





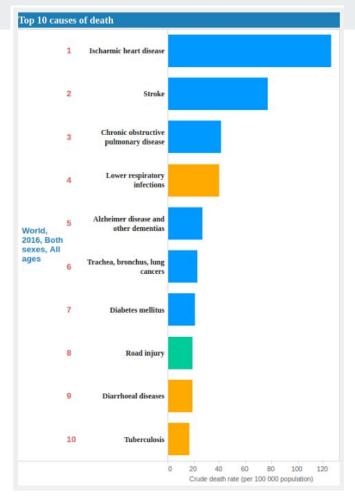
Master Thesis Defense: Bayesian Modeling in Neurological Diseases

Hüseyin Camalan

Supervisors: Prof.Dr. Kerstin Ritter Dr. Michelle Livne

- are difficult to cure
- damage to nerve tissue is largely irreversible

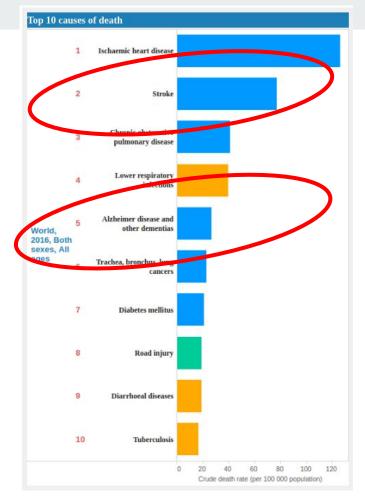
 Neurological diseases associated with aging present the worst portrait:



https://www.who.int/gho/mortality_burden_disease/causes_death/top_10/en/

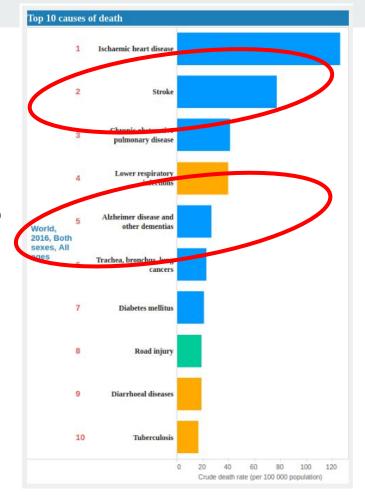
- are difficult to cure
- damage to nerve tissue is largely irreversible

 Neurological diseases associated with aging present the worst portrait:

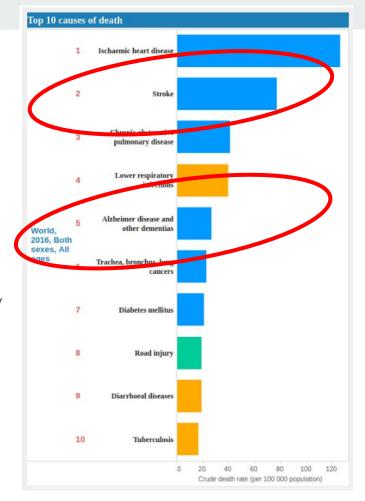


https://www.who.int/gho/mortality_burden_disease/causes_death/top_10/en/

- Both stroke and dementia increased twofold in the last two decades and are projected to increase twofold again
- Population distributions skewing towards older ages is a likely culprit in this increase



- From here onwards, focus will be on dementia/Alzheimer's disease
- However, most statements are mutually applicable and the separation between the two diseases is also not completely clear
 - e.g. vascular dementia



https://www.who.int/gho/mortality_burden_disease/causes_death/top_10/en/

Dementia

- Umbrella term for diseases that cause cognitive decline through degradation of brain tissue
- Various disease mechanisms at play
 - o vascular, oxidative, genetic, environmental (among others)
- Roughly %75 Alzheimer's disease (AD), followed by %20 vascular dementia
 - AD: characterized by memory loss and damage to corresponding brain regions (especially hippocampus)

Dementia

- Prevention efforts currently constitute the best option
 - mainly based around a healthy lifestyle and mental stimulation
 - prevention delays disease onset, not a definitive cure
- Early identification of at-risk-individuals could be valuable

Total potentially modifiable risk factors for dementia

Risk Factor	Relative risk for dementia	Prevalence (%)	Communality (%)	PAF (%)	Weighte PAF* (%	
Early life	•	**	-			
Less education (none or primary school only)	1.6	40.0	64.6	19.1	7.5	
Midlife (age 45-65)						
Hypertension	1.6	8.9	57.3	5.1	2.0	
Obesity	1.6	3.4	60.4	2.0	0.8	
Hearing loss	1.9	31.7	46.1	23.0	9.1	
Later life (age >65)	•	•			•	
Smoking	1.6	27.4	51.1	13.9	5.5	
Depression	1.9	13.2	58.6	10.1	4.0	
Physical inactivity	1.4	17.7	26.6	6.5	2.6	
Low social contact	1.6	11.0	45.9	5.9	2.3	
Diabetes	1.5	6.4	70.3	3.2	1.2	
Total adjusted for communality					35.0	

Table 1. Risk factors for dementia; relative risk for dementia, prevalence, communality and Population Attributable Fraction (PAF) for dementia

Goal:

• Build a model that can predict the risk of developing dementia/AD in the future

How to determine "risk"?

Goal:

• Build a model that can predict the risk of developing dementia/AD in the future

How to determine "risk"?

- Utilize probability theory
 - Use Bayes' rule to derive probabilities for AD given variables

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}$$

Bayesian Networks on Dementia/AD

- 1. Specify the problem using Bayes rule
- 2. Factorize joint probability distributions
- 3. Extract individual probability terms
- 4. Evaluate the Bayes rule

Test model performance on real-world data

• Alzheimer's Disease Neuroimaging Initiative (ADNI) Database

Detour: ADNI Database

- Alzheimer's Disease Neuroimaging Initiative (ADNI)
- Large scale longitudinal study of Alzheimer's disease (AD) patients, age-matched controls and patients with in-between statuses: mild cognitive impairment (MCI), significant memory concern (SMC)
- Contains demographic information, medical history, neuropsychological tests, genetic analyses, MRI scans, biological marker analyses, etc.

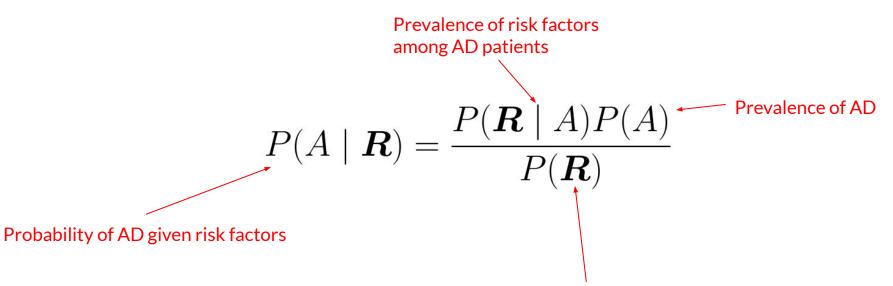
More info at https://adni.loni.usc.edu/

1. Specify the problem using Bayes rule

$$P(A \mid \mathbf{R}) = \frac{P(\mathbf{R} \mid A)P(A)}{P(\mathbf{R})}$$

- A: Alzheimer's disease, R: relevant variables/risk factors
- R is bold because it represents multiple variables, i.e. a joint probability distribution

1. Specify the problem using Bayes rule



Prevalence of risk factors in general population

2. Factorize joint probability distributions

- The equation is unsolvable until we break down the joint probability distributions P(R) and P(R|A)
- Two possible options (not exhaustive):
 - 1. Assume conditional independence between all variables (naive Bayes)
 - Simply multiply all individual probability terms
 - 2. Construct a Bayesian network of \mathbf{R} , which can then be used to break the term down to its individual parts (ideally based on evidence)
 - Use scientific evidence to build the network

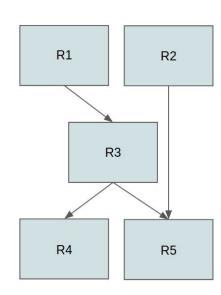
Naive Bayes

$$P(\mathbf{R} \mid A)P(A) =$$

$$P(R_1,R_N, A) = P(A) \prod_{i=1}^{N} P(R_i \mid A)$$

Bayesian Network

Assume R₁...R₅ are
variables that make up R



$$P(R_1, R_2, R_3, R_4, R_5) =$$

$$P(R_4 \mid R_3)P(R_5 \mid R_3, R_2)P(R_3 \mid R_1)P(R_2)P(R_1)$$

Bayesian Network of ADNI Variables

- AGE and APOE4 are highly connected to brain regions and test scores
- PTEDUCAT is connected to brain size and test scores
- PTMARRY is connected to test scores
- Brain areas are assumed to be conditionally independent to each other

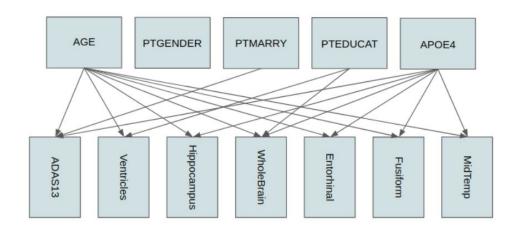


Figure 2: DAG for the selected ADNI database variables based on medical evidence. Vertical arrows indicate the direction of causality.

Extract individual probability terms

- The equation can now be solved once probabilities are plugged in
- How to look up probabilities (in the case of AD)?

Extract individual probability terms

- The Bayes rule equation can now be solved once probabilities are plugged in
- How to look up probabilities (in the case of AD)?

Options:

- 1. Look up scientific literature to find descriptive statistics about relevant groups
- 2. Extract probabilities from data

Extract individual probability terms

Four ways based on (i) type of variable and (ii) its position in the Bayesian network:

- 1. Variable with parent nodes in the network: use regression
 - a. Discrete: class probability estimates of a Logistic Regression model (not used in practice)
 - b. Continuous: PDF calculated from a Bayesian Ridge Regression model
- 2. Variable without parent(s): use histograms
 - a. Discrete
 - b. Continuous: smoothed histogram values

Testing on ADNI Database

Specific research questions:

- 1. Can we separate patients who were initially diagnosed as AD or clinically healthy? (AD-CN)
 - Extract a subset of the data that contain only these two groups
- Can we predict the future status of patients who are in-between AD and clinically healthy? (MCI-D)
 - o a.k.a. Mild Cognitive Impairment (MCI)
 - Extract a subset of the data that contains only MCI patients
 - Predict which MCI patients develop dementia in 2 years

Testing on ADNI Database

- Train, validate and test models using 5-fold nested crossvalidation
 - o 5 validation folds, i.e. roughly %65-%15-%20 training-validation-test split
 - Validation parameter is the decision threshold to classify a patient (P_{threshold})
 - Test Naive Bayes (henceforth "NB") and manually built Bayesian networks (henceforth "Manual")
 - Test models with different normalization procedures: no normalization, z-score normalization, min-max feature scaling

Testing on ADNI Database

- Use generic machine learning models as benchmarks
 - Multilayer Perceptron: one hidden layer with 100 neurons, 200 iterations, with ReLu activation function and momentum term
 - L2 regularization as validation parameter
 - C-SVM : linear kernel
 - regularization term C as validation parameter

Results

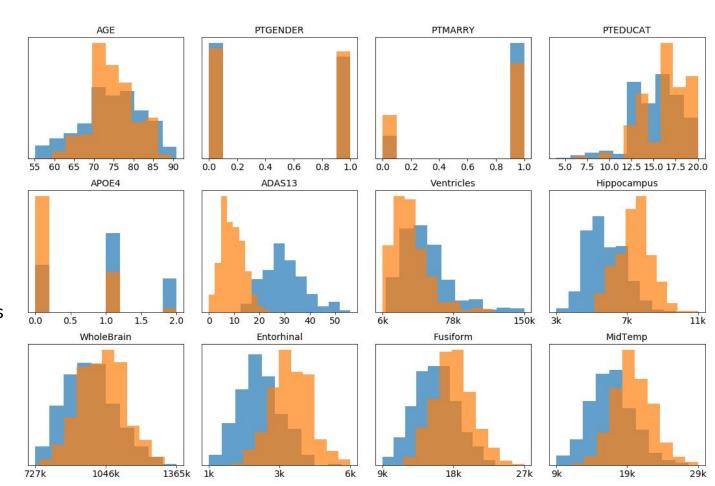
- 1. Variable distributions
- 2. Classification performance
- 3. Visualizations of model prediction behavior

1. Variable distributions

AD-CN Dataset

Orange - initially diagnosed as clinically normal

Blue - initially diagnosed as AD patient

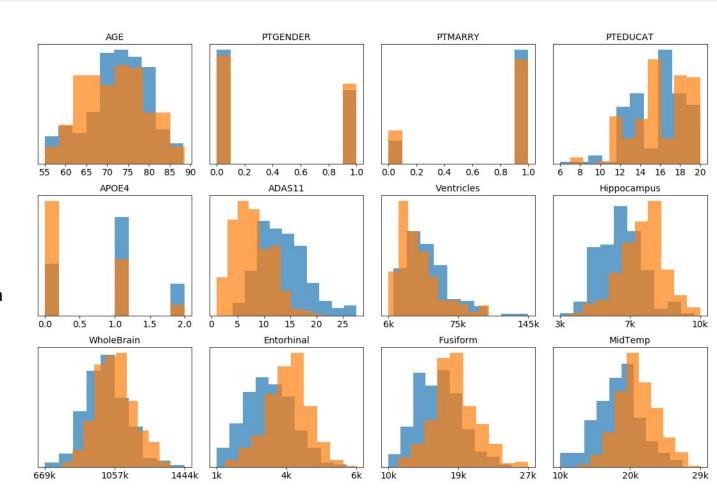


1. Variable distributions

MCI-D Dataset

Orange - does not develop dementia in two years

Blue - develops dementia in two years



2. Classification performance

AD-CN Dataset

- unnormalized > min-max > z-score
- Manual ~ NB
- MLP=C-SVM > Bayesian models
- Optimal P_{threshold} is consistently quite low

Model name	Balanced	ROC-AUC	Best parameter		
	accuracy	score			
NB - Unnormalized	.914	.901	$P_{threshold} = 0.1$		
NB - Normalized (z-score)	.667	.638	$P_{threshold} = 0.5$		
NB - Normalized (min-max)	.829	.834	$P_{threshold} = 0.1$		
Manual - Unnormalized	.884	.892	$P_{threshold} = 0.1$		
Manual - Normalized (z-score)	.630	.610	$P_{threshold} = 0.1$		
Manual - Normalized (min-max)	.813	.796	$P_{threshold} = 0.1$		
C-SVM	.972	.996	C = 0.4		
MLP	.971	.995	$\alpha = 0.001$		

2. Classification performance

MCI-D Dataset

- unnormalized ~ min-max > z-score
- Worse prediction than AD-CN
- Same as above

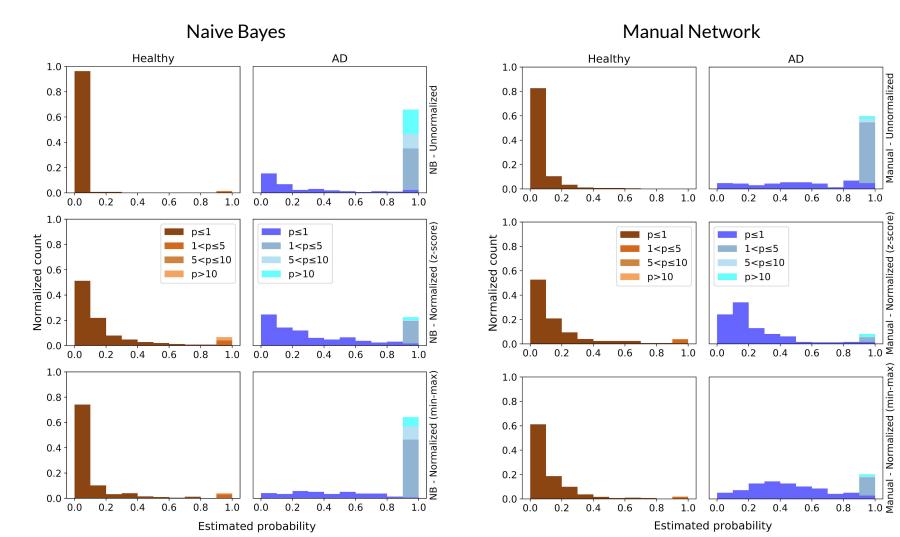
Model name	Balanced accuracy	ROC-AUC score	Best parameter
NB - Unnormalized	.709	.719	$P_{threshold} = 0.1$
NB - Normalized (z-score)	.558	.544	$P_{threshold} = 0.4$
NB - Normalized (min-max)	.714	.722	$P_{threshold} = 0.1$
Manual - Unnormalized	.718	.719	$P_{threshold} = 0.1$
Manual - Normalized (z-score)	.532	.539	$P_{threshold} = 0.4$
Manual - Normalized (min-max)	.713	.705	$P_{threshold} = 0.1$
C-SVM	.809	.892	C = 0.2
MLP	.797	.891	$\alpha = 1$

- 3. Visualizations of model prediction behavior
 - What is causing the predictions to be so high?
 - Are both class predictions affected by this behavior?

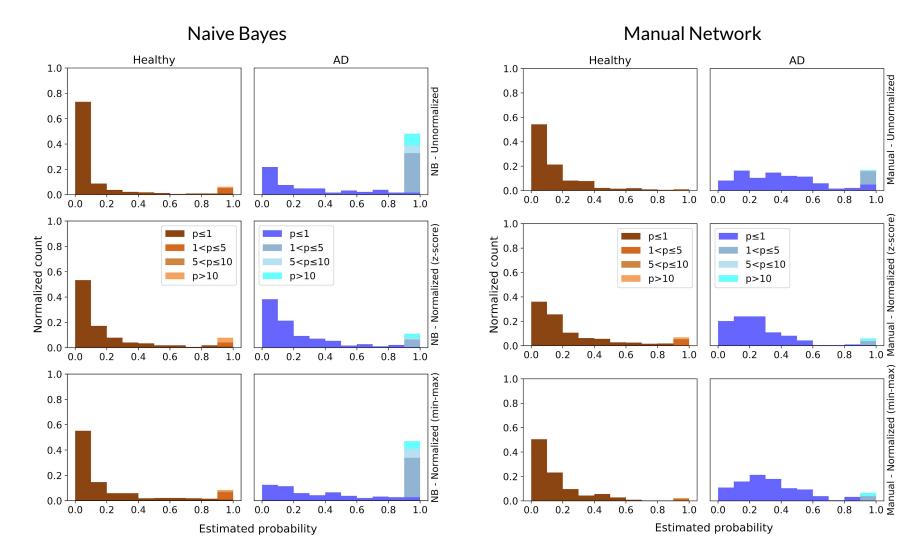
	1	2	5	10	100
NB - Unnormalized	0.724	0.778	0.869	0.918	0.988
NB - Normalized (z-score)	0.876	0.938	0.968	0.976	0.983
NB - Normalized (min-max)	0.711	0.814	0.918	0.965	0.997
Manual - Unnormalized	0.768	0.898	0.978	0.99	1.
Manual - Normalized (z-score)	0.953	0.977	0.986	0.988	0.991
Manual - Normalized (min-max)	0.917	0.976	0.987	0.991	0.997

Proportion of model predictions that are below specified values above (ideally, all predictions would be below 1)



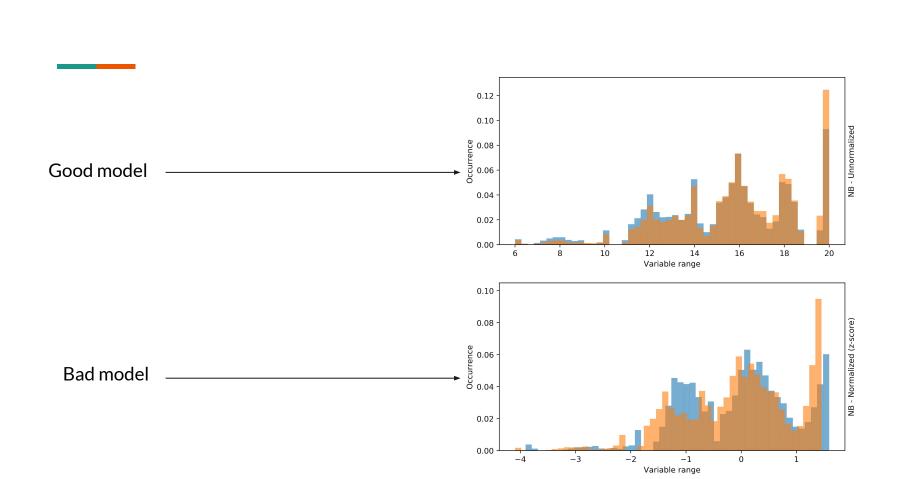






	AGE	PTGENDER	PTMARRY	PTEDUCAT	APOE4	ADAS13	Ventricles	Hippocampus	WholeBrain	Entorhinal	Fusiform	MidTemp
NB - Unnormalized	1.1	1.0	1.0	1.1	1.3	19.9	68.6	10.3	1.1	24.2	1.6	3.2
NB - Normalized (z-score)	1.2	1.0	1.1	877.1	1.3	1.1	3.1	3.7	3.1	1.0	4.2	1.8
NB - Normalized (min-max)	1.1	1.0	1.1	1.1	1.3	28.6	11.4	1.5	1.1	14.4	1.1	1.1
Manual - Unnormalized	1.1	1.0	1.1	1.1	1.3	2.6	1.1	1.3	1.2	1.3	1.1	1.1
Manual - Normalized (z-score)	1.2	1.0	1.1	879.9	1.3	1.1	1.0	1.0	1.0	1.1	1.0	1.0
Manual - Normalized (min-max)	1.1	1.0	1.1	1.1	1.3	1.1	1.1	1.2	1.1	1.2	1.2	1.1

Ratio of corresponding probability terms on the upper and lower hand of the Bayes rule (average value)



Discussion

- Large performance differences depending on type of normalization
 - Normalization should typically not affect results because the probability extraction methods are supposed to be scale invariant
 - Smoothing of empirical variable distributions may have introduced unintended artifacts
 - There is likely an undetermined numerical problem in the z-score normalization
- Models classify AD-CN better than MCI-D
- NB performed similarly to manual models
- Bayesian models slightly worse than generic ML models
 - o nature of the task may not be favoring Bayesian models

Discussion

- Advantages of Bayesian models
 - Designed to deal with uncertainties
 - May prove to be more useful depending on the problem
 - Possible to extend models without data
 - No regularization necessary
- Disadvantages of Bayesian models
 - o (Apparently) not optimal for typical classification tasks
 - o Probability estimations can be unrealistic

Future Directions

- Automatized Bayesian Networks
 - Building a Bayesian network on medical literature is an arduous process
 - Work scales up exponentially as variables increase
 - Conflicting evidence
 - Literature does not necessarily match data
 - Finding optimal Bayesian networks is an NP-complete problem
 - Algorithms exist, which tend to perform better than NB
 - e.g. Tree-augmented Naive Bayes

Future Directions

- How do model predictions relate to time?
- Consider the two questions:
 - "What is the probability for a patient to develop dementia?"
 - "What is the probability for a patient to develop dementia in X years?"
- Extract a new dataset with only MCI patients getting dementia and correlate it with the probability outputs of the Bayesian model

Future Directions

- Expand model with new variables
 - More biological markers, medical and family history
- Large amount of missing data
 - Requires imputation methods

Thank you for listening