

Module 1: Introduction

CAD data overview

The data mart is a random sample of patients in the Mass General Brigham (formerly Partner's Healthcare) EHR database who had at least one note of 500 characters and met an initial filter for **coronary artery disease** (CAD) defined as:

- ▶ ≥ 1 ICD9 code related to CAD (410.x, 411.x, 412.x, 413.x, 414.x).
- ▶ ≥ 1 mention for any CAD related concepts (eg. CAD, CAD procedures, CAD biomarkers, positive stress test).

Read in the CAD data

“label”: whether the patient has CAD, **extracted from chart review by a clinician.**

```
data(ehr_data)
data <- PhecapData(
  ehr_data, "healthcare_utilization", "label", 75,
  patient_id = "patient_id", seed = 123
)
data
```

```
## PheCAP Data
## Feature: 10000 observations of 587 variables
## Label: 119 yes, 62 no, 9819 missing
## Size of training samples: 106
## Size of validation samples: 75
```

Read in the CAD data

“main_ICD”, “main_NLP”: total number of billing codes or NLP mentions of the disease.

```
head(ehr_data[, c(1:5, 25:30)])
```

##	patient_id	label	main_ICD	main_NLP	healthcare_utilization	NLP10	NLP11	NLP12
## 1	1	NA	1	0	25	5	0	0
## 2	2	NA	41	157	187	72	0	2
## 3	3	NA	4	1	138	44	1	0
## 4	4	NA	0	0	67	9	0	0
## 5	5	NA	0	0	9	4	0	0
## 6	6	NA	4	2	4	0	0	0

##	NLP13	NLP14	NLP15
## 1	0	0	0
## 2	22	0	47
## 3	8	13	12
## 4	1	0	2
## 5	0	0	0
## 6	0	0	0

Read in the CAD data

“healthcare_utilization”: total number of notes the patient has.

```
head(ehr_data[, c(1:5, 25:30)])
```

##	patient_id	label	main_ICD	main_NLP	healthcare_utilization	NLP10	NLP11	NLP12
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Read in the CAD data

“CODx” (n = 10): the counts of a specific code “NLPx” (n = 574): the counts of a positive mention of a CUI

```
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```

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##	NLP13	NLP14	NLP15
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Basic descriptives

```
# Check for missing data.
```

```
colnames(ehr_data)[which(colMeans(is.na(ehr_data)) > 0)]
```

```
## [1] "label"
```

Basic descriptives

```
# Check for missing data.
```

```
colnames(ehr_data)[which(colMeans(is.na(ehr_data)) > 0)]
```

```
## [1] "label"
```

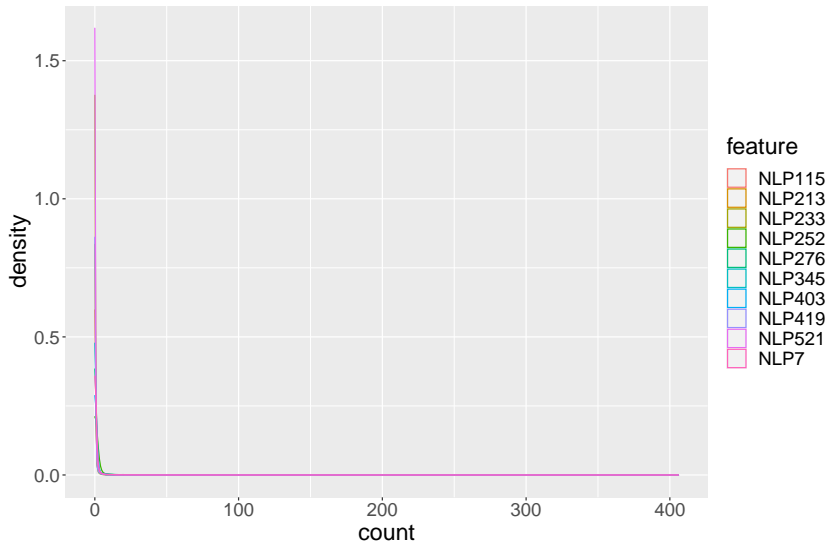
```
# Prevalence of the label.
```

```
mean(ehr_data$label, na.rm = TRUE)
```

```
## [1] 0.6574586
```


Feature distributions

Density plots of randomly selected 10 features



Prepare the data for model fitting

- ▶ We log transform all the features as they are highly skewed
- ▶ We orthogonalize all features against health care utilization for Module 2

(Please find more details in the `.Rmd` file.)