 J30.0 786.00 J92 J76.5 768.06 J56 J01.9 J70.1 J15.0 J39.2 494.1 516.8 519.4 770.9 J38.3 R06.09 J03.91 G47.37 327.2 J34.1 J12.0 J21.1 J01 P22.0 J12.2 J39.3 P25.3 786.02 J95.851 J31.1 P25.0 J15 J43.0 P23.1 495.2 478.31 P24.30 770.18 P24.31 J57 J63 J95.00 J69.0 J38.4 J09 277.0 J04.30 J95.5 J45.902 504 P24.11 J45 J03.01 P23.6 R06.1 519.0 786.1 J37.1 J15.29 J98.6 J44.9 J84.10 P27.9 J44.0 J96.00 517.3 E84.0 J45.998 516.9 J86.9 471 J63.2 491.0 J68.1 786.07 J98.19 P25 J66.8 768.3 518.84 J95.3 J30 J72 J44.1 519.0 786.3 J16 J84.2 770.85 J66.0 J20.2 519.11 770.00 J47.9 P27.1 770.87 P91.62 P22.9 786.03 J84.117 J84.113 516.30 770.16 P23.2 495.0 J67.6 J93.82 J98.51 516.37 770.89 768.8 J50 J04.2 J44 J12 327.24 J43.9 J77 J84.82 J20.8 510.9 770.13 P28 J31.2 478.32 478.70 496 J38.6 J41.0 J24 J68 J11.89 J45.909 J03.81 J89.9 518.89 P91.61 770.10 J67.7 J15.0 J39.2 494.1 516.2 G47.33 277.02 J38.2 J60 E84.11 R09.89 J47 277.01 J95.831 J35 P23.5 J94.8 P24.04.0 J69.8 517.2 R07.2 495.5 786.09 J20 J12.81 J45.31 J58 J45.51 J43.1 E84.19 P84 494 J55 J33.9 516.31 J30.9 P22.8 J98.59 J04.10 J38.1 J52 P25.8 P23.8 J62 516.33 J84.842 J54 J92.0 J32.1 769 J04.11 786.04 J68.9 J70.0 327.21 J90 P24.20 G47.32 770.83 P24.9 J12.1 J84.81 J67.1 J10.83 J35.2 J10.1 492 J514 768.2 327.27 J95.61 J88.7 J16.0 J20.7 478.0 471.1 R06.02 J15.6 J95.1 J02 J95.812 J15.4 J68.4 J96.01 514.0 J03.90 J35.1 516.35 J45.990 786.3 J35.2.6 J62.8 J91.0 500 J93.12 770.82 J84.01 516.1 J45.41 J88 327.25 J84.114 P27.3 471.9 J96.90 J1.81 518.82 495.3 J39.1 J98.11 J10.2 J80 519.8 J45.52 J96.12 518.83 J05.11 R06.4 770.17 J69.1 J67.4 J84.841 J99 J98.2 P26.8 J11 J63.1 J78 768.5 J85.2 J45.50 P26 P28.3 J15.9 J70.9 786.4 J36 J05 J95.861 J04.31 J67.9 J85.94 478.71 471.0 518.81 E84.8 J98 J19 J21.0 J94 J43.9 770.14 516.34 J30.81 510.0 J45.42 J13 J26 768.73 R22.2 J96.92	Respiratory
		727.66 727.04 726.12 726.31 71 29.1 I20.8 726.72 728.89 728.83 727.49 729.4 I25.3 I21.11 727.06 726.10 727.43 729.73 I25.42 726.60 727.81 726.90 726.73 727.50 729.0 729.39 728.6 727.51 729.6 I25.10 726.62 727.67 727.69 726.78 726.5 I25.811 728.2 I25.2 727.09 727.59 726.30 727.05 I21.29 726.2 727.83 I21.4 726.39 728.85 727.60 729.92 728.9 726.4 J26.4 726.91 727.01 729.82 728.5 726.64 726.32 726.61 728.4 727.69 I25.9 728.88 728.10 727.65 727.00 728.79 I24.1 728.87 I25.41 727.82 726.70 729.81 729.91 I24.0 727.42 727.63 725 727.9 I21.19 I20.0 729.99 728.82 I20.1 727.3 727.64 726.63 726.65 727.2 727.01 726.79 729.31 728.81 726.33 729.30 728.11 724.8 726.11 I25.89 728.12 729.72 728.0 727.41 729.90 727.02 726.0 I25.810 729.5 728.13 729.2 728.71 I21.3 728.3 727.1 I25.82 729.79 726.19 728.84 726.8 728.86 727.61 728.19 727.62 I21.09 I25.812 726.71	Rheumatism
		327.43 327.13 G47.37 G47.54 327.33 327.09 G47.01 I20.8 327.40 G47.35 G47.8 327.02 327.42 I25.3 I21.11 G47.51 327.15 G47.33 G47.419 327.32 327.11 G47.10 I25.42 327.20 327.27 327.51 G47.13 G47.27 327.41 G47.19 I25.10 G47.9 G47.22 G47.39 I25.811 327.00 327.36 327.30 G47.61 I25.2 327.34 G47.31 G47.69 I21.29 327.49 G47.14 I21.4 G47.50 327.53 327.31 I25.83 G47.29 G47.30 327.25 G47.36 327.35 G47.09 I25.9 G47.32 G47.52 327.24 I24.1 I25.41 G47.63 G47.23 I24.0 327.01 G47.11 G47.421 G47.20 327.10 G47.34 G47.00 327.29 I21.19 I20.0 I20.1 I20.1 327.21 327.44 G47.24 327.52 327.19 I24.8 327.8 I25.89 327.26 327.37 G47.12 G47.429 G47.53 327.22 I25.810 G47.26 G47.411 G47.62 G47.21 327.39 I21.3 327.12 I25.82 327.23 327.59 G47.25 327.14 I21.09 I25.812 G47.59	Sleep-Disorders
		R10.2 R10.11 R10.83 789.7 789.06 I20.8 789.02 789.1 R10.10 I25.3 I21.11 R10.812 789.42 789.63 789.04 789.2 R10.815 I25.42 R10.819 789.44 789.61 R10.811 789.34 789.47 R10.13 789.60 789.09 I25.10 789.67 I25.811 789.69 789.65 789.33 I25.2 789.01 I21.29 789.35 I21.4 R10.31 789.51 R10.12 I25.83 789.49 789.05 I25.9 R10.817 789.64 I24.1 I25.41 789.36 I24.0 R10.33 789.9 J21.19 I20.0 I20.1 R10.813 789.45 789.32 789.62 R10.9 789.43 789.40 I24.8 I25.89 789.46 789.41 R10.32 I25.810 789.00 I21.3 R10.84 789.31 I25.82 789.37 789.30 789.03 789.66 789.39 R10.814 R10.816 789.07 I21.09 I25.812 789.59	Symptoms-Abs-Pelvis
		R14.1 R13.14 I20.8 787.5 787.91 R19.4 R19.05 R19.01 R19.2 I25.3 I21.11 R11.11 R11.2 R19.07 R19.06 R19.09 R15.0 I25.42 787.3 R19.32 R13.13 R19.03 787.4 R19.30 787.21 R11.13 R15.9 I25.10 787.04 I25.811 I25.2 R11.0 787.20 I21.29 R19.35 R11.10 I21.4 R19.33 R19.04 787.29 787.03 I25.83 R16.0 R19.31 R12 R13.19 R17 R19.02 R15.1 R18.0 787.6 I25.9 R16.1 I24.1 I25.41 787.02 R15.2 I24.0 R13.12 R11.14 787.99 R13.11 787.23 I21.19 I20.0 I20.1 R10.19 787.23 R19.11 R19.8 I24.8 R19.37 I25.89 R13.10 R18.8 787.7 787.24 R19.34 787.01 I25.810 787.22 I21.3 R19.7 I25.82 R19.5 R19.00 I21.09 I25.812 787.1	Symptoms-Digestive
		R53.82 R65.10 R56.01 R50.81 R68.3 R59.9 780.39 I20.8 R53.1 R62.0 R55 R65.21 R62.51 780.64 I25.3 I21.11 780.1 780.63 780.65 R56.1 R68.0 R62.50 R64 780.59 H63.3 I25.42 780.96 R68.83 780.8 R56.00 H68.84 R62.52 R53.81 I25.10 R63.0 780.72 780.51 R68.82 780.91 R63.1 I25.811 I25.2 R68.12 I21.29 R63.2 R57.0 I21.4 R63.6 R63.4 R63.8 780.92 R57.9 I25.83 780.62 780.52 R65.20 R65.11 780.55 R68.81 R50.82 780.32 780.94 I25.9 780.95 780.71 I24.1 R50.84 I25.41 780.56 R68.11 780.09 I24.0 R50.9 R63.5 I25.19 I20.0 I20.1 780.99 780.97 780.61 R53.2 780.4 I24.8 R58 R69 780.2 R51 I25.89 R56.9 780.93 R52 780.03 R60.9 780.58 780.01 780.53 I25.810 780.31 780.57 R62.7 I21.3 I25.82 R61 780.79 780.50 R57.8 R68.13 780.02 780.54 780.60 R12.09 I25.812 R50.83 R68.89	Symptoms-General

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		786.7 786.50 R09.2 786.3 R06.4 786.51 R06.7 R09.82 I24.8 I25.10 786.04 786.8 R06.9 786.2 I25.89 I20.8 R07.0 786.02 I25.9 786.06 786.05 786.1 I25.811 R06.3 R06.2 R09.02 I24.1 I25.2 786.4 I25.41 I25.810 I25.3 I21.11 R06.81 R06.02 R06.1 786.07 R06.01 R06.6 I21.29 I21.3 786.00 786.6 786.9 I24.0 R05 I25.82 I21.4 R06.89 I25.42 R06.82 R09.3 R06.00 786.09 786.59 R09.89 R09.01 I21.19 I20.0 R07.2 R07.1 I20.1 I21.09 I25.812 786.03 R07.89 786.52 786.01 I25.83 R07.9
		R22.1 R23.4 R23.8 I24.8 I25.10 I25.89 I20.8 R23.2 782.2 I25.9 R22.2 I25.811 782.4 I24.1 I25.2 782.0 I25.41 I25.810 I25.3 I21.11 782.1 782.62 R21 R23.0 782.7 782.61 I21.29 I21.3 I24.0 R23.3 782.3 782.8 I25.82 I21.4 I25.42 782.5 I21.19 I20.0 I20.1 I21.09 I25.812 R23.1 R22.9 R20.3 782.9 I25.83
		R36.1 R36.9 788.35 788.61 788.36 I20.8 788.0 788.63 I25.3 I21.11 788.69 I25.42 R37 788.32 788.20 788.39 R32 R39.12 I25.10 R39.14 R31.9 788.65 788.38 R39.81 R35.8 R39.16 I25.811 R33.9 I25.2 I21.29 788.30 I21.4 788.37 R39.0 788.43 R39.13 R39.89 788.31 I25.83 788.99 788.7 R39.11 I25.9 I24.1 I25.41 R39.19 I24.0 788.91 I21.19 I20.0 788.8 R35.0 I20.1 788.21 788.33 788.42 I24.8 R35.1 R30.0 I25.89 R34 R33.8 788.62 I25.810 788.41 R39.15 I21.3 788.1 788.34 788.64 I25.82 788.5 788.29 I21.09 I25.812 R31.0 R31.1
Thyroid		E03.9 241.9 E04.1 E04.2 E05.90 I20.8 E05.21 I25.3 I21.11 245.2 243 241.0 E05.40 I25.42 E05.91 246.9 E07.89 E04.0 242.10 242.30 245.0 E07.0 I25.10 242.81 242.11 244.3 242.41 242.40 246.2 I25.811 240.0 E06.4 I25.2 I21.29 I21.4 242.21 241.1 E05.11 I25.83 E06.3 245.8 242.80 E05.20 E06.1 I25.9 E05.10 I24.1 I25.41 E07.81 E05.01 E01.8 245.4 I24.0 246.3 242.91 244.8 246.1 242.20 I21.19 I20.0 E01.2 242.01 I20.1 244.0 242.00 I24.8 245.1 E05.00 I25.89 244.9 246.0 E07.1 E06.9 I25.810 E00.9 244.1 E05.41 I21.3 244.2 242.90 240.9 245.9 E07.9 I25.82 E05.31 E05.30 245.3 E04.9 242.31 E06.0 246.8 E03.2 I21.09 I25.812 E06.5

Algorithm 1: GenESeSS

Data: A sequence x over alphabet Σ , $0 < \varepsilon < 1$
Result: State set Q , transition map δ , and transition probability $\tilde{\pi}$

/* Step One: Approximate ε -synchronizing sequence */

- 1 Let $L = \lceil \log_{|\Sigma|} 1/\varepsilon \rceil$;
- 2 Calculate the **derivative heap** D_ε^x equaling $\{ \hat{\phi}_y^x : y \text{ is a sub-sequence of } x \text{ with } |y| \leq L \}$;
- 3 Let \mathcal{C} be the convex hull of D_ε^x ;
- 4 Select x_0 with $\hat{\phi}_{x_0}^x$ being a vertex of \mathcal{C} and has the highest frequency in x ;
- /* Step Two: Identify transition structure */
- 5 Initialize $Q = \{q_0\}$;
- 6 Associate to q_0 the **sequence identifier** $x_{q_0}^{\text{id}} = x_0$ and the probability vector $d_{q_0} = \hat{\phi}_{x_0}^x$;
- 7 Let \tilde{Q} be the set of states that are just added and initialize it to be Q ;
- 8 **while** $\tilde{Q} \neq \emptyset$ **do**
- 9 Let $Q_{\text{new}} = \emptyset$ be the set of new states;
- 10 **for** $(q, \sigma) \in \tilde{Q} \times \Sigma$ **do**
- 11 Let $x = x_q^{\text{id}}$ and $d = \hat{\phi}_{x\sigma}^x$;
- 12 **if** $\|d - d_{q'}\|_\infty < \varepsilon$ **for some** $q' \in Q$ **then**
- 13 Let $\delta(q, \sigma) = q'$;
- 14 **else**
- 15 Let $Q_{\text{new}} = Q_{\text{new}} \cup \{q_{\text{new}}\}$ and $Q = Q \cup \{q_{\text{new}}\}$;
- 16 Associate to q_{new} the sequence identifier $x_{q_{\text{new}}}^{\text{id}} = x\sigma$ and the probability vector $d_{q_{\text{new}}} = d$;
- 17 Let $\delta(q, \sigma) = q_{\text{new}}$;
- 18 Let $\tilde{Q} = Q_{\text{new}}$;
- 19 Take a strongly connected subgraph of the labeled directed graph defined by Q and δ , and denote the vertex set of the subgraph again by Q ;
- /* Step Three: Identify transition probability */
- 20 Initialize counter $N[q, \sigma]$ for each pair $(q, \sigma) \in Q \times \Sigma$;
- 21 Choose a random starting state $q \in Q$;
- 22 **for** $\sigma \in x$ **do**
- 23 Let $N[q, \sigma] = N[q, \sigma] + 1$;
- 24 Let $q = \delta(q, \sigma)$;
- 25 Let $\tilde{\pi}(q) = \llbracket (N[q, \sigma])_{\sigma \in \Sigma} \rrbracket$;
- 26 **return** $Q, \delta, \tilde{\pi}$;

Algorithm 2: Log-likelihood

Data: A PFSA $G = (\Sigma, Q, \delta, \tilde{\pi})$ and a sequence x over alphabet Σ
Result: Log-likelihood $L(x, G)$ of G generating x

- 1 Calculate the state transition matrix Π and observation $\tilde{\Pi}$;
- 2 Calculate the stationary distribution over states ρ_G of G from Π ;
- 3 Calculate the stationary distribution of alphabet $\phi_\lambda^T = \rho_G^T \tilde{\Pi}$;
- 4 Initialize p by ρ_G and q by ϕ_λ ;
- 5 Let $L = 0$;
- 6 **for** i from 1 to $|x|$ **do**
- 7 Let σ be the i -th entry of x ;
- 8 Let $L = L - \log q|_\sigma$;
- 9 Let $p^T = \llbracket p^T \Gamma_\sigma \rrbracket$ where Γ_σ is defined in Eq. 8;
- 10 Let $q^T = p^T \tilde{\Pi}$;
- 11 **return** $L/|x|$;
