Lecture 6: Electronic Health Records (Part 2)
Announcements

Upcoming deadlines:

- A1 due Tue 10/18
- Project proposal due Fri 10/21
  - Remember that you must **train** a deep learning model somewhere in your project!
- Project partner finding session during review section this Friday, 1:30pm, Alway M106
Agenda for today

- Finishing up from last time: RNN (LSTM) models for EHR prediction tasks
- More on EHR data
- More on feature representations
- A first look at model interpretability: soft attention
Last time: overview of electronic health records

Patient chart in digital form, containing medical and treatment history.

At 24 hours after admission, predicted risk of inpatient mortality: 19.9%. Patient dies 10 days later.

Figure credit: Rajkomar et al. 2018
A real example of EHR data: MIMIC-III dataset

Examples of prediction tasks

**In-hospital mortality**

<table>
<thead>
<tr>
<th></th>
<th>Train</th>
<th>Test</th>
</tr>
</thead>
<tbody>
<tr>
<td>Negative</td>
<td>15480</td>
<td>2862</td>
</tr>
<tr>
<td>Positive</td>
<td>2423</td>
<td>374</td>
</tr>
</tbody>
</table>

Beginning of the ICU stay 48 hours → End of the ICU stay

**Decompensation**

<table>
<thead>
<tr>
<th></th>
<th>Train</th>
<th>Test</th>
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</thead>
<tbody>
<tr>
<td>Negative</td>
<td>2847401</td>
<td>513525</td>
</tr>
<tr>
<td>Positive</td>
<td>61013</td>
<td>9683</td>
</tr>
</tbody>
</table>

Beginning of the ICU stay → The moment the patient died → End of the ICU stay

24 hours

**Phenotypes**

<table>
<thead>
<tr>
<th></th>
<th>Train</th>
<th>Test</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>35621</td>
<td>6281</td>
</tr>
</tbody>
</table>

Beginning of the ICU stay → 25 phenotypes → End of the ICU stay

**Length-of-stay**

<table>
<thead>
<tr>
<th></th>
<th>Train</th>
<th>Test</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2925434</td>
<td>525912</td>
</tr>
</tbody>
</table>

Beginning of the ICU stay → remaining length of stay → End of the ICU stay

Harutyunyan et al. 2019
Remember: “vanilla” neural networks for predictions from clinical variables

Let us consider the task of **regression**: predicting a single real-valued output from input data

**Model input**: data vector $\mathbf{x} = [x_1, x_2, \ldots, x_N]$  
**Model output**: prediction (single number) $\hat{y}$

Example: predicting hospital length-of-stay from clinical variables in the electronic health record

$x = [\text{age, weight, …, temperature, oxygen saturation}]$  
$\hat{y} = \text{length-of-stay (days)}$
We can process a sequence of vectors $\mathbf{x}$ by applying a **recurrence formula** at every time step:

$$
\mathbf{h}_t = f_W(\mathbf{h}_{t-1}, \mathbf{x}_t)
$$

- New state
- Old state
- Input vector at some time step
- Some function with parameters $W$

**Slide credit:** CS231n
Long Short Term Memory (LSTM) Recurrent Networks

Unrolled Vanilla RNN

\[ h_t = \tanh(W_{hh}h_{t-1} + W_{xh}x_t) \]

\[ y_t = W_{hy}h_t \]

Unrolled LSTM

Different computation to obtain \( h_t \)

Figure credit: https://colah.github.io/posts/2015-08-Understanding-LSTMs/
Harutyunyan et al.

- Benchmarked LSTMs vs logistic regression on common prediction tasks using MIMIC-III data
- In-hospital mortality, decompensation, length-of-stay, phenotype classification
- Used a subset of 17 clinical variables from MIMIC-III

<table>
<thead>
<tr>
<th>Variable</th>
<th>MIMIC-III table</th>
<th>Impute value</th>
<th>Modeled as</th>
</tr>
</thead>
<tbody>
<tr>
<td>Capillary refill rate</td>
<td>chartevents</td>
<td>0.0</td>
<td>categorical</td>
</tr>
<tr>
<td>Diastolic blood pressure</td>
<td>chartevents</td>
<td>59.0</td>
<td>continuous</td>
</tr>
<tr>
<td>Fraction inspired oxygen</td>
<td>chartevents</td>
<td>0.21</td>
<td>continuous</td>
</tr>
<tr>
<td>Glasgow coma scale eye opening</td>
<td>chartevents</td>
<td>4 spontaneously</td>
<td>categorical</td>
</tr>
<tr>
<td>Glasgow coma scale motor response</td>
<td>chartevents</td>
<td>6 obeys commands</td>
<td>categorical</td>
</tr>
<tr>
<td>Glasgow coma scale total</td>
<td>chartevents</td>
<td>15</td>
<td>categorical</td>
</tr>
<tr>
<td>Glasgow coma scale verbal response</td>
<td>chartevents</td>
<td>5 oriented</td>
<td>categorical</td>
</tr>
<tr>
<td>Glucose</td>
<td>chartevents, labevents</td>
<td>128.0</td>
<td>continuous</td>
</tr>
<tr>
<td>Heart Rate</td>
<td>chartevents</td>
<td>86</td>
<td>continuous</td>
</tr>
<tr>
<td>Height</td>
<td>chartevents</td>
<td>170.0</td>
<td>continuous</td>
</tr>
<tr>
<td>Mean blood pressure</td>
<td>chartevents</td>
<td>77.0</td>
<td>continuous</td>
</tr>
<tr>
<td>Oxygen saturation</td>
<td>chartevents, labevents</td>
<td>98.0</td>
<td>continuous</td>
</tr>
<tr>
<td>Respiratory rate</td>
<td>chartevents</td>
<td>19</td>
<td>continuous</td>
</tr>
<tr>
<td>Systolic blood pressure</td>
<td>chartevents</td>
<td>118.0</td>
<td>continuous</td>
</tr>
<tr>
<td>Temperature</td>
<td>chartevents</td>
<td>36.6</td>
<td>continuous</td>
</tr>
<tr>
<td>Weight</td>
<td>chartevents</td>
<td>81.0</td>
<td>continuous</td>
</tr>
<tr>
<td>pH</td>
<td>chartevents, labevents</td>
<td>7.4</td>
<td>continuous</td>
</tr>
</tbody>
</table>

- **Logistic regression models**
  - Use hand-engineered feature vector to represent a time-series: min, max, mean, std dev, etc. of each feature in several subsequences (full series, first 10% of series, first 50%, last 10%, etc.)
  - If feature does not occur in subsequence (missing data), impute with mean value from training set
  - Categorical variables had meaningful numeric values -> no change
  - Zero-mean unit-variance standardization of all features
- **LSTM models**
  - Bucket time series into regularly spaced intervals, take the value (or last value, if multiple) of each variable in the interval to create observation $x_t$
  - Encode categorical variables using a one-hot vector (vector of 0s with a 1 in the observed position).
  - If variable is missing in a time bucket, impute using most recent observed measurement if it exists, and mean value from training set otherwise
  - Concat the values of each clinical variable with a binary mask indicating presence or not (i.e., missing and needed to impute) to form full observation feature vector $x_t$

Harutyunyan et al.: logistic regression vs LSTMs

Found better performance overall for LSTMs (S) vs logistic regression (LR). Also introduced more sophisticated variants and multi-task training (joint training of all tasks together).

<table>
<thead>
<tr>
<th>Model</th>
<th>AUC-ROC</th>
</tr>
</thead>
<tbody>
<tr>
<td>SAPS</td>
<td>0.720 (0.720, 0.720)</td>
</tr>
<tr>
<td>APS-III</td>
<td>0.750 (0.750, 0.750)</td>
</tr>
<tr>
<td>OASIS</td>
<td>0.760 (0.760, 0.761)</td>
</tr>
<tr>
<td>SAPS-II</td>
<td>0.777 (0.776, 0.777)</td>
</tr>
<tr>
<td>LR</td>
<td>0.848 (0.828, 0.868)</td>
</tr>
<tr>
<td>S</td>
<td>0.855 (0.835, 0.873)</td>
</tr>
<tr>
<td>S + DS</td>
<td>0.856 (0.836, 0.875)</td>
</tr>
<tr>
<td>C</td>
<td>0.862 (0.844, 0.881)</td>
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<tr>
<td>C + DS</td>
<td>0.854 (0.834, 0.873)</td>
</tr>
<tr>
<td>MS</td>
<td>0.861 (0.842, 0.878)</td>
</tr>
<tr>
<td>MC</td>
<td>0.870 (0.852, 0.887)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Model</th>
<th>Macro AUC-ROC</th>
</tr>
</thead>
<tbody>
<tr>
<td>LR</td>
<td>0.739 (0.734, 0.743)</td>
</tr>
<tr>
<td>S</td>
<td>0.770 (0.766, 0.775)</td>
</tr>
<tr>
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LR – logistic regression
S – standard LSTM
C – channel-wise LSTM
MS – multitask standard LSTM
DS – deep supervision
MC – multitask channel-wise LSTM

Figure credit: Harutyunyan et al. Multitask learning and benchmarking with clinical time series data. 2019.
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Figure credit: Harutyunyan et al. Multitask learning and benchmarking with clinical time series data. 2019.
Recall: Harutyunyan et al. imputed missing data

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More on missing data

A common problem with clinical variable data

- Missing completely at random (MCAR)
  - Missingness does not depend on the missing variable or on other variables
  - Ex: A portion of patient pain surveys (producing variable of patient pain level) are randomly lost or unreadable

- Missing at random (MAR)
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  - Ex: Male patients are less likely to complete patient pain surveys

- Missing not at random (MNAR)
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  - Ex: Patients with higher pain levels are less likely to complete patient pain surveys
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MNAR highest degree of bias / most challenging to accurately impute. Analysis of how well imputation methods work for MCAR / MAR / MNAR cases beyond the scope of this course -> just know that these are missingness characteristics that can make accurate imputation more or less challenging.
Strategies to impute data

- Simplest approaches:
  - Delete records with missing data
  - Fixed imputation of missing values with mean, median, previous value, interpolation, etc.
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- More sophisticated approaches:
  - K-nearest neighbors (impute based on feature value of k closest neighbors determined through non-missing values)
  - Predicting missing values (single imputation): Train regression or classification models to predict missing values based on other variables
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- An ongoing active area of research:
  - Methods incorporating deep learning generative models, etc.
Example of imputation through prediction in the widely used MICE Algorithm

Red = missing values across features A,B,C

van Burren, 2011. Figure credit: https://cran.r-project.org/web/packages/miceRanger/vignettes/miceAlgorithm.html
Example of imputation through prediction in the widely used MICE Algorithm

Fill in missing entries with initial values
(random, means, randomly drawn from distribution, etc.)

\(^1\)van Burren, 2011. Figure credit: https://cran.r-project.org/web/packages/miceRanger/vignettes/miceAlgorithm.html
Example of imputation through prediction in the widely used MICE Algorithm\(^1\)

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.93</td>
<td>1.40</td>
<td>1.53</td>
</tr>
<tr>
<td>0.24</td>
<td>0.46</td>
<td>0.76</td>
</tr>
<tr>
<td>0.95</td>
<td>1.24</td>
<td>1.46</td>
</tr>
<tr>
<td>0.23</td>
<td>0.57</td>
<td>1.28</td>
</tr>
<tr>
<td>0.90</td>
<td>1.28</td>
<td></td>
</tr>
<tr>
<td>0.15</td>
<td>0.63</td>
<td></td>
</tr>
<tr>
<td>0.47</td>
<td>1.14</td>
<td>1.45</td>
</tr>
</tbody>
</table>

Update missing values for feature A using regression model trained on all values (including red) of other features

---

\(^1\)van Burren, 2011. Figure credit: https://cran.r-project.org/web/packages/miceRanger/vignettes/miceAlgorithm.html
Example of imputation through prediction in the widely used MICE Algorithm\(^1\)

Update missing values for feature B using regression model trained on all values (including red and updated/yellow) of other features

\(^1\)van Burren, 2011. Figure credit: https://cran.r-project.org/web/packages/miceRanger/vignettes/miceAlgorithm.html
Example of imputation through prediction in the widely used MICE Algorithm

In this example, features A and B are known to be strongly correlated. See correlation including imputed values improve over updates.

\[ R^2 = 0.9345 \]

\[ R^2 = 0.4106 \]

\[ R^2 = 0.9311 \]

\[ R^2 = 0.8771 \]

\(^1\text{van Burren, 2011. Figure credit: https://cran.r-project.org/web/packages/miceRanger/vignettes/miceAlgorithm.html}\)
Example of imputation through prediction in the widely used MICE Algorithm\(^1\)

\begin{center}
\begin{tabular}{|c|c|c|}
\hline A & B & C \\ \hline 0.93 & 1.40 & 1.53 \\ 0.24 & 0.46 & 0.76 \\ 0.95 & 1.24 & 1.46 \\ 0.23 & 0.57 & 1.28 \\ 0.90 & 0.46 & 1.28 \\ 0.15 & 0.42 & 1.53 \\ 0.47 & 0.54 & 0.63 \\ 0.89 & 1.23 & 1.45 \\ \hline
\end{tabular}
\end{center}

Continue this update process for feature C, and then circle back to feature A and repeat process in cycles until imputed values for all features have converged.

\(^1\)van Burren, 2011. Figure credit: https://cran.r-project.org/web/packages/miceRanger/vignettes/miceAlgorithm.html
Example of imputation through prediction in the widely used MICE Algorithm\(^1\)

Continue this update process for feature C, and then circle back to feature A and repeat process in cycles until imputed values for all features have converged.

Full MICE Algorithm (multiple imputation) repeats this for N random initializations of the dataset and then aggregates for final imputation + uncertainty measure. We will not cover different initialization methods and implications.

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\(^1\)van Burren, 2011. Figure credit: https://cran.r-project.org/web/packages/miceRanger/vignettes/miceAlgorithm.html
Sources of EHR data

- Open-source EHR datasets (MIMIC-III/IV, MIMIC-CXR, …)
- Restricted EHR data from individual institutions
  - Major vendors: EPIC, Cerner, etc.
- Also: insurance claims data
  - Fills in blanks of patient health outside the hospital!
    - Visits with other care providers outside the hospital EHR system
    - Pharmacy visits
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- Restricted EHR data from individual institutions
  - Major vendors: EPIC, Cerner, etc.
- Also: insurance claims data
  - Fills in blanks of patient health outside the hospital!
    - Visits with other care providers outside the hospital EHR system
    - Pharmacy visits

Challenge: many of these data sources are in their own formats. How do we use multiple data sources?
OMOP Common Data Model

- Observational Medical Outcomes Partnership (OMOP)
- Created from public-private partnership involving FDA, pharmaceutical companies, and healthcare providers
- Standardized format and vocabulary
- Allows conversion of patient data from different sources into a common structure for analysis
- Intended to support data analysis

Figure credit: https://www.ohdsi.org/wp-content/uploads/2014/07/Why-CDM.png
OMOP Common Data Model

Figure credit: https://ohdsi.github.io/TheBookOfOhdsi/images/CommonDataModel/cdmDiagram.png
STARR: Stanford Hospital Data in OMOP

Stanford Electronic Health Records in OMOP
STARR-OMOP is Stanford Electronic Health Record data from its two Hospitals in a Observational Medical Outcomes Partnership (OMOP) Common Data Model (CDM). Use OMOP for observational science, population health science, collaborative network studies and reproducible data science.

Standardized Data
- Standardized vocabulary
- Transparent data transformations
- High mapping rate
FHIR

- Fast healthcare interoperability resources (FHIR)
- Web-based standards / framework for secure exchange of electronic healthcare information across disparate sources
- Based on “resource” elements that contain information to be exchanged, as a JSON or XML object

Figure credit: https://www.hl7.org/fhir/DSTU1/shot.png
Figure credit: Choi et al. OHDSI on FHIR Platform Development with OMOP CDM mapping to FHIR Resources. 2016.
FHIR

FHIR-based information exchange between different sources

Figure credit: Choi et al. OHDSI on FHIR Platform Development with OMOP CDM mapping to FHIR Resources. 2016.
Data from all sources can be written in an OMOP data repository for analysis.

Figure credit: Choi et al. OHDSI on FHIR Platform Development with OMOP CDM mapping to FHIR Resources. 2016.
OHDSI (parent of OMOP) also provides tools and resources for data analysis.

Figure credit: Choi et al. OHDSI on FHIR Platform Development with OMOP CDM mapping to FHIR Resources. 2016.
SMART on FHIR is a platform for building third-party apps that interface with health data in e.g. EHRs, through FHIR.


Figure credit: Choi et al. OHDSI on FHIR Platform Development with OMOP CDM mapping to FHIR Resources. 2016.
Aside: improving EHR technology and utility major current issue in healthcare

- **Have already seen one challenge: interoperability**
  - EHR systems were built and adopted very quickly -- not enough time to design for interoperability

- **Are EHRs being used meaningfully?**
  - Clinicians spending huge amount of time on documentation and interfacing with EHR system -> burnout and reduced patient interaction
  - Lots of pain points. What are the benefits?

- **Ongoing efforts to reduce pain points**
  - Improving user experience and AI-assisted documentation (dictation, autocomplete, etc.)

- **Ongoing efforts to improve value**
  - Data analytics, clinical decision support
Rajkomar et al. 2018

- Clinical predictions from patients’ entire raw EHR records, in FHIR format
- De-identified EHR data from two US academic centers with 216,221 adult patients
- Prediction tasks: in-hospital mortality, 30-day unplanned readmission, prolonged length of stay, patients’ final discharge diagnoses
- 46,864,534,945 total data points across data (every event, every word in note, etc.)

Data representation

Data representation

Each element is mapped to a token ID (e.g. medication=zosyn), with a token “feature type”

Every unique token is numerically represented by an “embedding vector” that will represent the token in the model. The embedding vector values are learned; similar tokens will probably have similar embedding vectors.

## Token Embeddings

A one-hot token input is multiplied by an embedding matrix to produce a token embedding.

<table>
<thead>
<tr>
<th>0.5</th>
<th>0.2</th>
<th>0.1</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.6</td>
<td>0.1</td>
<td>0.6</td>
</tr>
<tr>
<td>0.5</td>
<td>0.8</td>
<td>0.2</td>
</tr>
<tr>
<td>0.7</td>
<td>0.9</td>
<td>0.3</td>
</tr>
<tr>
<td>0.3</td>
<td>0.5</td>
<td>0.1</td>
</tr>
<tr>
<td>...</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.7</td>
<td>0.8</td>
<td>0.1</td>
</tr>
</tbody>
</table>

1xN token input (one-hot selection of token) \( \times \) N x D embedding matrix = D-dim token embedding

\[
\begin{bmatrix}
0 & 0 & 1 & 0 & 0 & 0 & \ldots & 0 \\
\end{bmatrix} \times \begin{bmatrix}
0.5 & 0.8 & 0.2 \\
\end{bmatrix} = \begin{bmatrix}
[0.5 & 0.8 & 0.2] \\
\end{bmatrix}
\]
Token embeddings

\[
\begin{bmatrix}
0 & 0 & 1 & 0 & 0 & 0 & 0 & \ldots & 0
\end{bmatrix}
\times
\begin{bmatrix}
0.5 & 0.2 & 0.1 \\
0.6 & 0.1 & 0.6 \\
0.5 & 0.8 & 0.2 \\
0.7 & 0.9 & 0.3 \\
0.3 & 0.5 & 0.1 \\
\vdots \\
0.7 & 0.8 & 0.1
\end{bmatrix}
= \begin{bmatrix}
0.5 & 0.8 & 0.2
\end{bmatrix}
\]

D-dim token embedding

In general, learning embedding matrices are a useful way to map discrete data into a semantically meaningful, continuous space! Will see frequently in natural language processing.
Computational graph input to RNN

\[ W \]

\[ h_0 \rightarrow f_W \rightarrow h_1 \rightarrow f_W \rightarrow h_2 \rightarrow f_W \rightarrow h_3 \rightarrow \ldots \rightarrow h_T \]

\[ \text{reshape} \]

\[ f_E \]

\[ x_1 \rightarrow f_E \rightarrow x_2 \rightarrow f_E \rightarrow x_3 \rightarrow f_E \rightarrow \]
Computational graph input to RNN

\[ W \]

\[ h_0 \xrightarrow{f_W} h_1 \xrightarrow{f_W} h_2 \xrightarrow{f_W} h_3 \xrightarrow{\ldots} h_T \]

- \( M \times N \) one-hot token embeddings (\( M \) feature tokens at the timestep, \( N \) tokens in vocab)

- \( f_E \)

- \( x_1 \), \( x_2 \), \( x_3 \)
Computational graph input to RNN

$W$

$h_0 \xrightarrow{f_W} h_1 \xrightarrow{f_W} h_2 \xrightarrow{f_W} h_3 \xrightarrow{\ldots} h_T$

$E = \begin{bmatrix}
e_{11} & e_{12} & e_{13} \\
e_{21} & e_{22} & e_{23} \\
e_{31} & e_{32} & e_{33} \\
e_{41} & e_{42} & e_{43} \\
e_{51} & e_{52} & e_{53}
\end{bmatrix}$

N x D embedding matrix (N words in vocab, D-dimensional embedding)
Computational graph input to RNN

\[ \begin{align*}
W & \rightarrow h_0 \rightarrow f_W \rightarrow h_1 \rightarrow f_W \\
\text{reshape} & \rightarrow f_E \rightarrow x_1 \\
\text{reshape} & \rightarrow f_E \rightarrow x_2 \\
\text{reshape} & \rightarrow f_E \rightarrow x_3 \\
\end{align*} \]

Matrix multiplication of \( f_E \) with \( x \) selects embedding vectors corresponding to tokens (M x D output)

### Example

1xN token input (one-hot selection of token)

\[
\begin{bmatrix}
0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & \ldots & 0
\end{bmatrix} \times
\begin{bmatrix}
0.5 & 0.2 & 0.1 \\
0.6 & 0.1 & 0.6 \\
0.5 & 0.8 & 0.2 \\
0.7 & 0.9 & 0.3 \\
0.3 & 0.5 & 0.1 \\
0.7 & 0.8 & 0.1 \\
\vdots
\end{bmatrix}
= \begin{bmatrix}
0.5 & 0.8 & 0.2 \\
\end{bmatrix}
\]

D-dim token embedding

\[ E = \begin{bmatrix}
\begin{array}{ccc}
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e_{51} & e_{52} & e_{53}
\end{array}\end{bmatrix} \]
Computational graph input to RNN

Reshape into a 1 x MD vector -> input into RNN at each timestep

\[ E = \begin{array}{ccc}
  e_{11} & e_{12} & e_{13} \\
  e_{21} & e_{22} & e_{23} \\
  e_{31} & e_{32} & e_{33} \\
  e_{41} & e_{42} & e_{43} \\
  e_{51} & e_{52} & e_{53}
\end{array} \]

Serena Yeung  
BIODS 220: AI in Healthcare  
Lecture 6 - 51
Embedding matrix has values that are randomly initialized at the beginning, then learned through training (backpropagation)!
Computational graph input to RNN

Embedding matrix has values that are randomly initialized at the beginning, then learned through training (backpropagation)!
(shown for N = 5, D = 3)

Note that E is used at each timestep in computational graph of RNN

\[ E = \begin{bmatrix} e_{11} & e_{12} & e_{13} \\
                 e_{21} & e_{22} & e_{23} \\
                 e_{31} & e_{32} & e_{33} \\
                 e_{41} & e_{42} & e_{43} \\
                 e_{51} & e_{52} & e_{53} \end{bmatrix} \]
Rajkomar et al. RNN (LSTM) input

Rajkomar et al. RNN (LSTM) input

One vector representation for each token “feature type” (e.g. medication, procedure). Embeddings of multiple tokens corresponding to a same feature type are combined through averaging.

A little bit of added complexity: each feature type has its own embedding dimension $D$. A hyperparameter!

Rajkomar et al. RNN (LSTM) input

Also include an embedding representation of time delta from last RNN input.

One vector representation for each token “feature type” (e.g. medication, procedure). Embeddings of multiple tokens corresponding to a same feature type are combined through averaging.

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A little bit of added complexity: each feature type has its own embedding dimension D. A hyperparameter!

Refer to paper for other details, e.g. bucketing of continuous data types into discrete token IDs.

Rajkomar et al. Compared deep learning approach with baselines (e.g. logistic regression), and using all variables in data (flattened vector) vs hand-crafted features from subset of variables.

<table>
<thead>
<tr>
<th>Inpatient Mortality, AUROC(^1) (95% CI)</th>
<th>Hospital A</th>
<th>Hospital B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Deep learning 24 hours after admission</td>
<td>0.95 (0.94-0.96)</td>
<td>0.93 (0.92-0.94)</td>
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<tr>
<td>Full feature enhanced baseline at 24 hours after admission</td>
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<td>Full feature simple baseline at 24 hours after admission</td>
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<td>Baseline (aEWS(^2)) at 24 hours after admission</td>
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<td>Full feature enhanced baseline at discharge</td>
<td>0.75 (0.73-0.76)</td>
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<tr>
<td>Full feature simple baseline at discharge</td>
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<td>0.73 (0.72-0.74)</td>
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<tr>
<td>Baseline (mHOSPITAL(^3)) at discharge</td>
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<tr>
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1 Area under the receiver operator curve  
2 Augmented early warning score  
3 Modified HOSPITAL score  
4 Modified Liu score  

Rajkomar et al.

Evaluated model at different time points, e.g., at admission, 24 hrs after admission, discharge

Compared deep learning approach with baselines (e.g. logistic regression), and using all variables in data (flattened vector) vs hand-crafted features from subset of variables

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\(^1\) Area under the receiver operator curve
\(^2\) Augmented early warning score
\(^3\) Modified HOSPITAL score
\(^4\) Modified Liu score

Also trained a model with “soft attention” on a simpler task (in-hospital mortality, subset of data variables) to obtain interpretability.

Soft attention

- Weight input variables by an “attention weights” vector \( p \)

- Learn to dynamically produce \( p \) for any given input, by making it a function of the input \( x \) and a fully connected layer \( f_A \) (with learnable parameters \( A \))

- By optimizing for prediction performance, network will learn to produce \( p \) that gives stronger weights to the most informative features in \( x \)!
Soft attention

- Weight input variables by an “attention weights” vector $p$
- Learn to dynamically produce $p$ for any given input, by making it a function of the input $x$ and a fully connected layer $f_A$ (with learnable parameters $A$)
- By optimizing for prediction performance, network will learn to produce $p$ that gives stronger weights to the most informative features in $x$!

$$\text{Input } x = [x_1, x_2, ..., x_D]$$
$$\text{Attention weights } p = [p_1, p_2, ..., p_D]$$
$$\text{Attention-weighted input } z = [z_1, z_2, ..., z_D]$$
$$\text{Learnable fully connected layer } f_A \text{ with weights } A$$
Soft attention

- Weight input variables by an "attention weights" vector $p$
- Learn to dynamically produce $p$ for any given input, by making it a function of the input $x$ and a fully connected layer $f_A$ (with learnable parameters $A$)
- By optimizing for prediction performance, network will learn to produce $p$ that gives stronger weights to the most informative features in $x$!

Input $x = [x_1, x_2, ..., x_D]$

Attention weights $p = [p_1, p_2, ..., p_D]$

Attention-weighted input $z = [z_1, z_2, ..., z_D]$

Learnable fully connected layer $f_A$ with weights $A$

Output $y$

Rest of the neural network

Soft attention weighting

$p$ is output of a softmax function -> attention weights sum to 1

Learnable fully connected layer $f_A$ with weights $A$
Soft attention in RNNs

Note that $f_A$ produces attention weights as a function of both current input $x$ as well as previous hidden state $h$!
Soft attention in RNNs

Note that $f_A$ produces attention weights as a function of both current input $x$ as well as previous hidden state $h$!

Attention weights $p_i$ indicate features that the model gives the most importance to at every time-step.
Soft attention in RNNs

Soft attention weighting

\[ h_0 \xrightarrow{f_W} h_1 \xrightarrow{f_W} h_2 \xrightarrow{f_W} h_3 \xrightarrow{\cdots} h_T \]

Soft attention weighting

\[ x_1 \xrightarrow{f_A} p \]

Soft attention weighting

\[ x_2 \xrightarrow{f_A} p \]

Soft attention weighting

\[ x_3 \xrightarrow{f_A} p \]

Note that \( f_A \) produces attention weights as a function of both current input \( x \) as well as previous hidden state \( h \)!

Attention weights \( p_i \) indicate features that the model gives the most importance to at every time-step \( i \)

Weight matrix \( A \) shared across multiple timesteps in computational graph.
Active areas of research

- Improving prediction models for clinically meaningful tasks
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  - Another popular task: early warning for critical conditions such as sepsis
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- Improving prediction models for clinically meaningful tasks
  - Another popular task: early warning for critical conditions such as sepsis
  - Multimodal modeling: more effective joint reasoning over different modalities of data (e.g. text, lab results, images, etc.)
Summary

Today’s topics

- More on EHR data, missing values, and data formats
- More on feature representations
- A first look at model interpretability: soft attention

Next lecture

- More on text data and representations