

Disease Prediction Using Machine Learning and Electronic Health Records

Narges Razavian

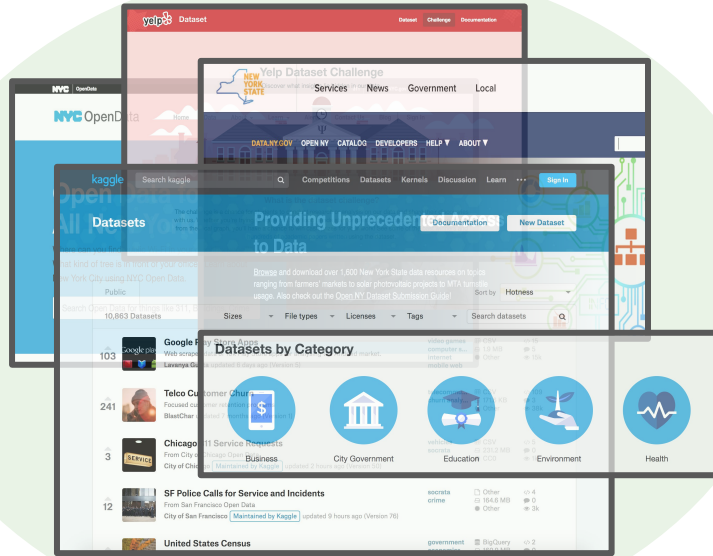
Assistant Professor

NYU Langone Medical Center

Departments of Radiology and Population Health

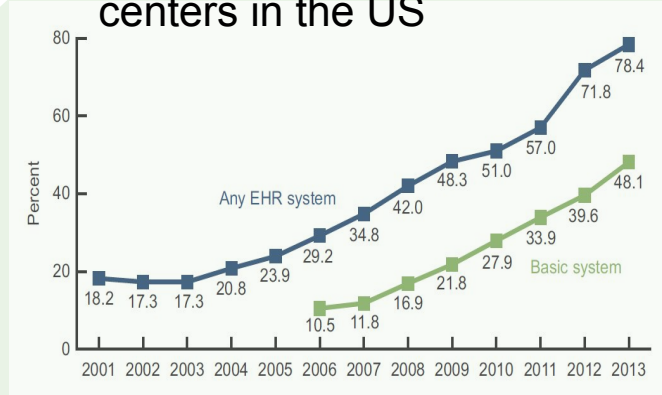


Changing Landscape of Digital Data



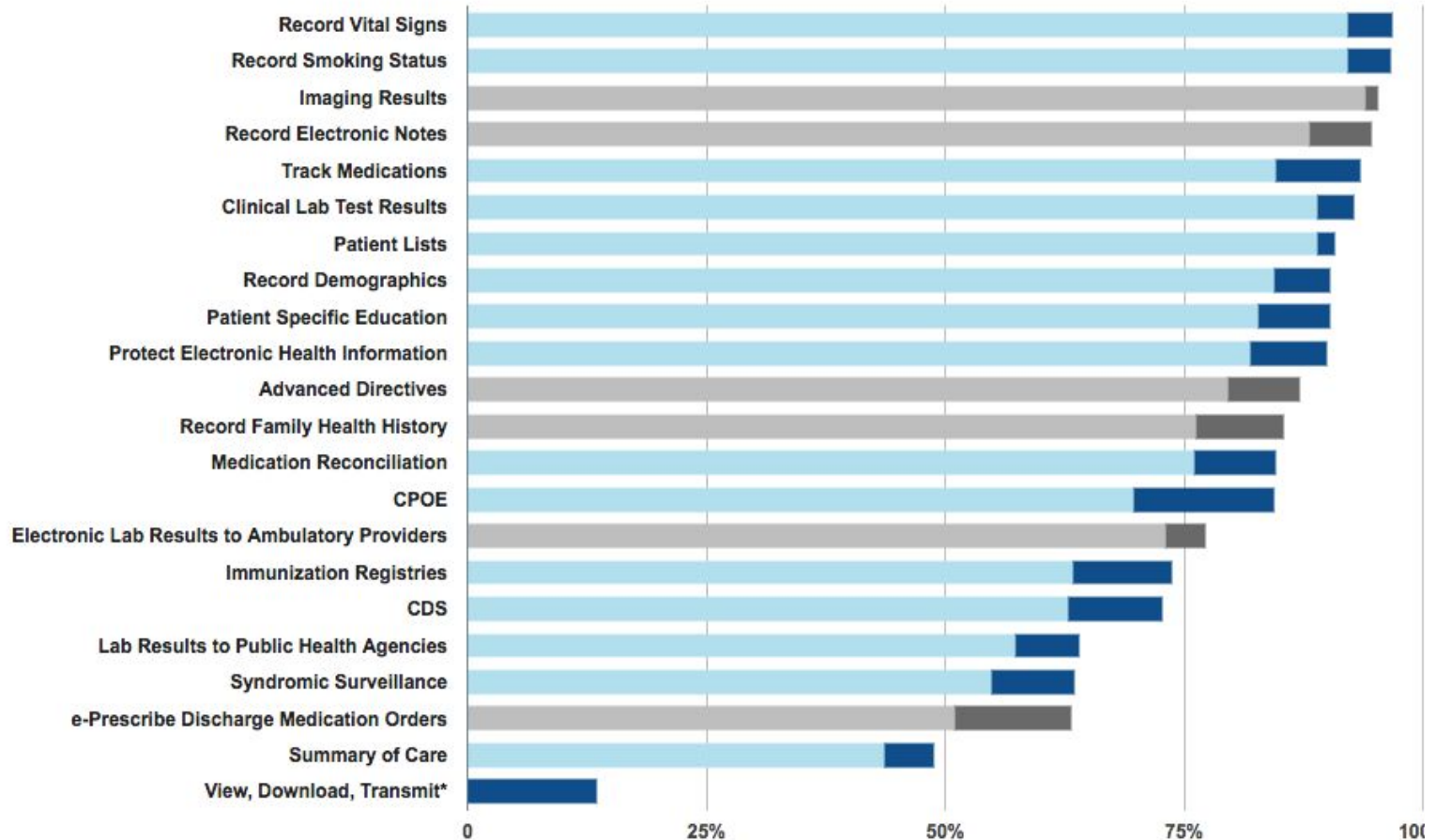
Environment, food,
housing, transportation,
crime, education,
etc. etc.

EHR adoption by healthcare centers in the US

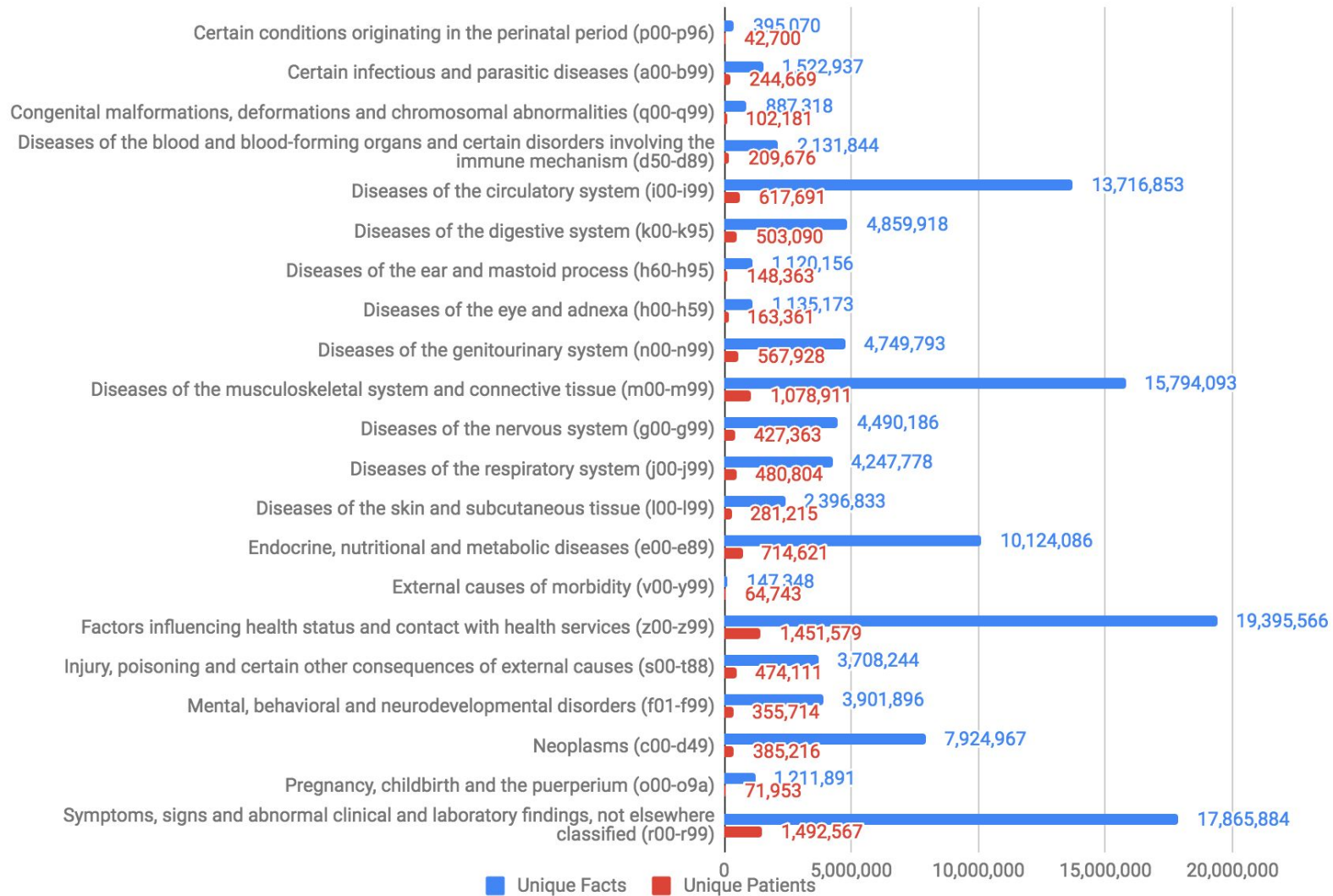


Electronic Health Records
at scale of millions per
year

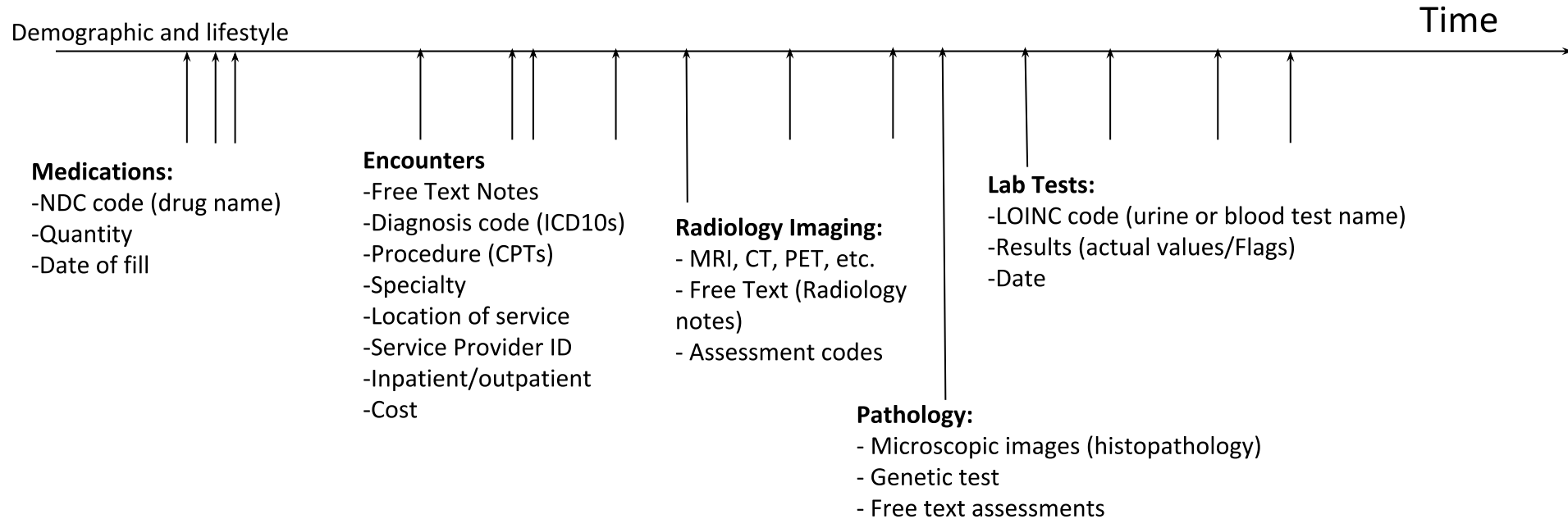
What is captured in the EHR?



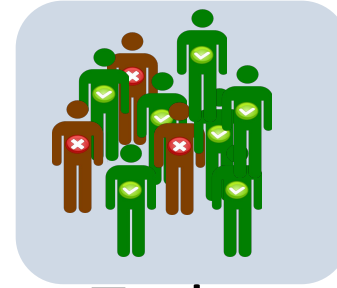
Source: healthcare.gov



Electronic Health Records



Electronic Health Records for future outcome prediction

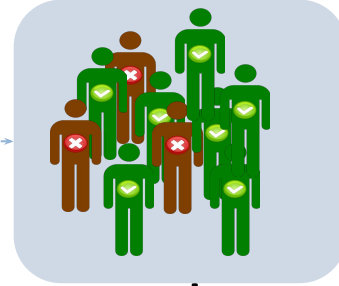


Today

Electronic Health Records for future outcome prediction



A Few Years Ago



Today

Electronic Health Records for future outcome prediction



A Few Years Ago



Today



Demographic and lifestyle

Medications:

- NDC code (drug name)
- Quantity
- Date of fill

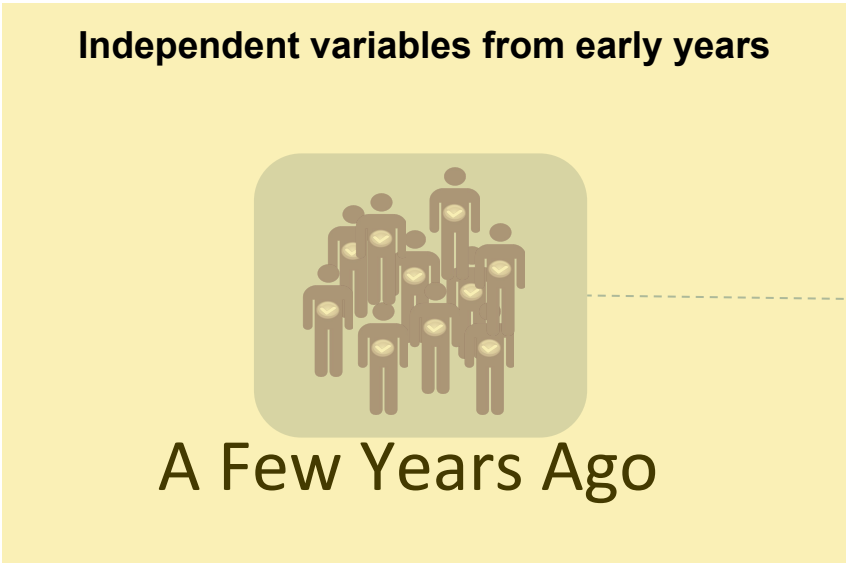
Encounter Records

- Free Text Notes
- ICD9/10 diagnosis code
- CPT code (procedure)
- Specialty
- Location of service
- Service Provider ID
- Inpatient/outpatient
- Cost

Lab Tests:

- LOINC code (urine or blood test name)
- Results (actual values/Flags)
- Date

Electronic Health Records for future outcome prediction




- Medications:**
- NDC code (drug name)
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Electronic Health Records for future outcome prediction

Independent variables from early years



A Few Years Ago

Target outcome in the future



Today



Demographic and lifestyle

Medications:

- NDC code (drug name)
- Quantity
- Date of fill

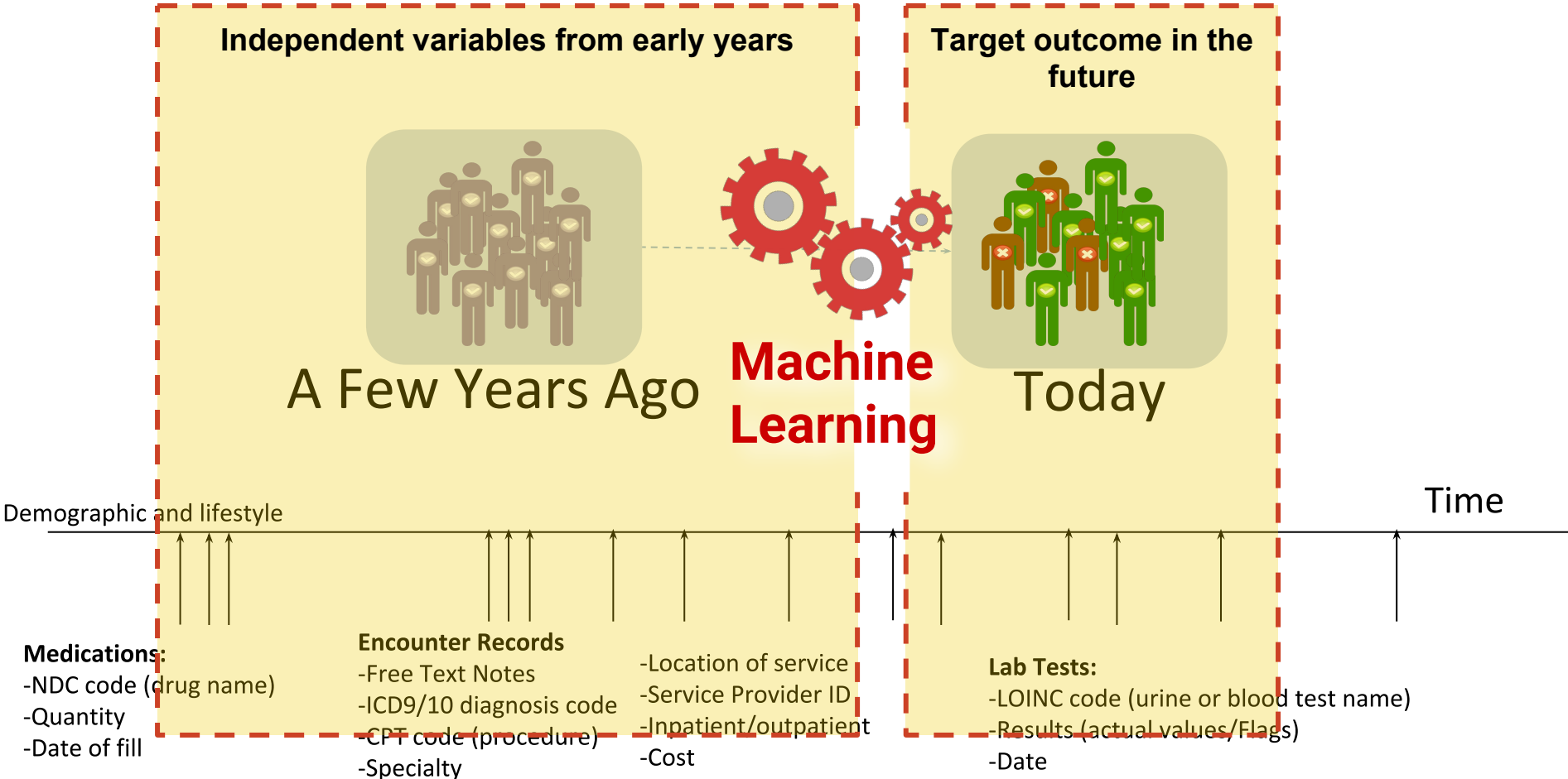
Encounter Records

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Electronic Health Records for future outcome prediction



Challenges:

Multi-modal (Time series, Text, Images)

Biased data

Explanations of model decisions

Challenges:

Multi-modal (Time series, Text, Images)

Biased data

Explanations of model decisions

Using Structured Data for Early Detection

NYU Collaborators

David Sontag

Rahul Krishnan

Uri Shalit

Jake Marcus

YD Choi

Yoni Halpern

NYU Medical School Collaborators

Saul Blecker

Ann Marie Schmidt

Yin Aphinyanaphong

Leora Horwitz

My Students



Anant Gupta

Graduate Student, Courant Institute,
Department of Computer Science, NYU

Research: Deep Learning and Machine
Learning on Electronic Health Records,
Predicting Preventable Diseases



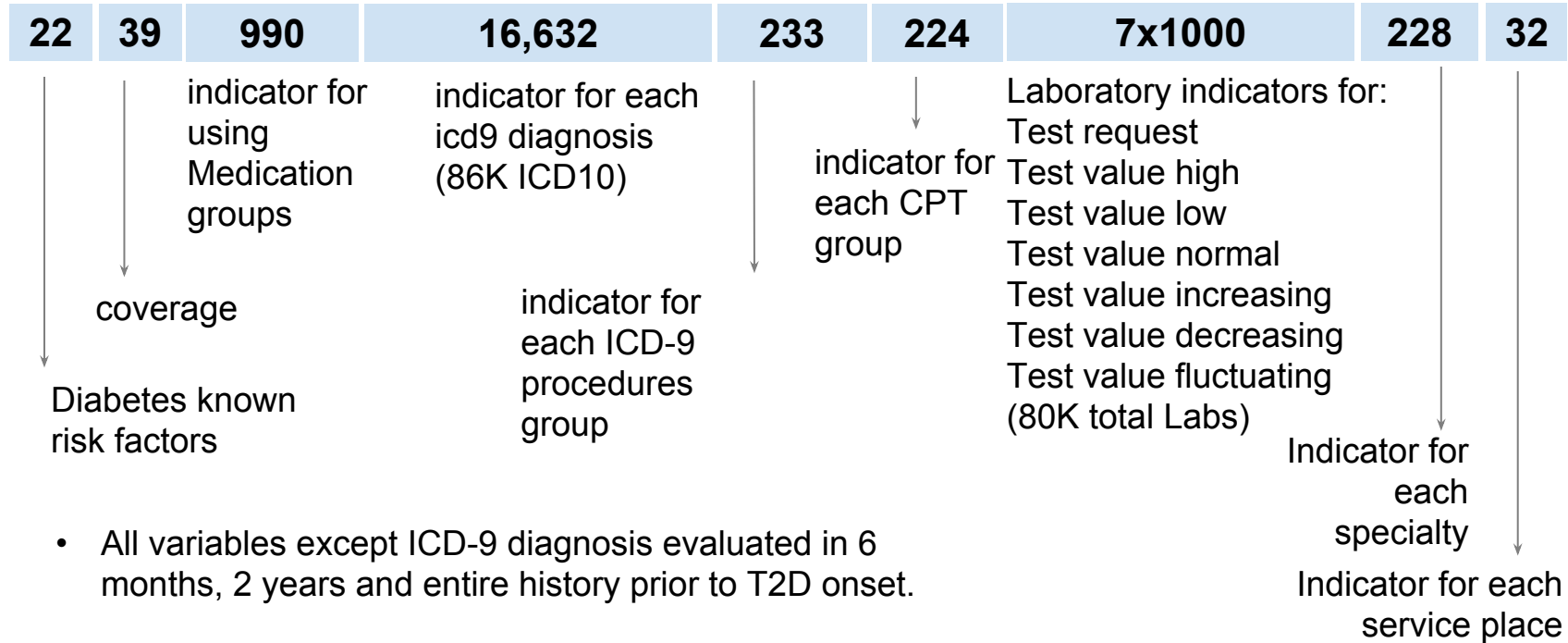
Rob Hammond

Graduate Student, NYU Center for Data
Science

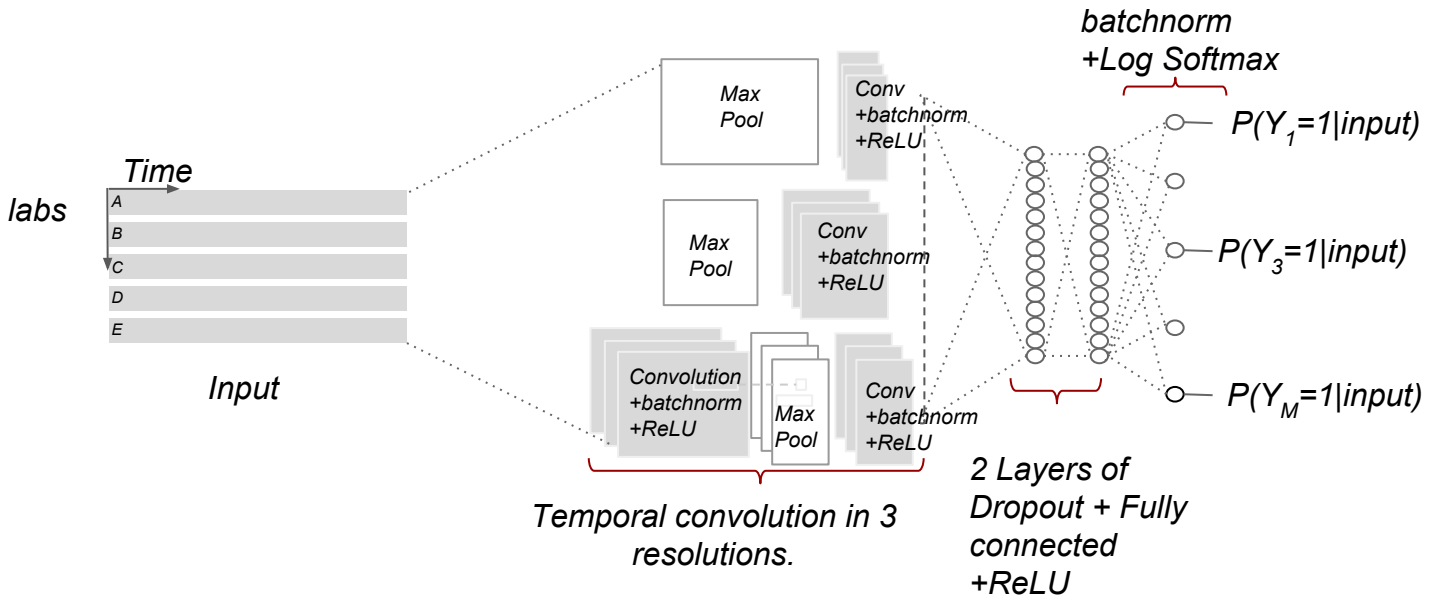
Data Scientist, NYU Langone Medical Center

Research: Machine Learning Models for
Electronic Health Records, Predicting
Childhood Obesity

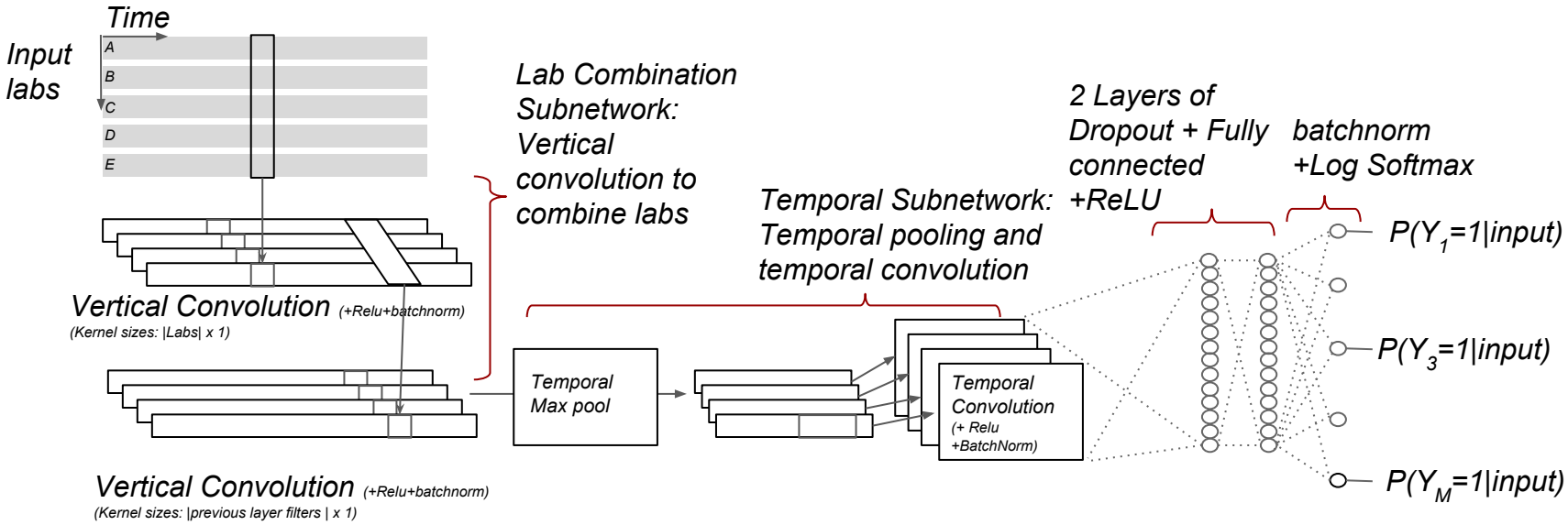
42K variables (before) to 280K variables (now), each across time



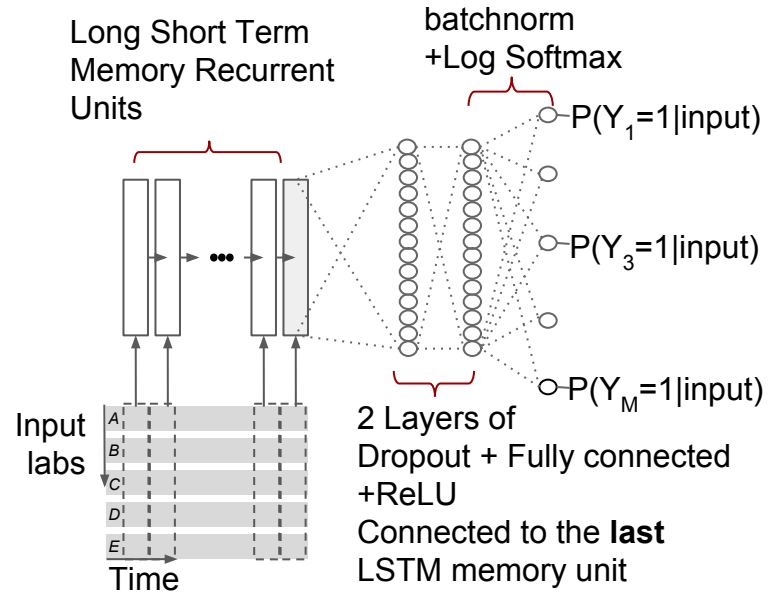
Learning features and Deep Learning/Multitask learning



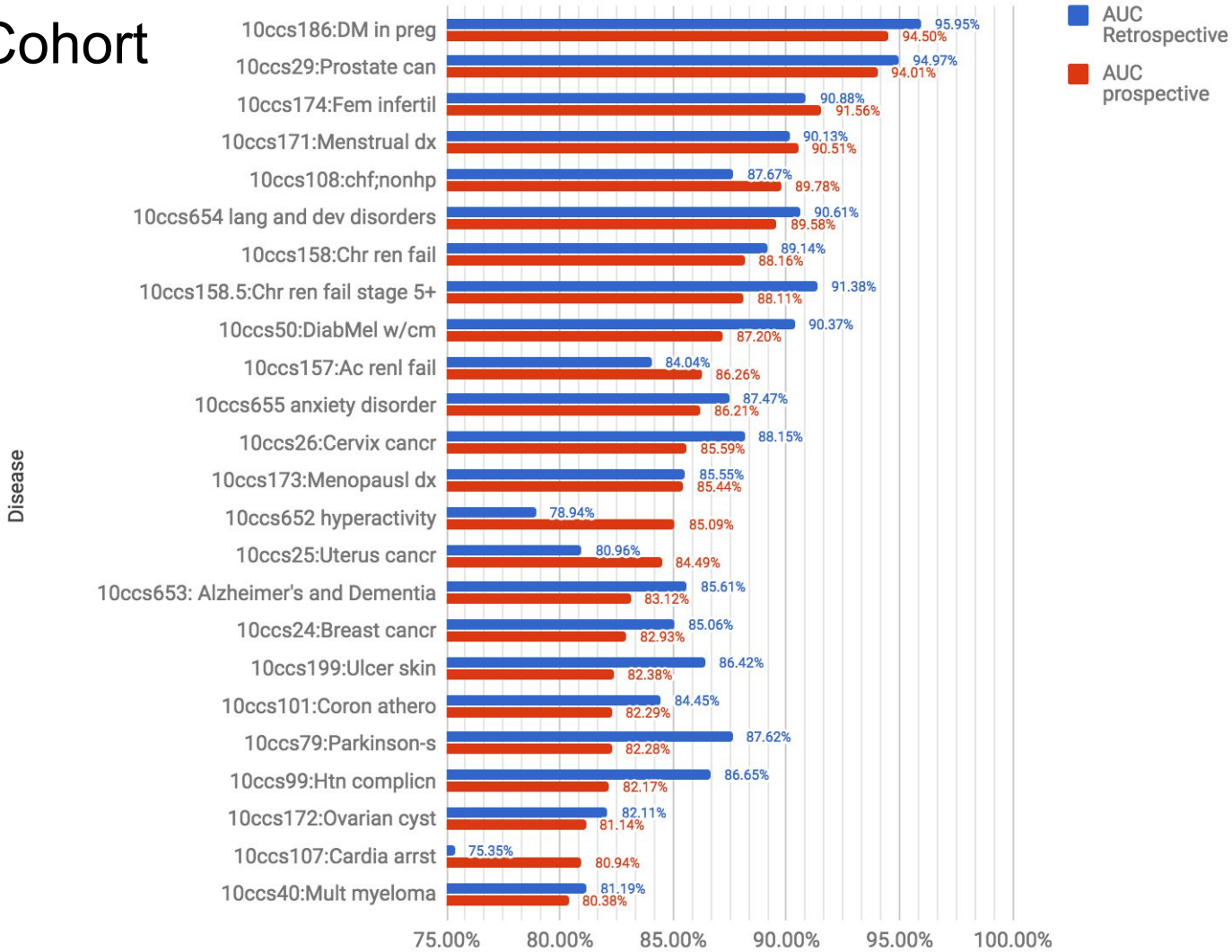
Learning features and Deep Learning/Multitask learning



Learning features and Deep Learning/Multitask learning



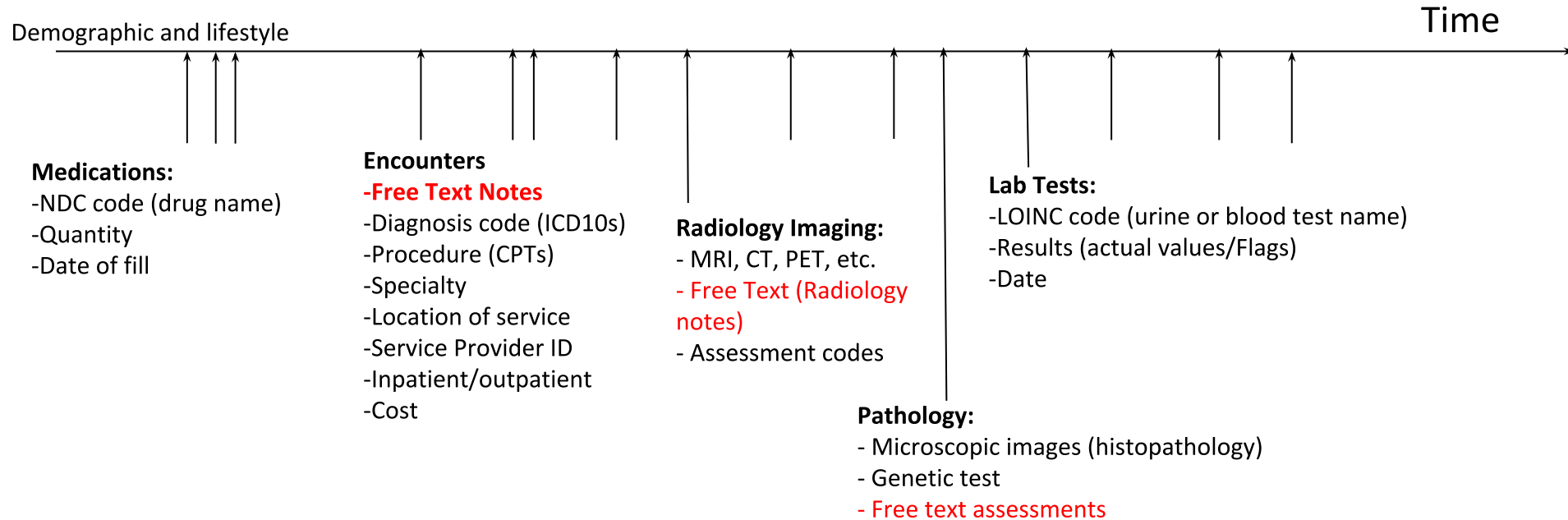
NYUMC Cohort



Applicable to many more outcomes and tasks

- Early prediction of childhood obesity
- Using environmental factors to predict childhood obesity
- Predicting diabetes and diabetes complications
- Detecting undocumented but existing diseases (all diseases)
- Using lab values only to predict future diseases
- Predicting medication adherence
- Predicting appointment no-shows
- etc. etc. etc....

How to handle *Clinical Notes*?



Using AI + Clinical Notes for Early Detection



Jingshu Liu

Graduate Student, NYU Department of
Computer Science

Research: Deep Learning and Natural
Language Processing for Clinical Notes



Zachariah Zhang

Graduate Student, NYU Center for Data
Science

Research: Deep Learning and Natural
Language Processing for Clinical Notes



Sheng Liu

Graduate Student, NYU Center for Data
Science

Research: Deep Learning and Natural
Language Processing for Clinical Notes on
ICU data

NYU Collaborators

Kyunghyun Cho
Sam Bowman

NYU Medical School Collaborators

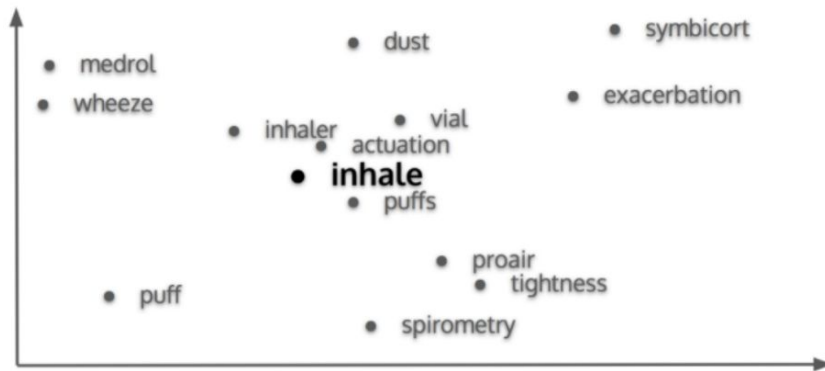
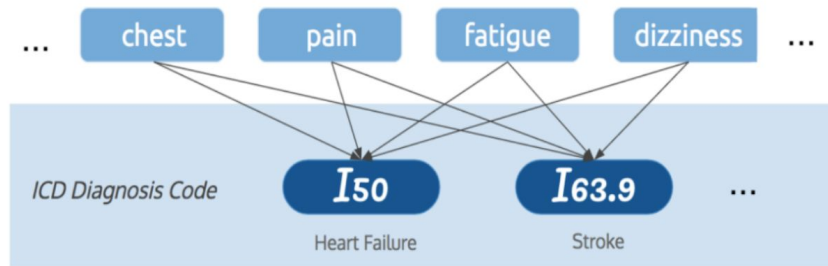
Yin Aphinyanaphong
Leora Horwitz
Himanshu Grover
Jerko Steiner
Marina Marin

Clinical Notes: Abbreviated, Messy, Unstructured, *not* English, not grammatical, not intended to be.

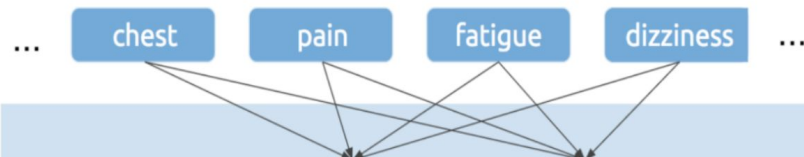
An example of a real note - de-identified:

Patient received via stretcher from ED in NAD. Ambulated without any difficulties. Patient states that he is due for Fentanyl lollipop 600mcg at 1800. PA [**Last Name (un) 1**] made aware of patient's arrival and pain meds. To assess patient at bedside. Handoff given to RN. Patient sleeping comfortably in bed in NAD. Call bell within reach. Safety maintained. Patient off the floor to xray. Patient stable. Handoff report given by [**Name8 (MD) 1**], RN. IV fluids running well. Patient is resting comfortably at this assessment. Call bell within reach. The care of this patient has transferred to PA [**Last Name (un) 1**]. Current disposition: placed in observation. At this time, the care of this patient was transferred to the Emergency Medicine service for ED observation. Reassessment Vital Signs: [**2016-04-29**] 1457 BP: 120/80 Pulse : 75 Temp: 36.2 ?C (97.2 ?F) Resp: 15 SpO2: 100% Temp (24hrs) Max:36.8 ?C (98.3 ?F) Pain Score: 8 - Eight [**First Name8 (NamePattern2) 2**] [**Last Name (NamePattern1) 3**] is a 37 y. o. male placed in observation under the Abdominal Pain Protocol. Pertinent results: Upper GI Series/Abd XR with contrast into the small bowel Please follow-up on: Follow-up abd XR at 8pm to eval for contrast into the rectum Plan of care in the observation unit: serial abdominal exams, advancement of diet, repeat abdominal XR

Learning Semantics First - *Learning Embeddings*

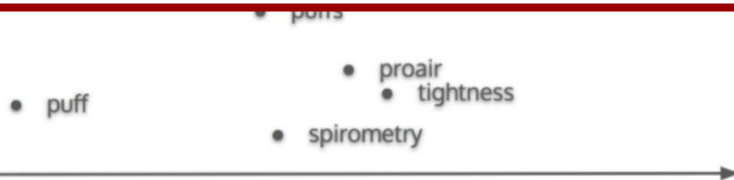


Learning Semantics First - *Learning Embeddings*

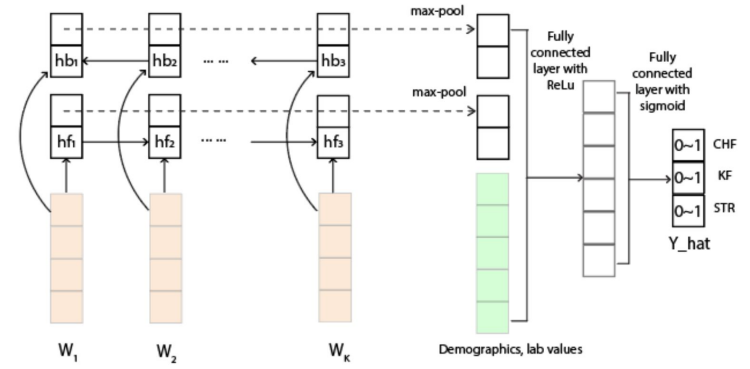
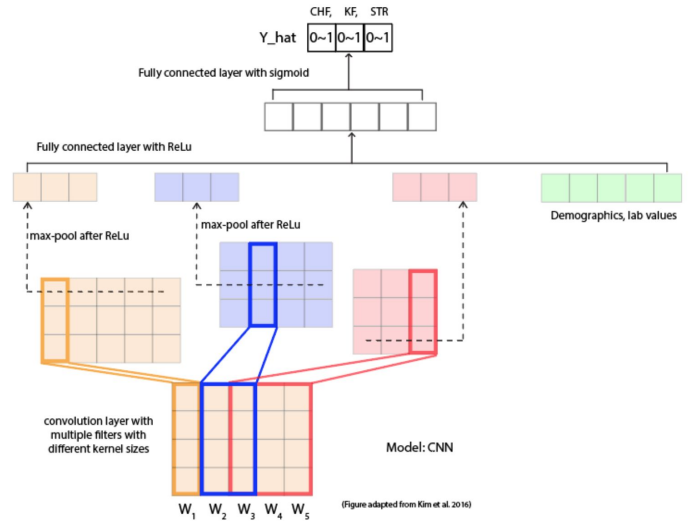


All code & instructions and *trained embeddings* for
24,960 clinical terms:

<https://github.com/NYUMedML/DeepEHR>
(Fully open-sourced)



Extracting Structured Data from the Notes & Combining with Text Data



Dealing with Time

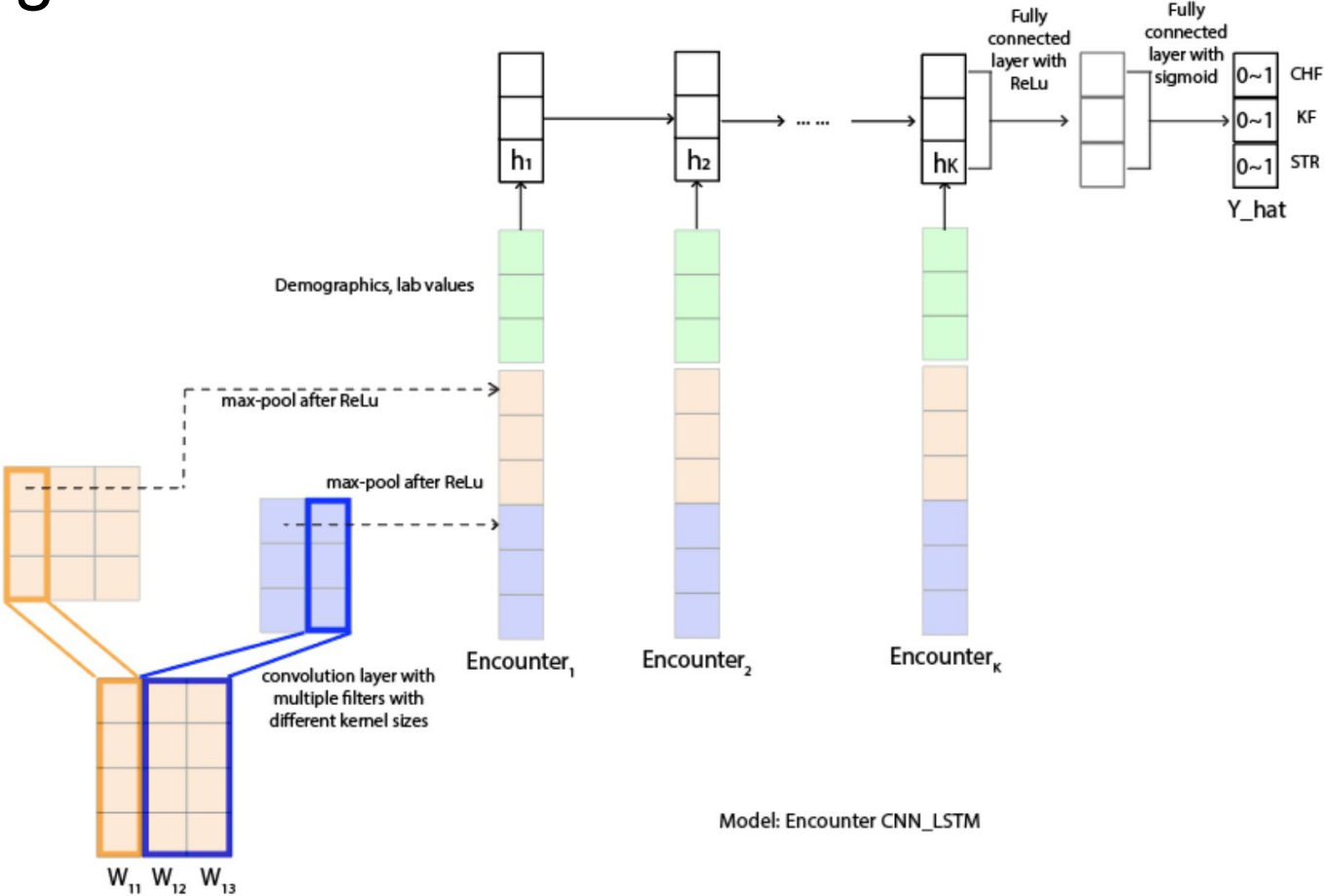
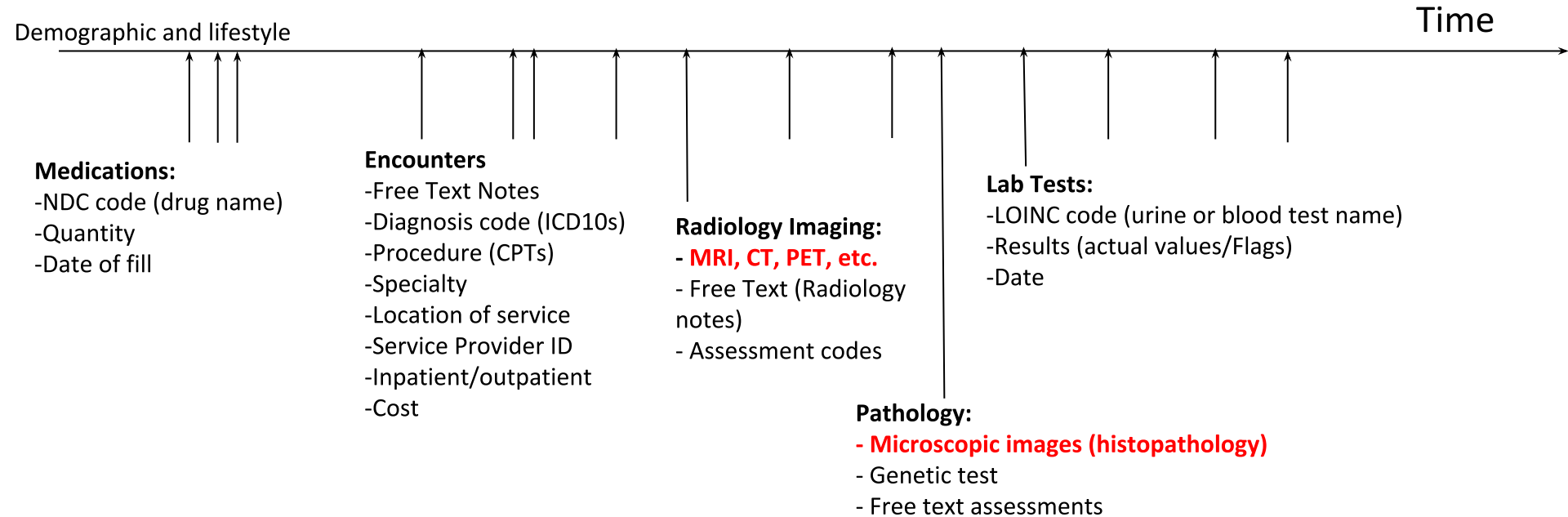


Table 1: Number of Records by Target Diseases (Negative Cases : Positive Cases)

Target	Training Set	Validation Set	Test Set
Congestive Heart Failure	644K : 4080	93K : 574	184K : 1167
Kidney Failure	616K : 10051	88K : 1428	176K : 2809
Stroke	653K : 3195	94K : 406	187K : 916

	Heart Failure	Kidney Failure	Stroke
Logistic Reg Lab/Demo	0.781	0.724	0.70
LSTM Lab/Demo	0.813	0.743	0.699
Logistic Reg Notes	0.810	0.752	0.708
CNN PubMed Embeddings	0.844	0.799	0.711
CNN Single Task	0.847	0.796	0.706
CNN	0.854	0.802	0.714
CNN + Neg Tag	0.867	0.811	0.727
CNN + Neg Tag + Dense	0.880	0.812	0.733
CNN + Neg Tag + Dense + Lab/Demo	0.893	0.822	0.749
BiLSTM	0.869	0.807	0.738
BiLSTM + Neg Tag	0.875	0.811	0.745
BiLSTM + Neg Tag + Dense	0.892	0.823	0.739
BiLSTM + Neg Tag + Dense + Lab/Demo	0.900	0.833	0.753
Enc CNN-LSTM	0.859	0.797	0.727
Enc CNN-LSTM + Lab/Demo	0.885	0.812	0.740

How to handle images?



Using Histopathology Images for Lung Cancer subtype and mutation detection



Nicolas Coudray

Image Analysis Specialist, Applied
Bioinformatics Laboratories, NYU Lagnone
Medical Center

Research: Deep Learning for Histopathology
and Medical Imaging



Shaivi Kochar

Graduate Student, NYU Tandon School of
Engineering

Research: Visualization of Deep Learning
Models and Generative Adversarial Networks
for Histopathology Models



Xianzhi (Viola) Cao

Graduate Student, NYU Center for Data
Science

Research: Deep Learning and Natural
Language Processing for Clinical Notes

NYU Medical School Collaborators

Aristotelis Tsirigos

David Fenyo

Paulo Ocampo

Matija Snuderl

Classification and mutation prediction from non–small cell lung cancer histopathology images using deep learning <https://www.nature.com/articles/s41591-018-0177-5>

MENU ▾

nature
medicine

Article | Published: 17 September 2018

Classification and mutation prediction from non–small cell lung cancer histopathology images using deep learning

Nicolas Coudray, Paolo Santiago Ocampo, Theodore Sakellaropoulos, Navneet Narula, Matija Snuderl, David Fenyő, Andre L. Moreira, Narges Razavian ✉ & Aristotelis Tsirigos ✉

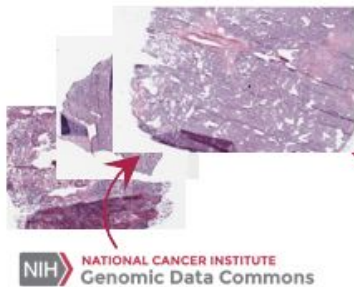
Nature Medicine **24**, 1559–1567 (2018) | [Download Citation](#) ↓

Abstract

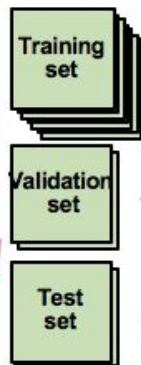
Visual inspection of histopathology slides is one of the main methods used by pathologists to assess the stage, type and subtype of lung

Our Approach

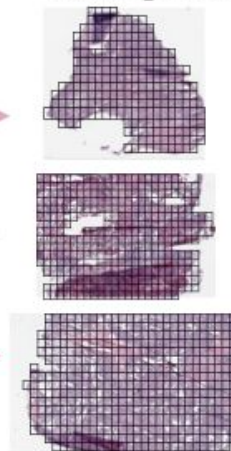
d1 Download from GDC database



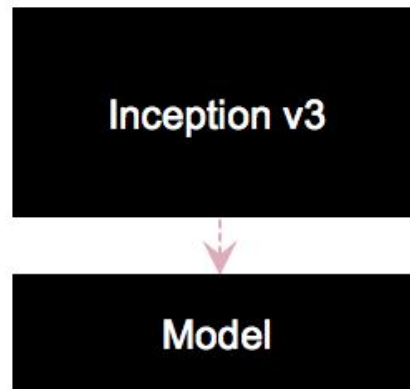
d2 Separate in 3 datasets



d3 Tile and filter out background tiles



d4 Per-tile training



d5 Testing and per-slide tile aggregation



Results

AUC after aggregation by...

Classification	Information	AUC after aggregation by...	
		... average predicted probability	... percentage of positively classified tiles
Normal vs Tumor (20x tiles)	a) Inception v3, fully-trained	0.993 [0.974-1.000]	0.990 [0.969-1.000]
	b) Inception v3, transfer learning	0.847 [0.782-0.906]	0.844 [0.777-0.904]
LUAD vs LUSC (20x tiles)	c) Inception v3, fully-trained	0.950 [0.913-0.980]	0.947 [0.911-0.978]
	d) Same as (c) but aggregation done solely on tiles classified as "tumor" by A	0.952 [0.915-0.981]	0.949 [0.912-0.980]
LUAD vs LUSC (5x tiles)	Inception v3, fully-trained	0.942 [0.907-0.971]	0.906 [0.851-0.951]
	Normal	0.984 [0.947-1.000]	0.985 [0.953-1.000]
3 classes. Normal vs LUAD vs LUSC at 20x	LUAD	0.969 [0.933-0.994]	0.970 [0.937-0.993]
	LUSC	0.966 [0.935-0.990]	0.964 [0.932-0.989]
	Micro-average	0.970 [0.950-0.986]	0.969 [0.949-0.985]
	Macro-average	0.976 [0.949-0.993]	0.976 [0.950-0.993]
3 classes. Normal vs LUAD vs LUSC at 5x	Normal	0.997 [0.993-0.998]	0.988 [0.962-1.000]
	LUAD	0.965 [0.942-0.983]	0.938 [0.896-0.971]
	LUSC	0.977 [0.960-0.991]	0.964 [0.937-0.986]
	Micro-average	0.980 [0.972-0.987]	0.966 [0.948-0.980]
	Macro-average	0.981 [0.968-0.991]	0.964 [0.939-0.980]

n=244 slides for LUAD vs LUSC classifiers and n=170 slides for the others, all from 137 patients.

Predicting gene mutational status from whole-slide images

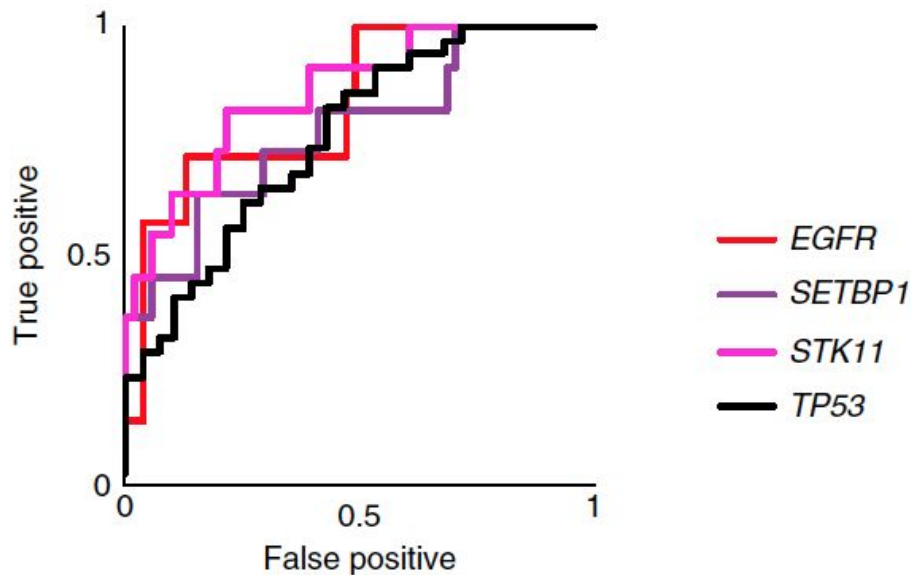


Table 1 | AUC achieved by the network trained on mutations (with 95% CIs)

Mutations	Per-tile AUC	Per-slide AUC after aggregation by...	
		... average predicted probability	... percentage of positively classified tiles
<i>STK11</i>	0.845 (0.838-0.852)	0.856 (0.709-0.964)	0.842 (0.683-0.967)
<i>EGFR</i>	0.754 (0.746-0.761)	0.826 (0.628-0.979)	0.782 (0.516-0.979)
<i>SETBP1</i>	0.785 (0.776-0.794)	0.775 (0.595-0.931)	0.752 (0.550-0.927)
<i>TP53</i>	0.674 (0.666-0.681)	0.760 (0.626-0.872)	0.754 (0.627-0.870)
<i>FAT1</i>	0.739 (0.732-0.746)	0.750 (0.512-0.940)	0.750 (0.491-0.946)
<i>KRAS</i>	0.814 (0.807-0.829)	0.733 (0.580-0.857)	0.716 (0.552-0.854)
<i>KEAP1</i>	0.684 (0.670-0.694)	0.675 (0.466-0.865)	0.659 (0.440-0.856)
<i>LRP1B</i>	0.640 (0.633-0.647)	0.656 (0.513-0.797)	0.657 (0.512-0.799)
<i>FAT4</i>	0.768 (0.760-0.775)	0.642 (0.470-0.799)	0.640 (0.440-0.856)
<i>NF1</i>	0.714 (0.704-0.723)	0.640 (0.419-0.845)	0.632 (0.405-0.845)

n = 62 slides from 59 patients.

Predicting gene mutational status from whole-slide images

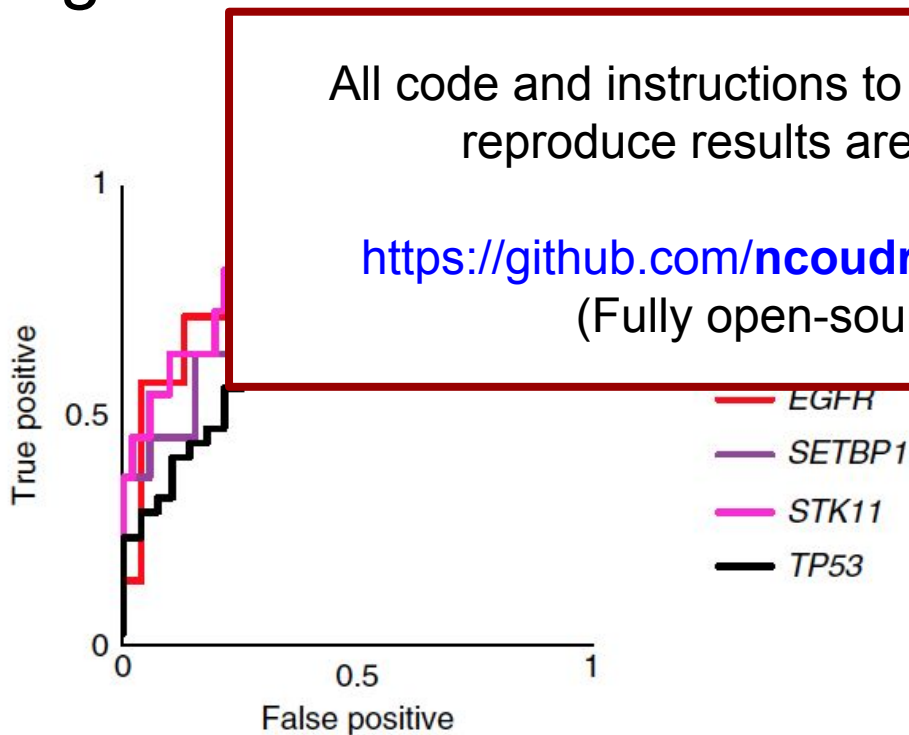


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			8- 0.782 (0.516-0.979)
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	0.723)	0.845)	

n = 62 slides from 59 patients.

Implications and Summary

- AI can fundamentally change how we
 - Screen for Conditions
 - Generate hypotheses
 - Recruit for clinical trials
 - Develop treatments
- Many many supervised learning tasks for next few years
 - Predicting *current* and *future* diseases
 - Predicting from Time series, Text and Images and Between them to save time/costs
- *Deployment and workflow changes* remain challenging

Thank you
Questions and Comments:
narges.razavian@nyumc.org

<https://github.com/ncoudray/DeepPATH>

<https://github.com/NYUMedML/DeepEHR>