The Heritage Health Prize

Modeling Healthcare in Ten Minutes

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Hi, I’m Thomson.

Currently:
Data Scientist at Lookout Mobile Security, visiting scholar at NYU Courant.

I enjoy:
Rowing, road cycling, SC2, finding good rueben sandwich places.

This presentation:
Has been adapted from a IEEE BioMedCom talk. To fit in 10 minutes.

Agenda

- Introduction to the Heritage Health Prize
- The Datasets
- Preliminary Models
- Random Decision Trees
- Parallelization
- Summary

Introduction to the HHP

The Datasets
Preliminary Models
Random Decision Trees
Parallelization

Motivation

- **Hospitalization in the United States**
  - ~71 million people were admitted into the hospital last year
  - Of these 71 million people, 11 million of them were classified as “unnecessary”, resulting in $30bn in unnecessary expenditure.
    - The majority (83%) of these admissions were made by GPs and Managed Care Organizations.
- **Question**
  - Is there a data-driven approach that GPs can use to assist their diagnoses and decrease false positives?

Source: Friedwel, J. (2010)

Heritage Health Prize

- **Heritage Health Prize** (**HHP**)
  - Modeling competition administered by Kaggle, with data from the HPN.
  - Given the last three years of HPN patient claims…
  - Can you predict the number of hospitalization days in the next year?

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What's in the **data**?

Members Table (113000 x 3)

```
> head(members)
  MemberID AgeAtFirstClaim Sex
1 14723353            70-79   M
2 75706636            70-79   M
3 17320609            70-79   M
4 69690888            40-49   M
5 33004608              0-9   M
6 63690883            40-49   F
```

Rx Table (Y1/Y2/Y3, 818241 x 4)

```
> head(drug.count)
  MemberID Year         DSFS DrugCount
1 48925661   Y2  9-10 months         7+
2 90764620   Y3  8- 9 months          3
3 61221204   Y1  2- 3 months          1
4 63628544   Y3  1- 2 months          1
5 46949606   Y2 10-11 months          3
6 72110751   Y2  9-10 months          1
```

Claims Table (Randomized claims for Y1, Y2, Y3, 2668990 x 14)

```
> head(claims)
  MemberID ProviderID Vendor   PCP Year  Specialty          PlaceSvc PayDelay        DSFS     PCG CharlsonIndex ProcedureGroup SupLOS
1 42286978    8013252 172193 37796   Y1    Surgery            Office       28 8- 9 months NEUMENT           0            MED      0
2 97903248    3316066 726296  5300   Y3   Internal            Office       50 8- 9 months NEUMENT           0            MED      1
3  2759427    2997752 140343 91972   Y3   Internal            Office       14  0- 1 month  METAB3           0             EM      1
4 73570559    7053364 240043 70119   Y3 Laboratory     Independent Lab       24  0- 1 month  METAB3           0            SCS      0
5 11837054    7557061 496247 68968   Y2    Surgery Outpatient Hospital       27 4- 5 months FXDISLC         1-2             EM      1
6 45844561    1963488   4042 55823   Y3 Pediatrics            Office       25 3- 4 months NEUMENT           0             EM      0
```

Labs Table (361484 x 4)

```
> head(lab.count)
  MemberID Year         DSFS LabCount
1 69258001   Y3 2- 3 months         1
2 10143167   Y1  0- 1 month         2
3  1054357   Y1  0- 1 month         6
4 56583841   Y3 6- 7 months         4
5 70967047   Y2  0- 1 month         2
6 88850854   Y2 3- 4 months         5
```

DaysInHospital Tables (Y2/Y3)

```
> head(hospital.y2)
  MemberID ClaimsTruncated DaysInHospital
1 24027423               0              0
2 98324177               0              0
3 33899367               1              1
4  5481382               0              1
5 69908334               0              0
6 29951458               0              0
```

Right censored at 15 days!

Bringing it Together

- Split claims by year, use only claims that are attached to a member with a hospitalization record:

```
> clean.1 <- getCleanClaims("Y1", hospital.y2)
> clean.2 <- getCleanClaims("Y2", hospital.y3)
> clean.3 <- getCleanClaims("Y3", hospital.y4)
```

```
getCleanClaims <- function(x="Y1", y=hospital.y2){
        sand <- claims[claims$Year==x,]
        all.in <- sand$MemberID %in% y$MemberID
        sand <- sand[all.in,]
}
```

- Create tables of `counts' for each factor and merge it with `Members.csv`:

```
> head(makeTab(clean.1$MemberID, clean.1$PlaceSvc))
MemberID Ambulance Home Independent Lab Inpatient Hospital Office
10000665         0    2                0                  1      0
10001082         0    0                2                  0      0
10001258         3    1                0                  2      2
10001471         0    0                4                  0      8
10001818         1    0                0                  0      0
10002388         0    0                3                 13      7
```

```
makeTab <- function(x,y) {
  temp <- table(x,y)
  class(temp) <- "matrix"
  temp <- as.data.frame(temp, stringsAsFactors = FALSE)
  temp <- cbind(row.names(temp),temp)
  temp[,1] <- as.numeric(as.character(temp[,1]))
  colnames(temp) <- c("MemberID",colnames(temp)[-1])
  temp
  }
```

- Do this for **all** factors: 12 specialties, 8 places, 45 PCGs, 17 procedures, 5 Charlson indices, 1359 PCPs, 14699 ProviderIDs, and 6387 Vendors.

Data Transforms

- We now have three files (call them `right` files) with one unique member ID on each row and lots of columns:

```
> dim(right.a)
[1] 76038   22443
> dim(right.b)
[1] 71435   22443
> dim(right.c)
[1] 70942   22443
```

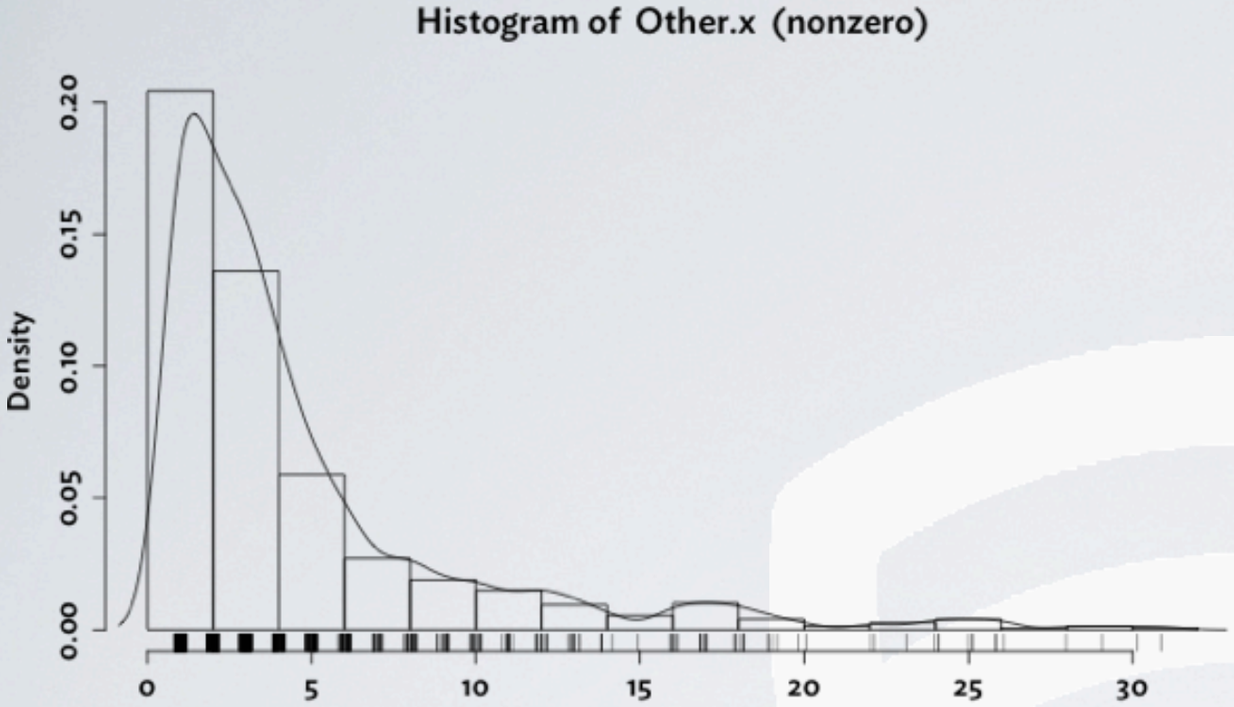
- **Very** sparse matrix! What does the data look like?

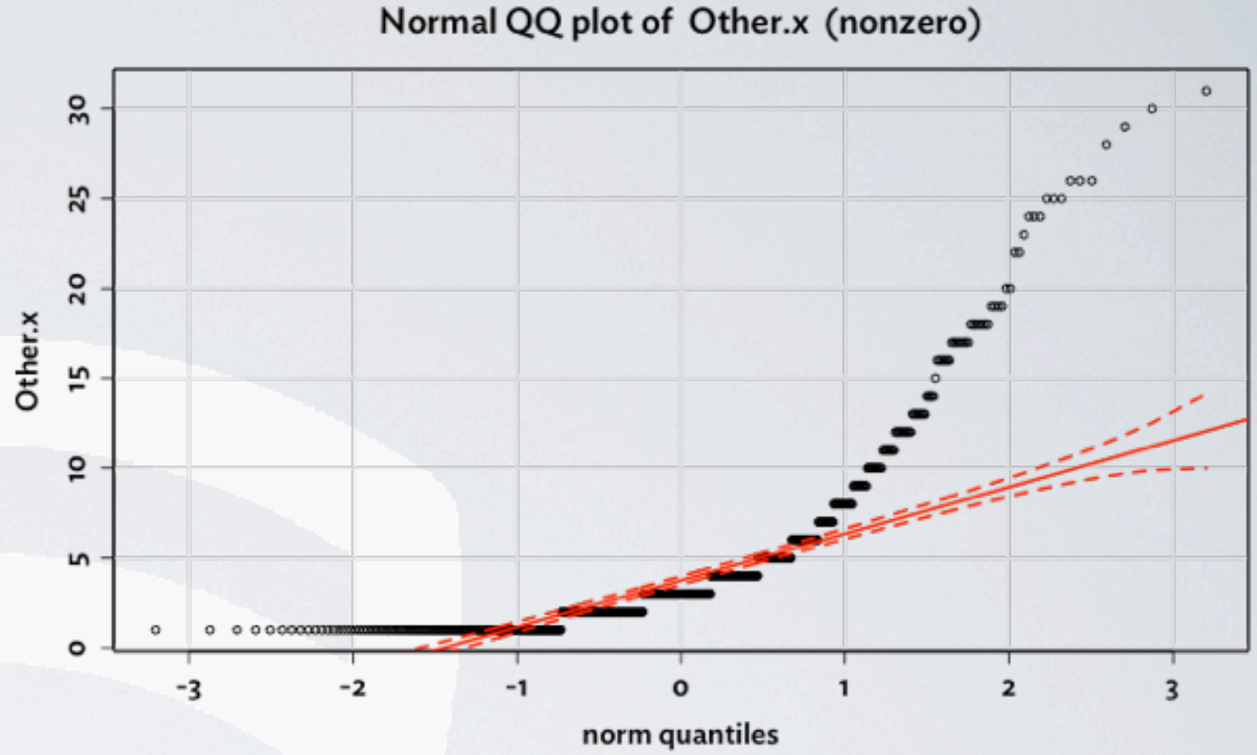
```
> summary(right.a$Other.x)
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
 0.00000  0.00000  0.00000  0.05086  0.00000 32.00000
```

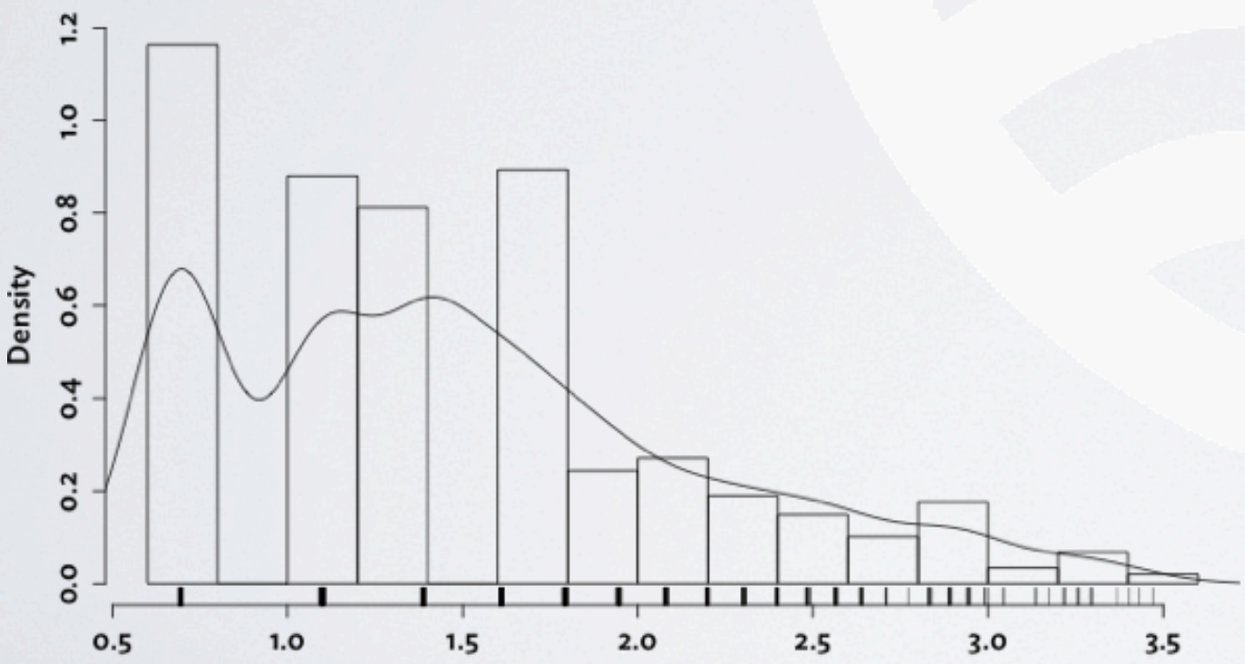
That looks pretty skewed. What if we took the log(1+x) transform?

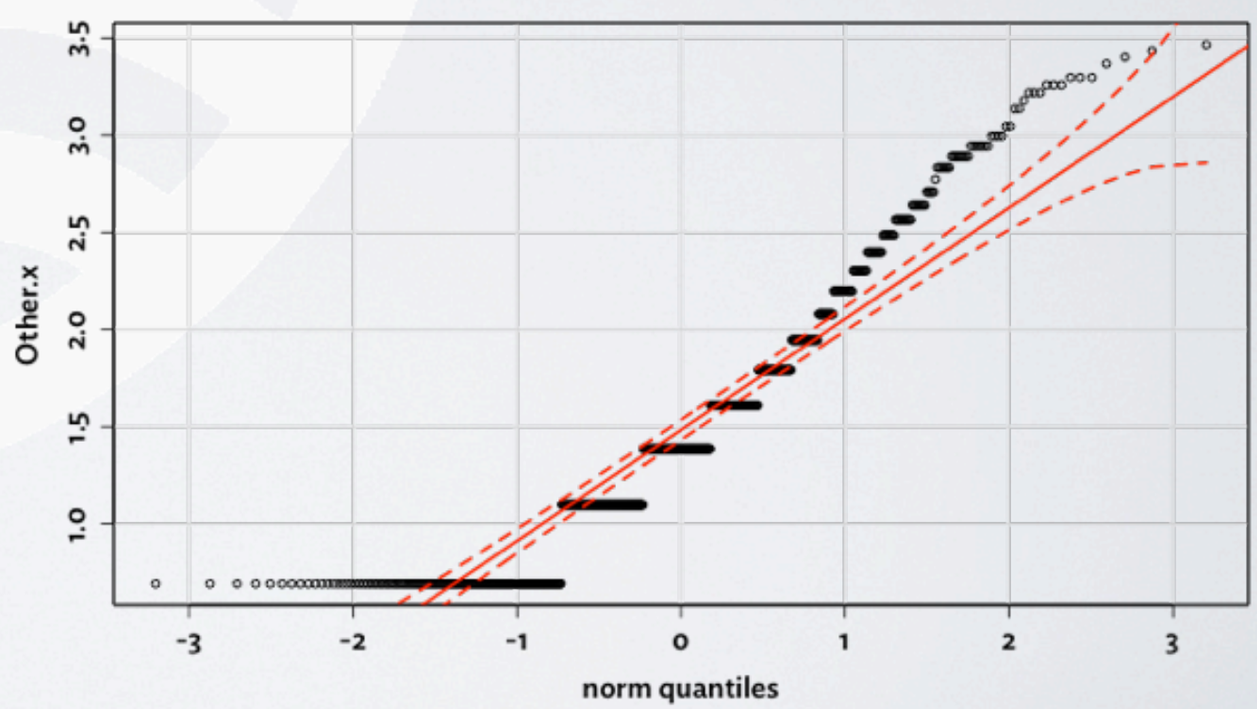
```
> right.a$Other.x <- log1p(right.a$Other.x)
> summary(right.a$Other.x)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.00000 0.00000 0.00000 0.01878 0.00000 3.43200
```

It looks better? What did we just do?









Introduction to the HHP

The Datasets

Preliminary Models

Random Decision Trees

Parallelization

Future Goals

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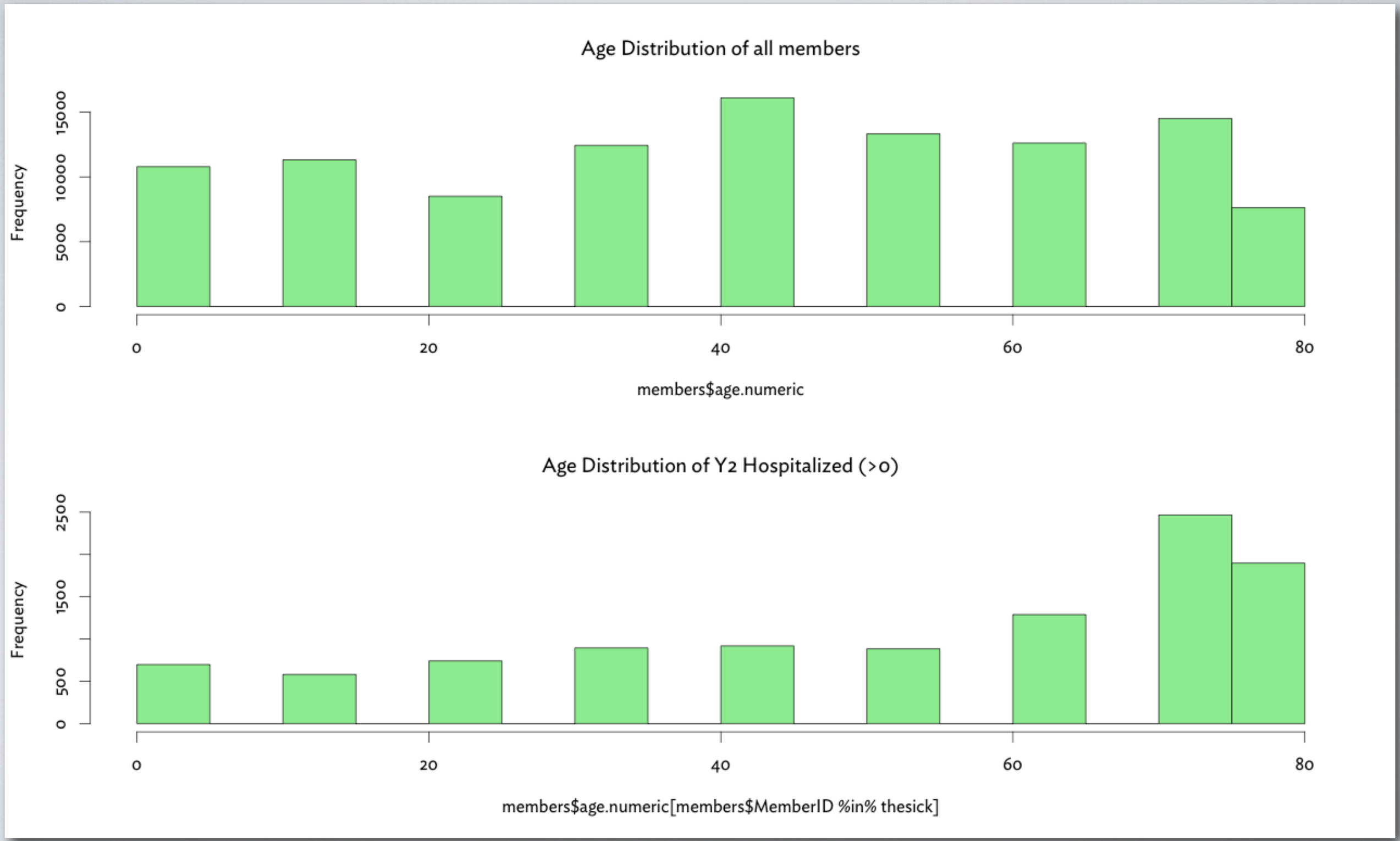
Model Evaluation

- Entries will be judged by comparing
  - the predicted number of days a member will spend in the hospital reflected in the entry,
  - with the actual number of days a member spent in the hospital in `DaysInHospital_Y4` (not given to competitors).
- Prediction accuracy will be evaluated based on the following metric:

$$\epsilon = \sqrt{\frac{1}{n}\sum_{i}^{n}[\log(p_i + 1) - \log(a_i + 1)]^2}$$

This is the root mean squared log error (RMSLE) of an outcome.

First Model



First Model

- Recall a Linear Model:

$$Y_i = \beta_0 + \beta_1\phi_1(X_{i1}) + \cdots + \beta_p\phi_p(X_{ip}) + \epsilon_i$$

- Let's create a simple linear regression of Age, and number of claims:

```
> model.1 <- lm(log(DaysInHospital) ~ AgeAtFirstClaim + num.claims, data=training)
> model.1

Call:
lm(formula = log(DaysInHospital ~ AgeAtFirstClaim + num.claims)

Coefficients:
       (Intercept)  AgeAtFirstClaim  num.claims
          -0.03551          0.07836     0.07504
> prediction <- predict(model, testing)
> prediction <- expm1(prediction)
> summary(prediction)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.01664 0.10240 0.18400 0.20080 0.28700 0.51810
```

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> prediction <- predict(model, testing)
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> summary(prediction)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.01664 0.10240 0.18400 0.20080 0.28700 0.51810
```

- RMSLE: 0.478246 (+.0918), Placement: 82nd of 255 teams

`Kitchen Sink' Model

- Let's now add counts for all Condition Groups, Procedures, Place of care, and Charlson Comorbidity score:

```
> model.1 <- lm(training[,2:105], log(training$DaysInHospital))
> prediction <- predict(model, testing)
> prediction <- expm1(prediction)
> summary(prediction) # Kitchen Sink model
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.00134 0.11240 0.19463 0.21892 0.28700 2.42792
> summary(prediction.old) # Three-variable model
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.01664 0.10240 0.18400 0.20080 0.28700 0.51810
```

`Kitchen Sink' Model

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   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.00134 0.11240 0.19463 0.21892 0.28700 2.42792
> summary(prediction.old) # Three-variable model
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.01664 0.10240 0.18400 0.20080 0.28700 0.51810
```

- RMSLE: 0.463167 (+.0034), Placement: ~~82nd~~ 45th of 398 teams

Preventing overfitting

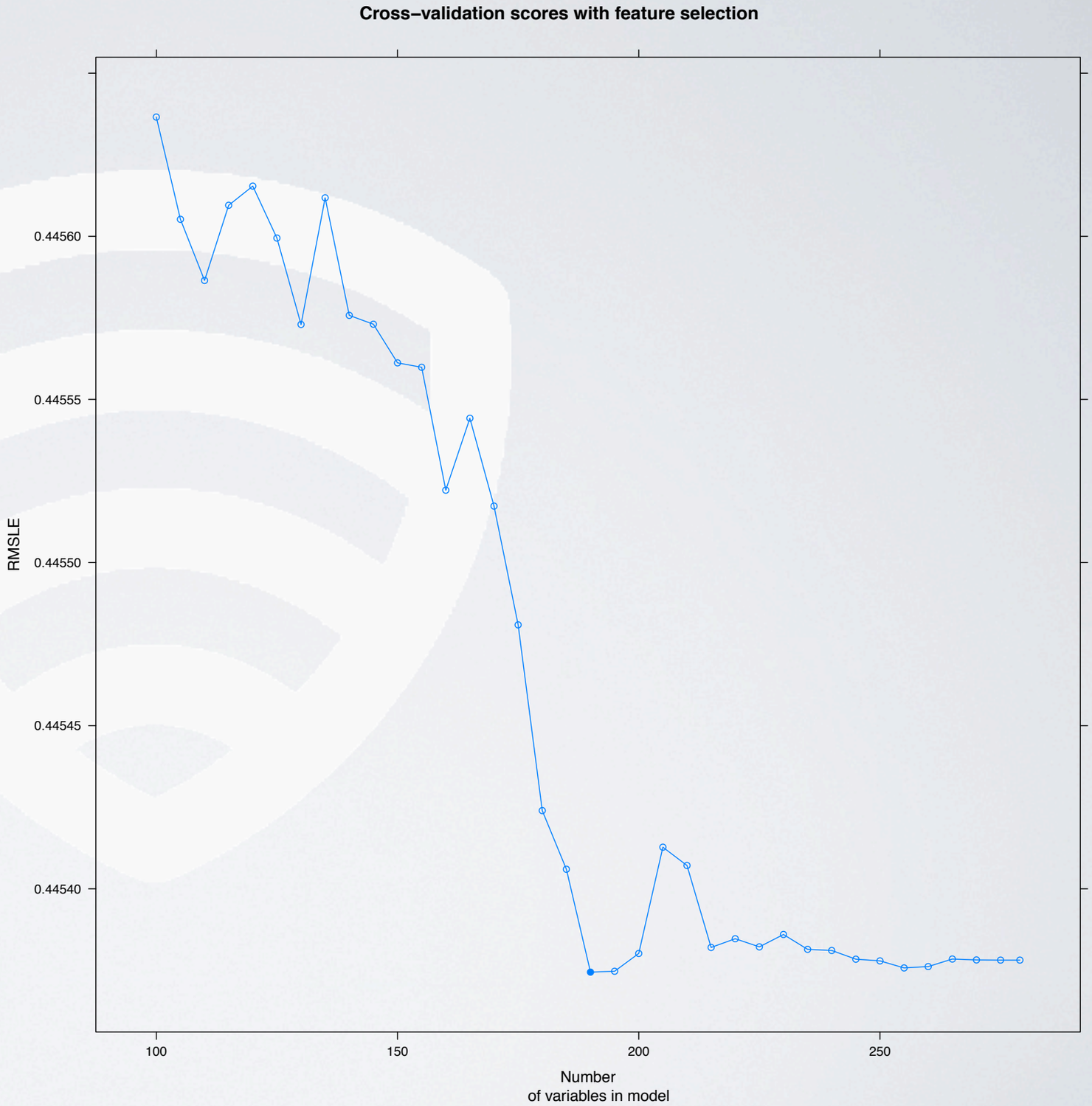
- Recursive Feature Selection
  - Train model with all predictors
  - Calculate model performance
  - Calculate variable importance/rankings

```
For (S in seq(1, numPred, by = 1)) do
      Keep the S most important variables
      Train the model using these variables
      Calculate model performance
      Recalculate variable importance/rankings
end
```

  - Calculate the model performance over all subsets S
  - Determine the final ranks of each predictor
  - Return list of predictors based on the optimal S value.

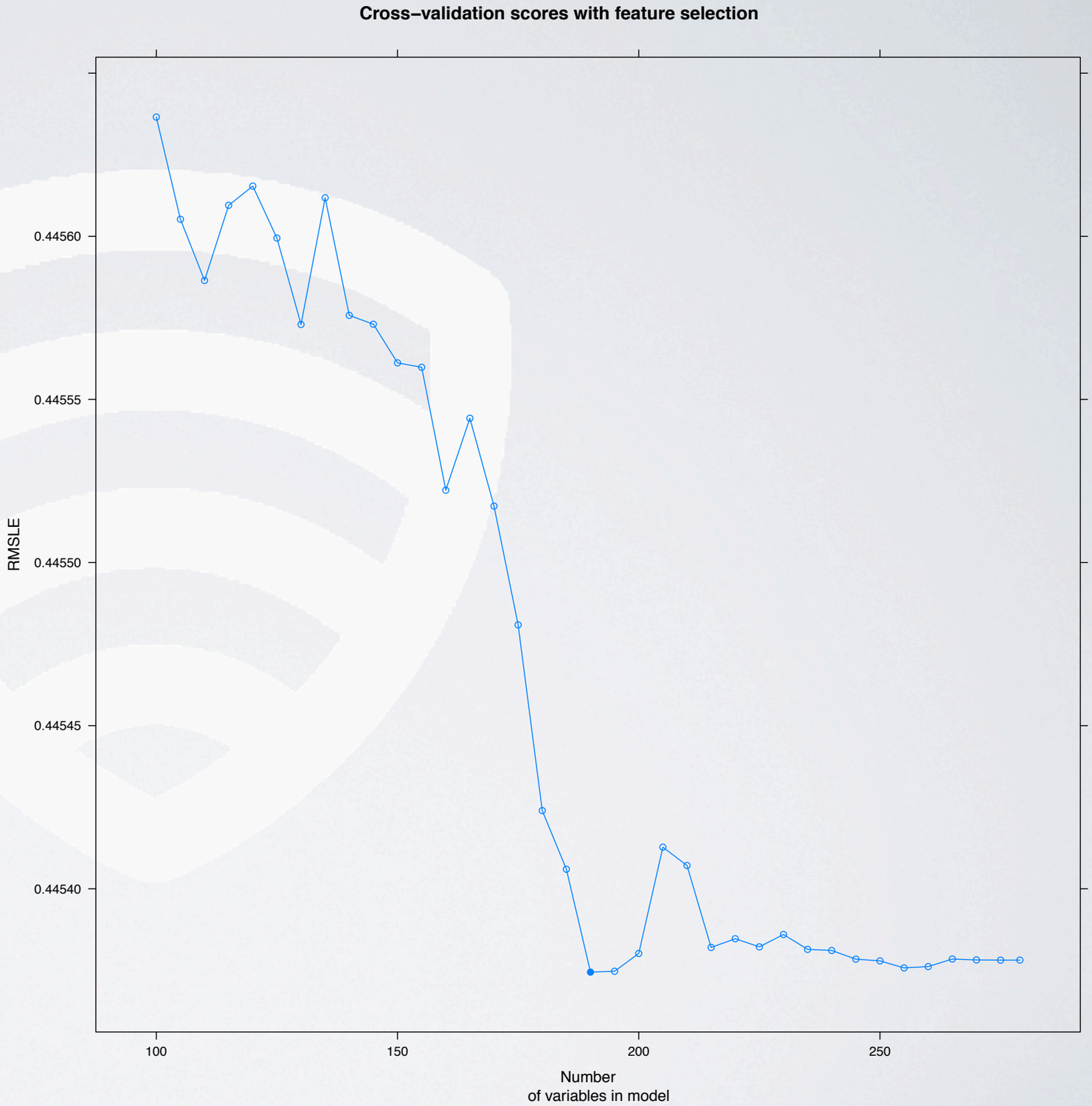
Optimised Kitchen Sink

- Ran recursive feature selection on entire training set of 22443 predictors
- Converged on 190 strongest predictors in linear model



Optimised Kitchen Sink

- Ran recursive feature selection on entire training set of 22443 predictors
- Converged on 190 strongest predictors in linear model
- RMSLE: 0.463002 (+.0021)



Optimised Kitchen Sink

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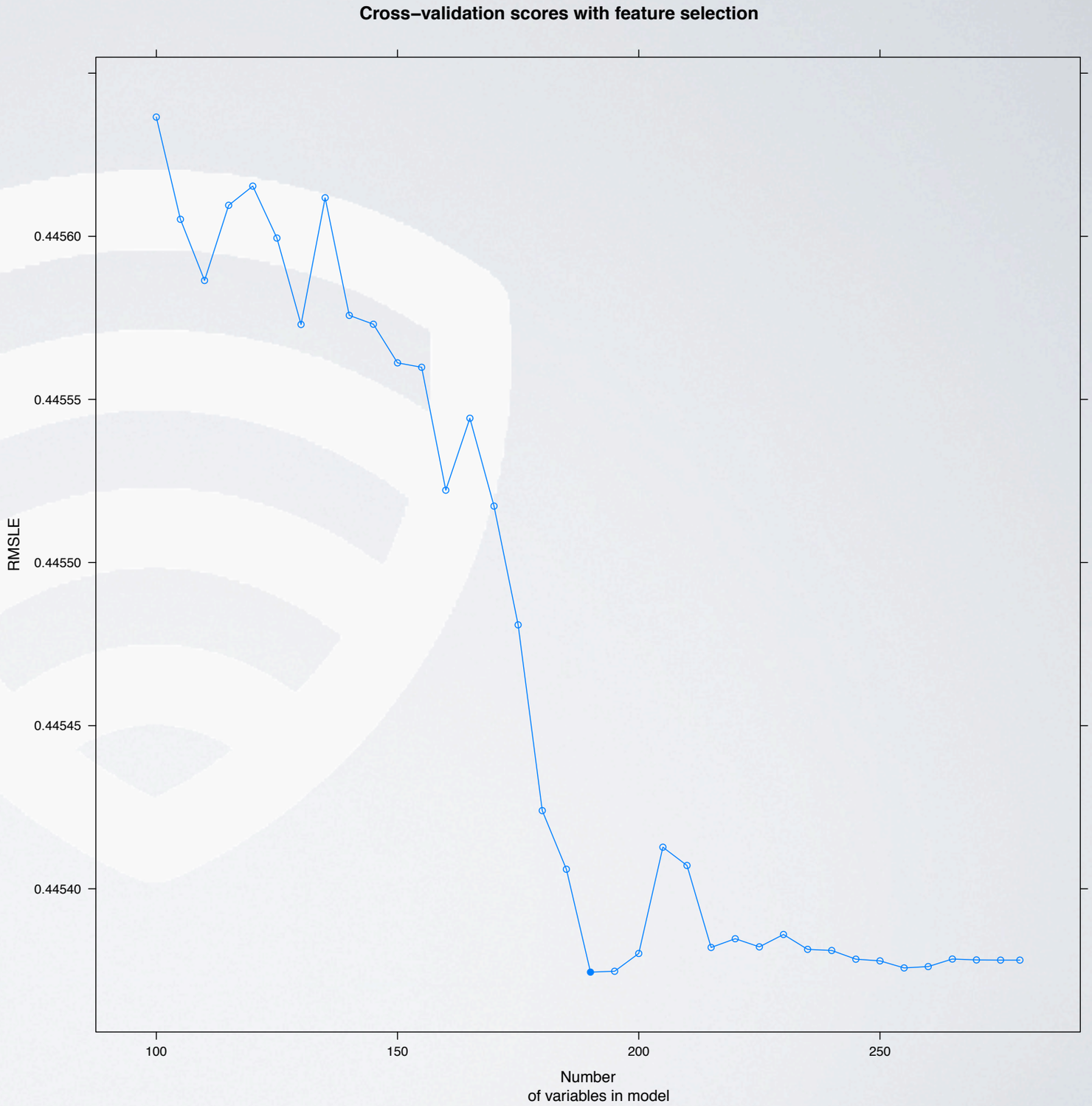
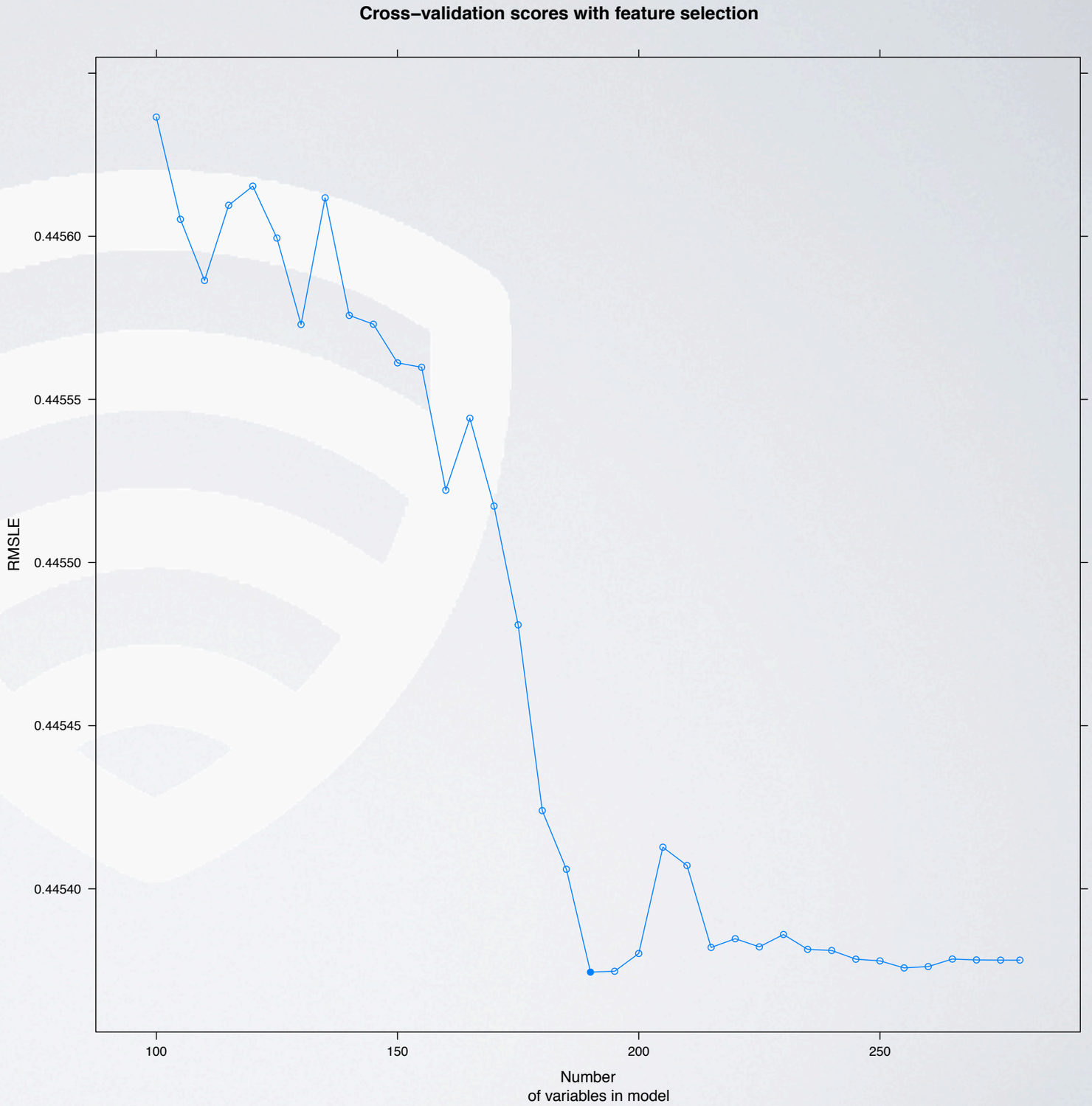
- RMSLE: 0.463002 (+.0021)
- Placement:



Optimised Kitchen Sink

- Ran recursive feature selection on entire training set of 22443 predictors
- Converged on 190 strongest predictors in linear model
- RMSLE: 0.463002 (+.0021)
- Placement:

~~45th~~ 35th of 410 teams



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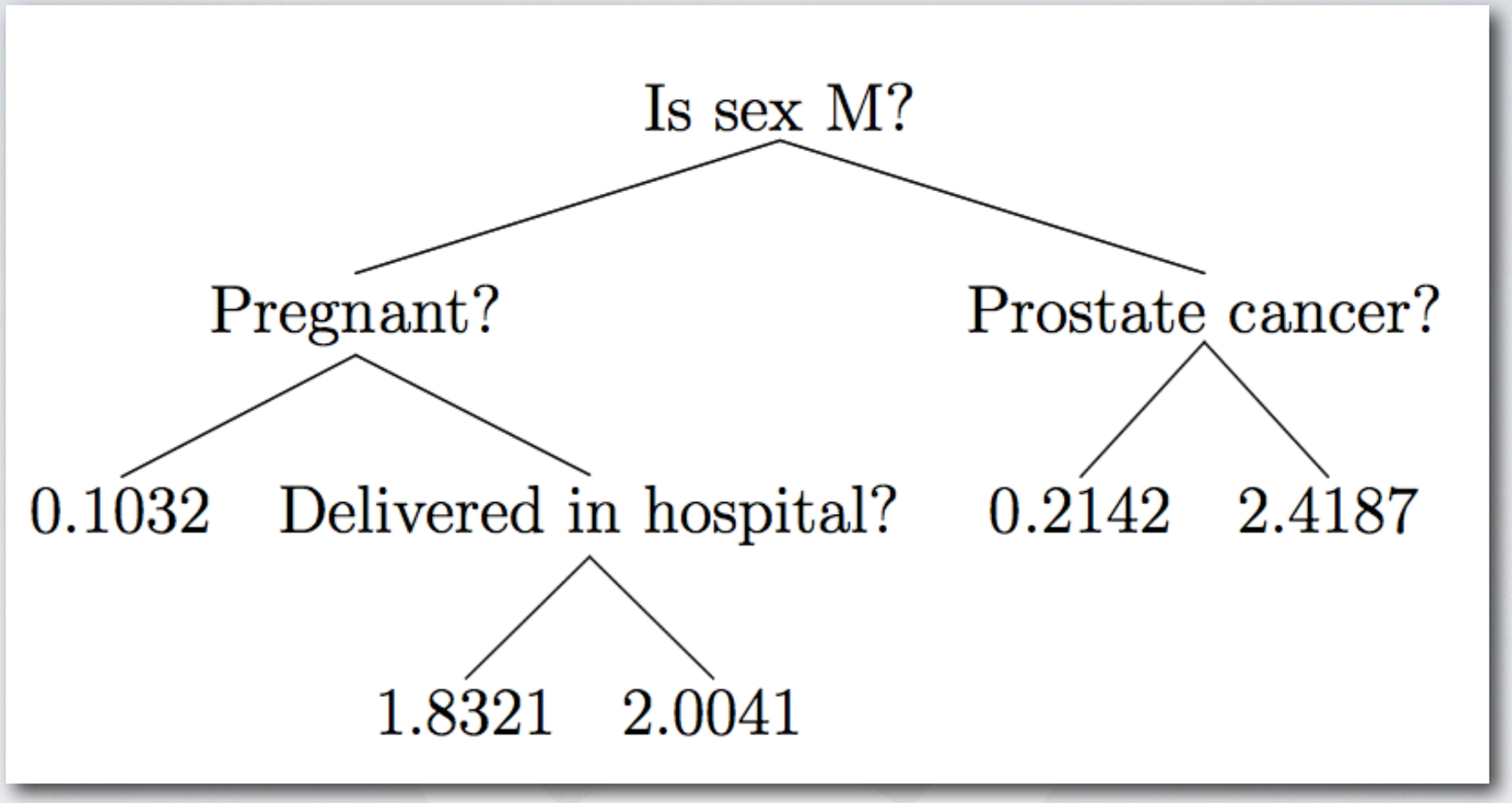
Introduction to Decision Trees



- Simple Decision Tree on Sex, PRGNCY, and CANCER1
- To create a tree, you take your training set and recursively partition subsets of predictors until splitting no longer adds value to the predictions.
- Excellent for discrete data, but still prone to overfitting.

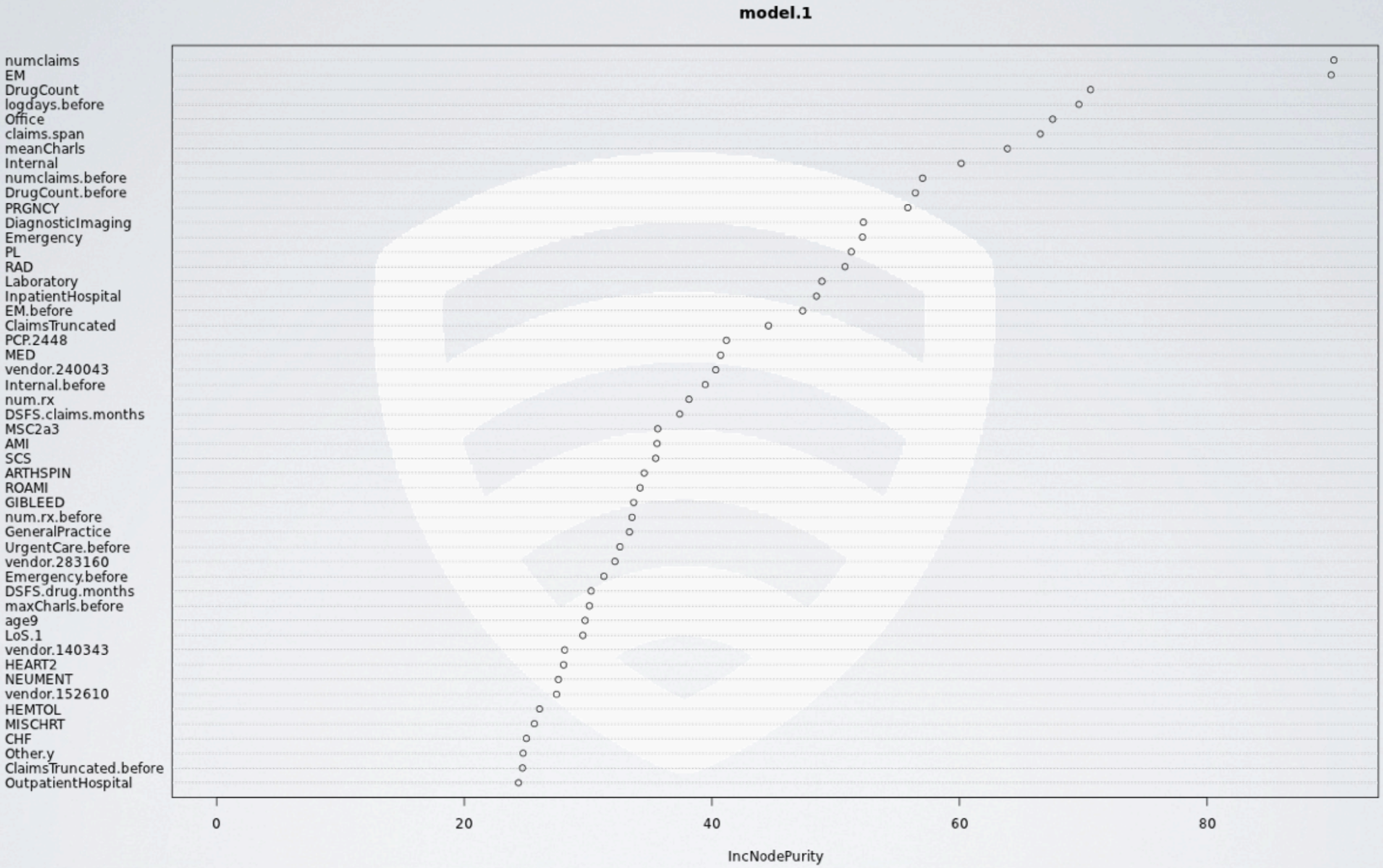
Random Decision Trees

- Ensemble regressor that consists of many trees (in our case, ~500k) that are calculated on random subsets of the data, using random subsets of predictors for each tree split.

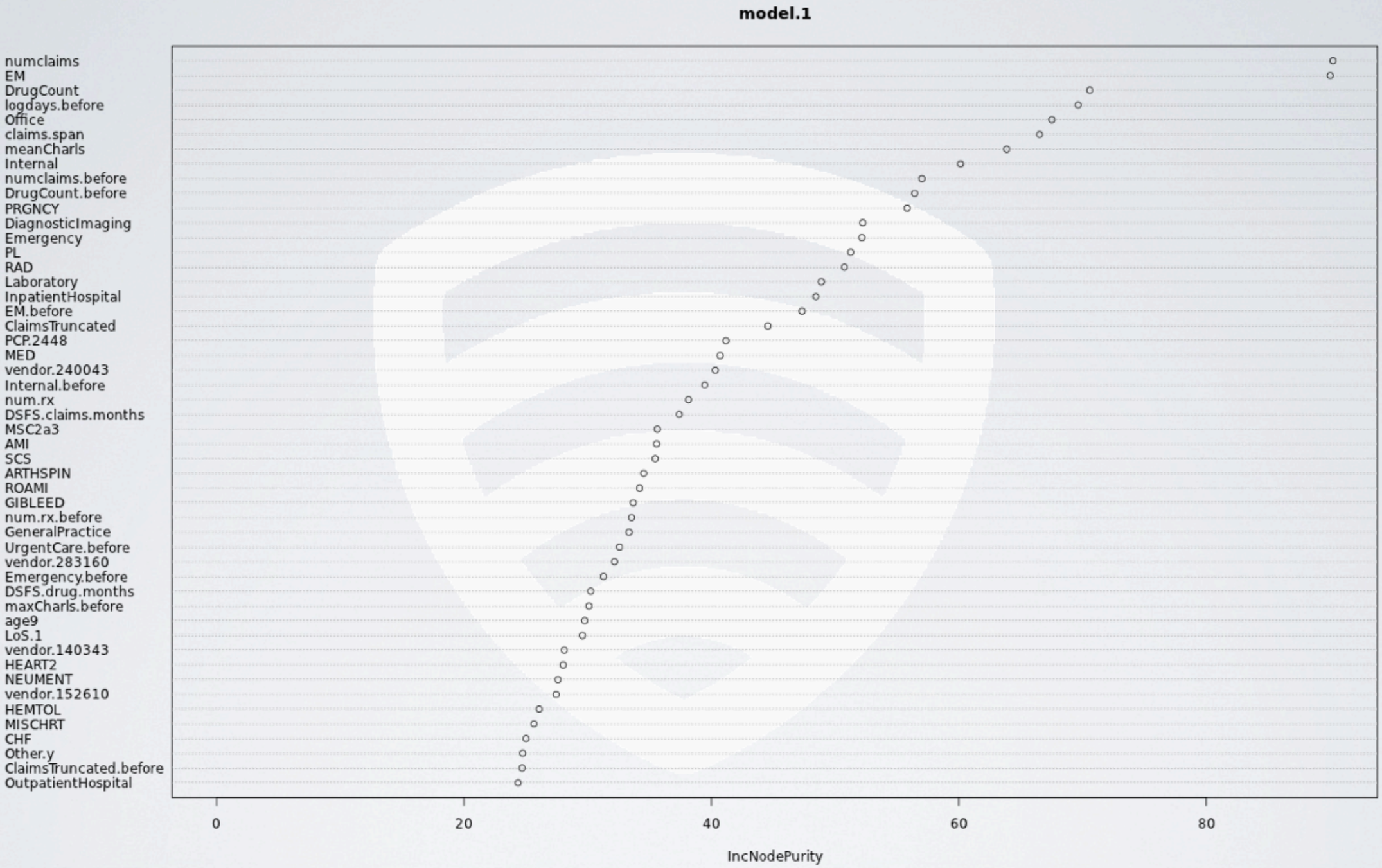
- Each tree is fully grown (i.e. like computing a recursive partitioning 500k times)

- To make a prediction, each test case is pushed down every tree and an average is taken for all trees.

```
> model.1 <- randomForest(x=model.training, y=model.training.response,
                          ntree = 500000, nodesize=50, mtry=3,keep.forest=TRUE)
```



```
> model.1 <- randomForest(x=model.training, y=model.training.response,
                          ntree = 500000, nodesize=50, mtry=3,keep.forest=TRUE)
```



RMSLE: 0.462973 Placement: ~~35th~~ 34th of 427 teams

Just one problem...

```
> a <- Sys.time()
> model.1 <- randomForest(x=model.training, y=model.training.response,
                          ntree = 500000, nodesize=50, mtry=3,keep.forest=TRUE)
> b <- Sys.time()
> b - a
Time difference of 7.336037 hours
```

- Growing 500,000 trees with the competition data on a single Intel i7 desktop takes about seven hours.
- Tuning and hill-climbing is infeasible.
- We’re going to need to run this on multiple cores.

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Using foreach

```
> a <- Sys.time()
> registerDoMC(256)
> mcoptions <- list(preschedule = FALSE, set.seed = FALSE)
> model.1 <- foreach(ntree = rep(2000,256), .combine = combine, .packages =
"randomForest") > %dopar%
+          randomForest(x=model.training, y=model.training.response,
+                  ntree = ntree, nodesize=50, mtry=3,
+                    .options.multicore=mcoptions,keep.forest=TRUE)
> b <- Sys.time()
Time difference of 3.19432 minutes
```

- `foreach` forks R as many times as you have cores (256).
- With respect to `randomForest`, each core runs 2000 trees,
- and then combines them into a ~500k forest when execution is finished.

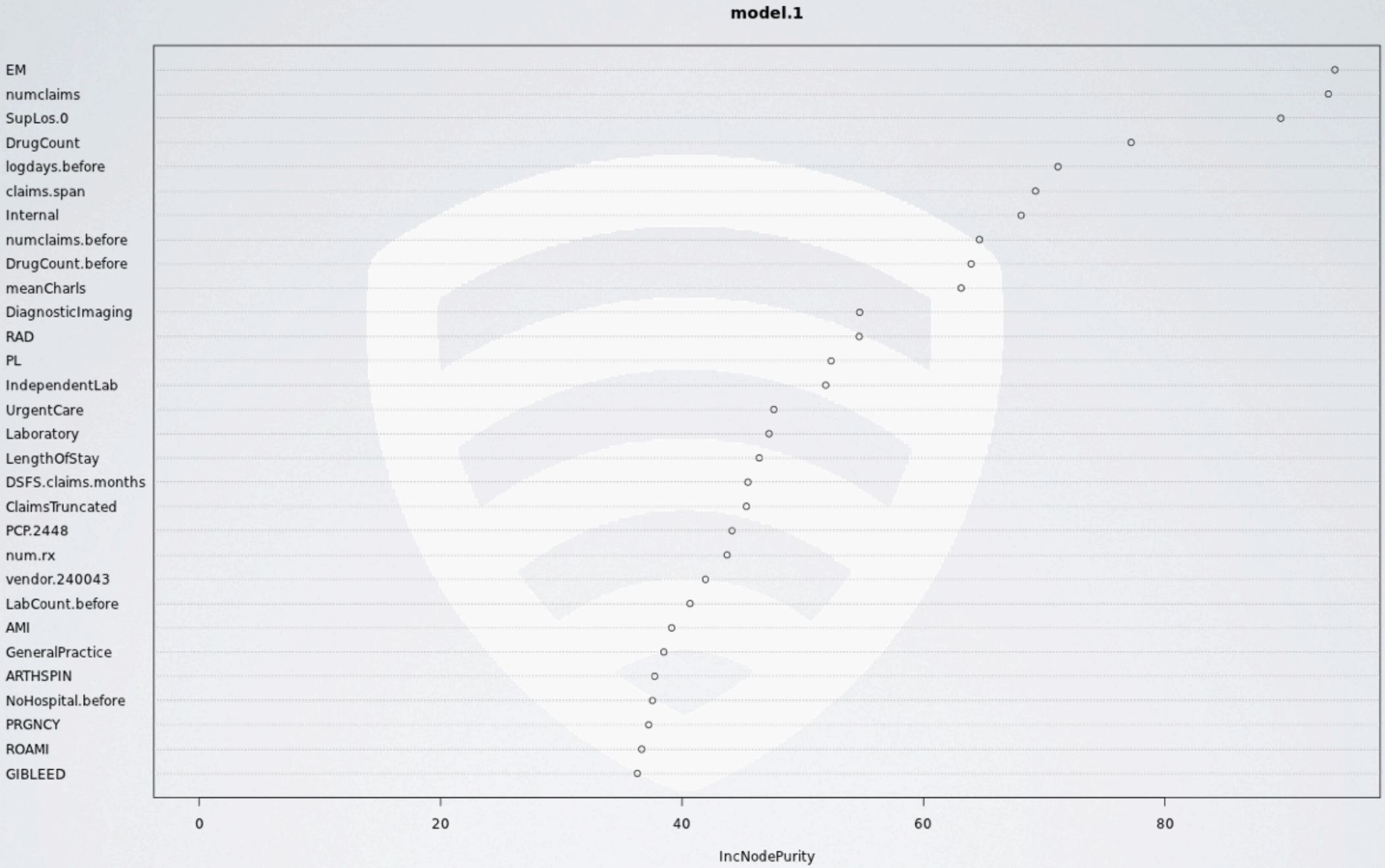
Recursive Feature Selection, with `mcapply`

```
> control.rfe.rf <- rfeControl(functions = hhp.functions,
                               rerank = TRUE,
                               workers = 256,
                               method = "repeatedcv",
                               number = 25,
                               returnResamp = "final",
                               computeFunction = mclapply,
                               computeArgs=list(mc.preschedule = FALSE,
                                                mc.set.seed = FALSE)
                              )
> sizes <- seq(200, 24442 ,by=100)
> model.1 <- rfe(model.training, model.training.response, sizes,
                 metric = "HHP", maximize = FALSE,
                 rfeControl = control.rfe.lm)
```

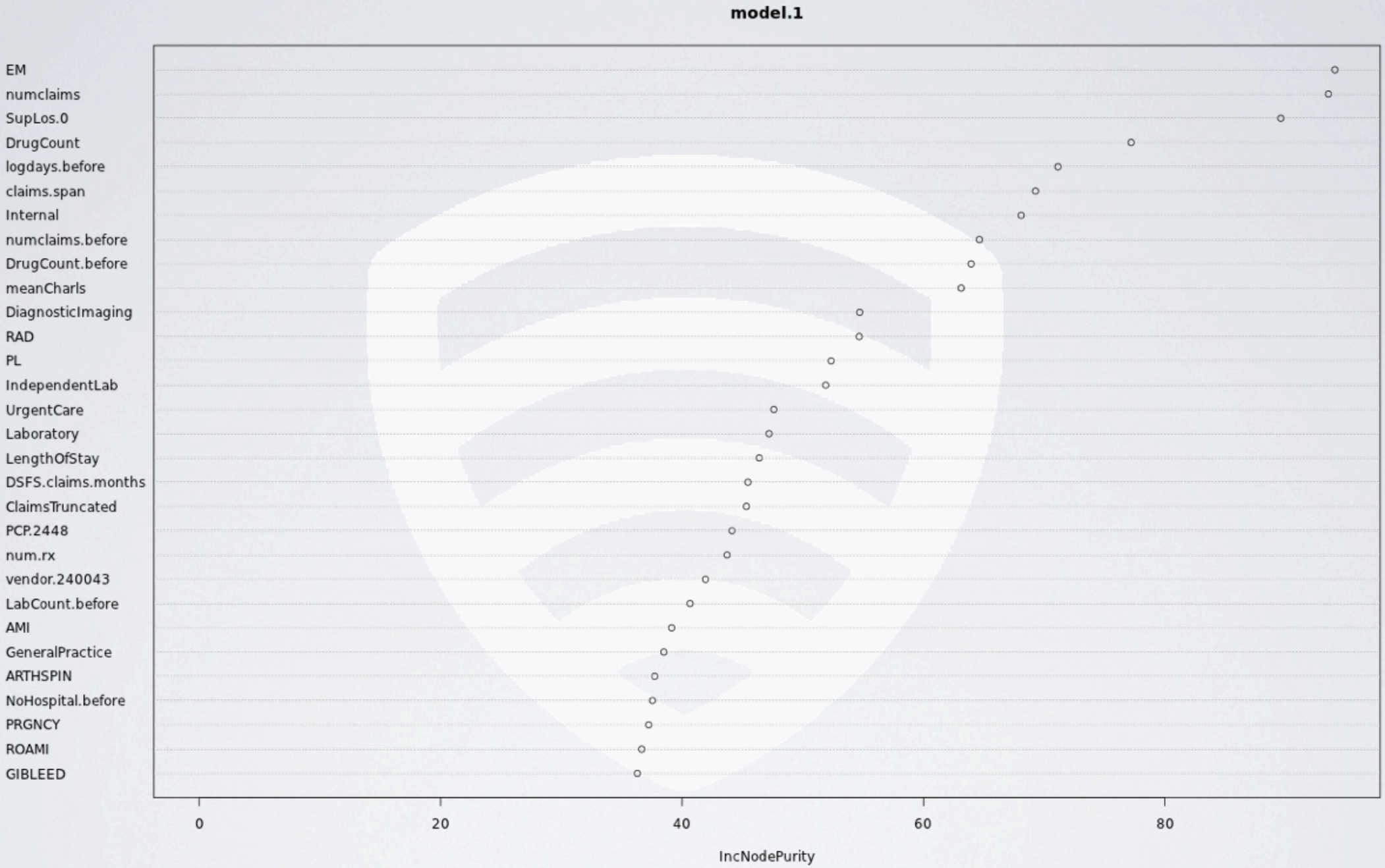
- Same process as linear RFS, excepts runs a 500k `randomForest` for each subset of predictors.

- Runs in total, about 10,000 500k `randomForests`.

Game on



Game on



RMSLE: 0.462678 Placement: ~~34th~~ 24th of 447 teams

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Summary

- **Simple, robust models are easy and will get you places**
  - Three variables put us in the top 40%
- **Visualizing data is always the first step**
  - Anscombe's Quartet
- **80% of my time was spent cleaning the data**
  - Better data will always beat better models

Questions?

End

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Appendix

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Looking at `Claims.csv`

Claims Table (Randomized claims for Y1, Y2, Y3, 2668990 x 14)

```
> head(claims)
  MemberID ProviderID Vendor   PCP Year  Specialty           PlaceSvc PayDelay       DSFS     PCG CharlsonIndex ProcedureGroup SupLOS
1 42286978    8013252 172193 37796   Y1    Surgery             Office       28 8- 9 months NEUMENT            0            MED      0
2 97903248    3316066 726296  5300   Y3   Internal             Office       50 8- 9 months NEUMENT            0            MED      1
3  2759427    2997752 140343 91972   Y3   Internal             Office       14  0- 1 month  METAB3            0             EM      1
4 73570559    7053364 240043 70119   Y3 Laboratory     Independent Lab       24  0- 1 month  METAB3            0            SCS      0
5 11837054    7557061 496247 68968   Y2    Surgery Outpatient Hospital       27 4- 5 months FXDISLC          1-2             EM      1
6 45844561    1963488   4042 55823   Y3 Pediatrics             Office       25 3- 4 months NEUMENT            0             EM      0
```

```
> levels(claims$Specialty)
 [1] "Anesthesiology"           "Diagnostic Imaging"
 [3] "Emergency"                "General Practice"
 [5] "Internal"                 "Laboratory"
 [7] "Obstetrics and Gynecology" "Other"
 [9] "Pathology"                "Pediatrics"
[11] "Rehabilitation"           "Surgery"
```

```
> levels(claims$ProcedureGroup)
 [1] "ANES" "EM"   "MED"  "PL"   "RAD"  "SAS"  "SCS"  "SDS"  "SEOA" "SGS"
[11] "SIS"  "SMCD" "SMS"  "SNS"  "SO"   "SRS"  "SUS"
```

```
> levels(claims$PlaceSvc)
[1] "Ambulance"           "Home"                "Independent Lab"
[4] "Inpatient Hospital"  "Office"              "Other"
[7] "Outpatient Hospital" "Urgent Care"
```

```
> levels(claims$CharlsonIndex)
[1] "0"   "1-2" "2-3" "4-5" "5+"
```

```
> levels(claims$PrimaryConditionGroup)
 [1] "AMI"      "APPCHOL"  "ARTHSPIN" "CANCRA"   "CANCRB"   "CANCRM"
 [7] "CATAST"   "CHF"      "COPD"     "FLaELEC"  "FXDISLC"  "GIBLEED"
[13] "GIOBSENT" "GYNEC1"   "GYNECA"   "HEART2"   "HEART4"   "HEMTOL"
[19] "HIPFX"    "INFEC4"   "LIVERDZ"  "METAB1"   "METAB3"   "MISCHRT"
[25] "MISCL1"   "MISCL5"   "MSC2a3"   "NEUMENT"  "ODaBNCA"  "PERINTL"
[31] "PERVALV"  "PNCRDZ"   "PNEUM"    "PRGNCY"   "RENAL1"   "RENAL2"
[37] "RENAL3"   "RESPR4"   "ROAMI"    "SEIZURE"  "SEPSIS"   "SKNAUT"
[43] "STROKE"   "TRAUMA"   "UTI"
```

```
> length(levels(claims$Vendor))
[1] 6387
```

```
> length(levels(claims$PCP))
[1] 1359
```

```
> length(levels(claims$ProviderID))
[1] 14699
```

Final Result

- After all the preprocessing's done, we now have three `right` files:

```
> dim(log.right.a)
[1] 76038   22443
> dim(log.right.b)
[1] 71435   22443
> dim(log.right.c)
[1] 70942   22443
```

- We make two dataframes called `training` and `testing`:

```
> training <- merge(log.right.a, log.right.b, by.x = "MemberID", by.y= "MemberID", sort=FALSE)
> testing <- merge(log.right.b, log.right.c, by.x = "MemberID", by.y= "MemberID", sort=FALSE)
```

- `training` contains data on Y1 and Y2 claims, with Y2 hospitalisation days.

- `testing` contains data on Y2 and Y3 claims, with Y3 hospitalisation days.

- All of our models will now be trained from the `training` dataset, and cross-validated on the `testing` set.

When is the HHP?

- Main competition runs from April 2011 - April 2013.
- There are three Milestone Prizes awarded in August 2011, February 2012, and September 2012.
- Registration and Team Mergers deadline is October 2, 2012.
- The Grand Prize Deadline is on April 4, 2013.

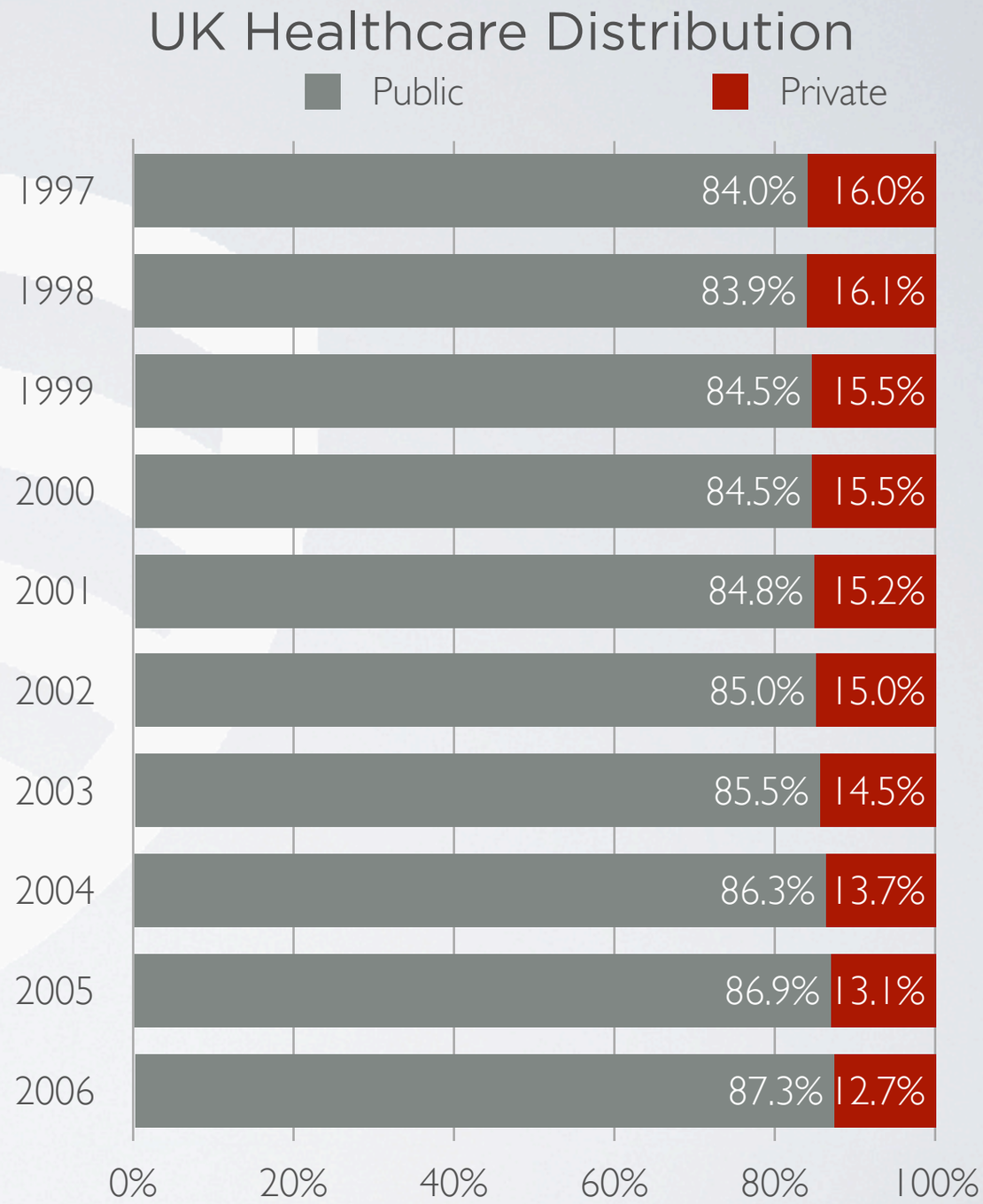
Date	Event	Prize
31 August 2011	First Milestone	1st: $30,000, 2nd: $20,000
13 February 2012	Second Milestone	1st: $50,000, 2nd: $30,000
4 September 2012	Third Milestone	1st: $60,000, 2nd: $40,000
4 April 2013	Final Prize	1st: $3,000,000, 2nd: $500,000

Healthcare in the United Kingdom

- Publicly funded, devolved organisations in England, Scotland and Wales (NHS), and Northern Ireland (HSC).

- Free at point-of-need for all permanent residents and foreign students.

- Private options available, but very small minority.



Source: ONS

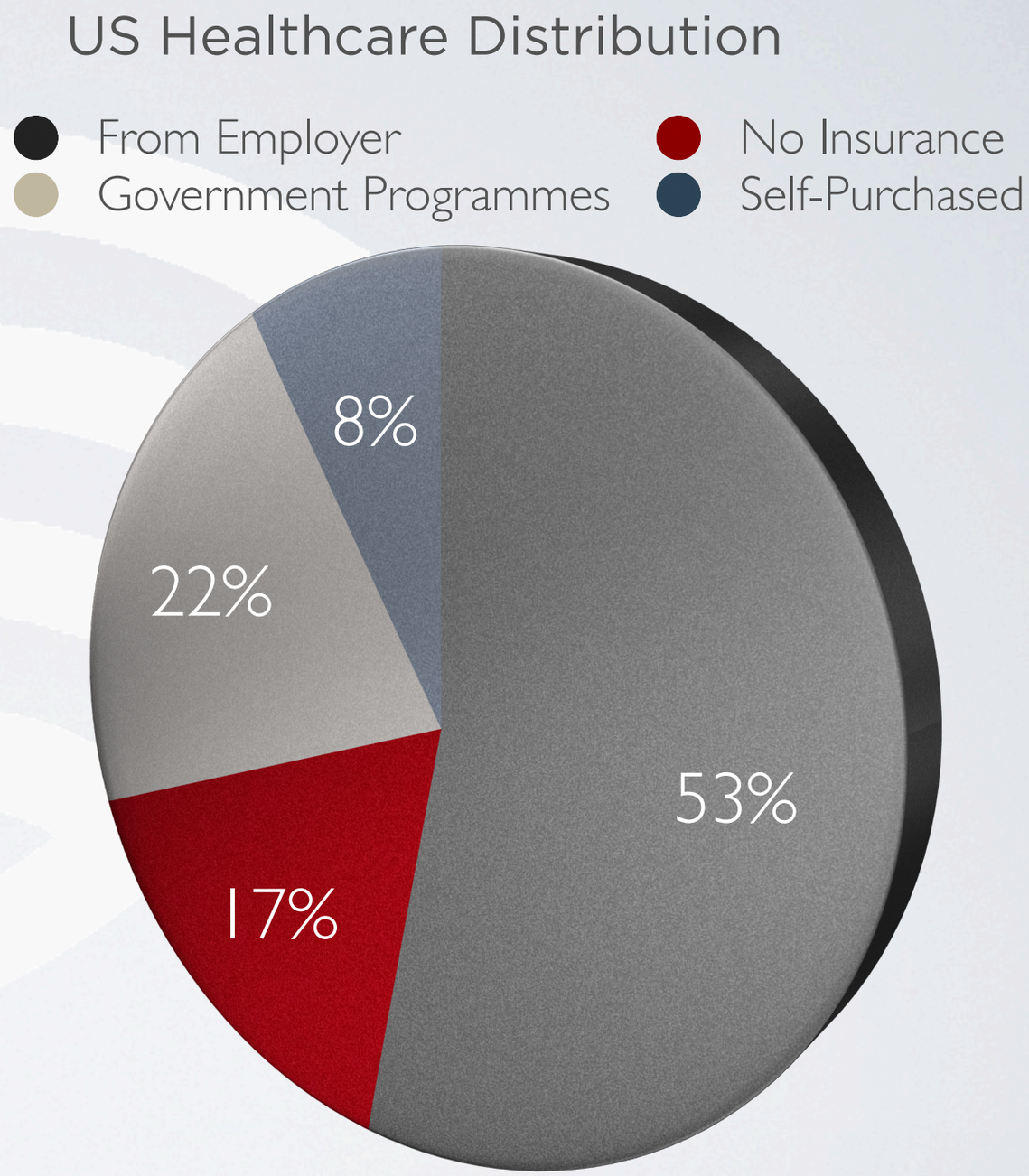
Healthcare in the United States

- Public options usually available to veterans, the elderly, and low-income families. (Reduced cost)

- Private options primarily administered through Managed Care Organisations, that may or may not also either sell insurance for their services.

  - (Conflict of interest?)

- 17.4% of Americans (~52.2m) are uninsured.



Source: HIPAA

What is the **HPN**?

- Heritage Provider Network (HPN): Non-insurance selling physician network that serves most of Southern California in the United States.

- 2,100 Primary Care Physicians (PCP), 30,000 Specialists.

- Comprehensive Electronic Health Records (EHR) are used and stored in their data infrastructure.

What if we added everything?

- Let's now add the rest of the columns for VendorID, PCP, and Provider ID? (remember, we had 22443 variables)

```
> model.1 <- lm(training, log(training$DaysInHospital))
> prediction <- predict(model, testing)

> prediction <- expm1(prediction)
Warning message:
In predict.lm(object, x) :
  prediction from a rank-deficient fit may be misleading
> summary(prediction) # Everything
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-2.1942 0.23955 0.25342 0.25594 0.89322 5.11723
> summary(prediction) # Kitchen Sink model
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.00134 0.11240 0.19463 0.21892 0.28700 2.42792
```

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- Kitchen Sink RMSLE: 0.463167

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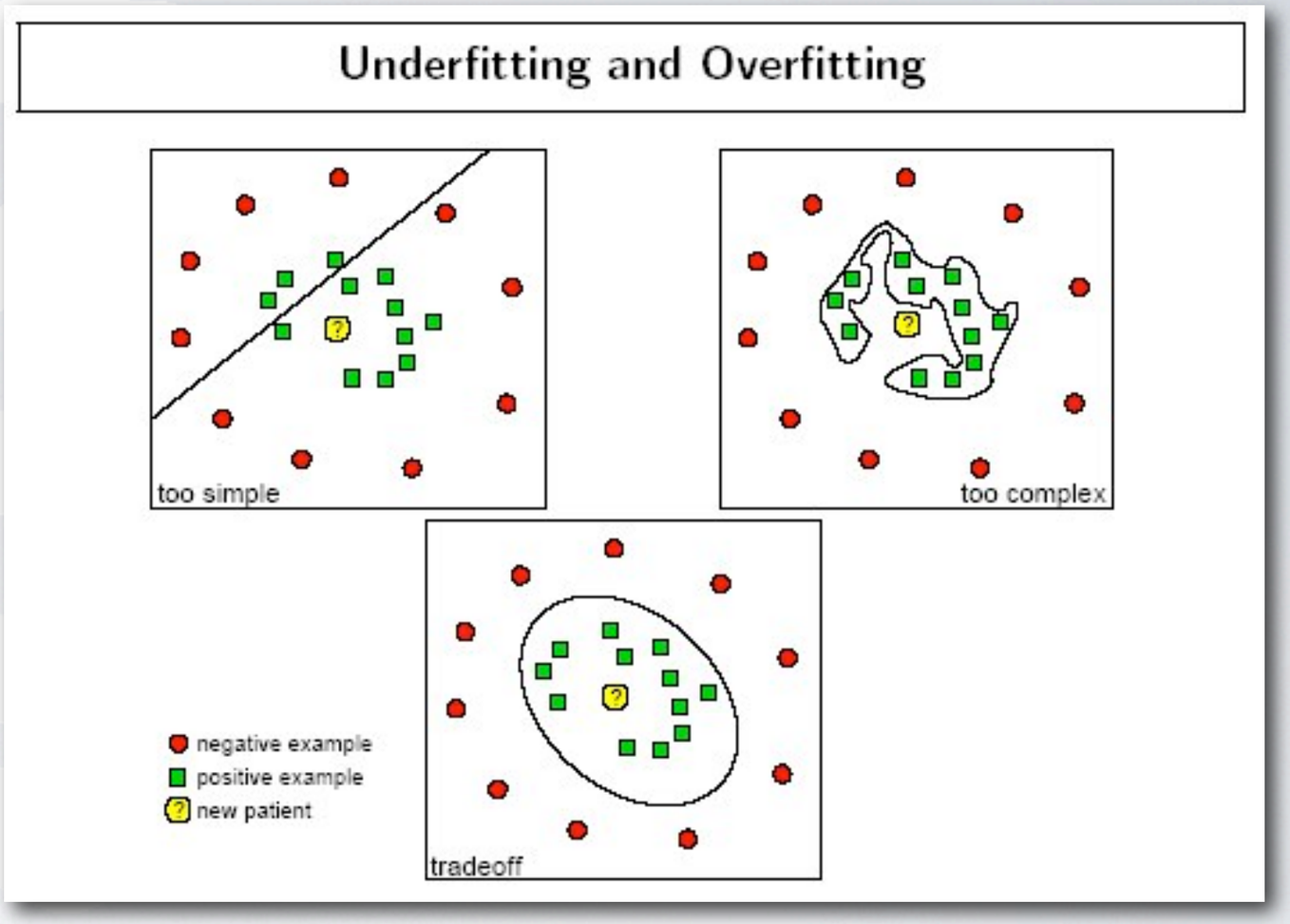
```

- Kitchen Sink RMSLE: 0.463167
- Everything RMSLE: 0.529431 -- why is this?

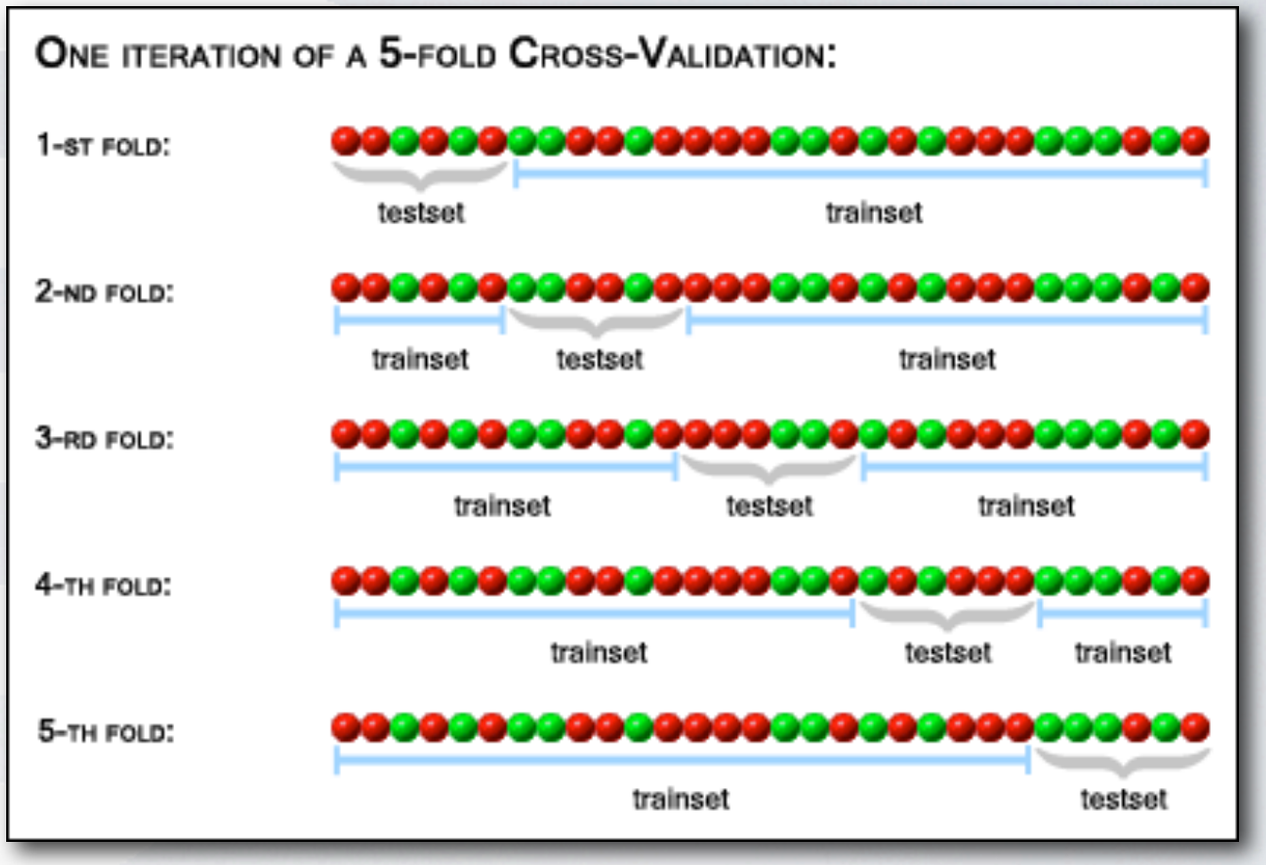
Overfitting

- By adding every predictor into our OLS linear regression, we are regressing for random error in the data.
- Even though our regression explains the training set well, it will fail to explain any other dataset as it is just too complicated given the number of observations (~70k).



Ways to overcome overfitting

- n-fold cross-validation:
  - Split original training set into n samples.
  - Choose one sample to be the validation set-the other samples serve as the training set and models are run.
  - Repeat this n times, each sample taking turns as the validation set
  - The model results are averaged.
  - This process is repeated many times to minimize RMSLE.

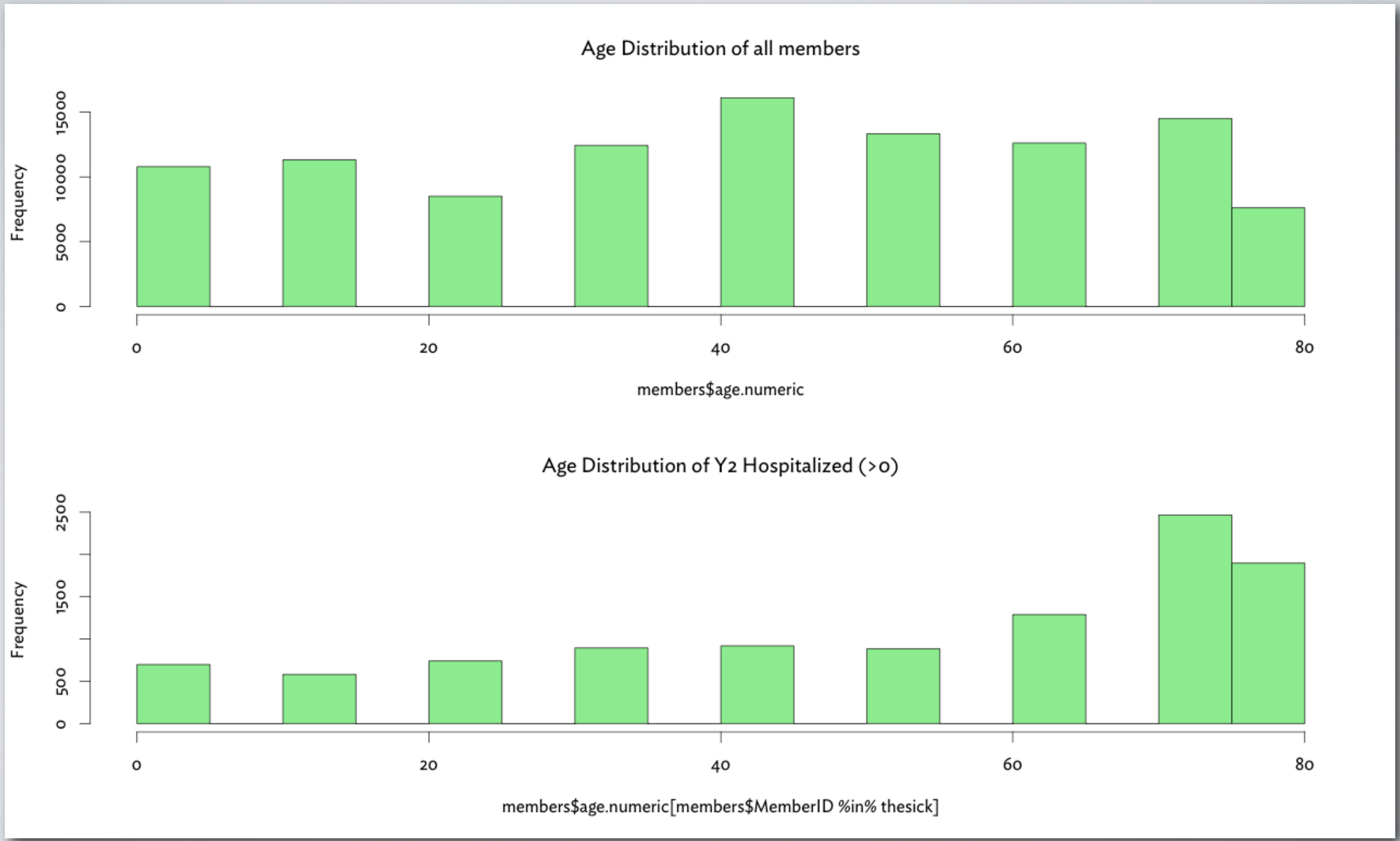


Copyright?

Regarding the trademark on Random Forest:

> “I don’t mean I am using a ‘Random Forest’: I am using an ‘ensemble of decision trees’ that happen to be generated - you know - randomly. Like in a forest.”
>
> Chris Raimondi, HHP Competitor

First Model



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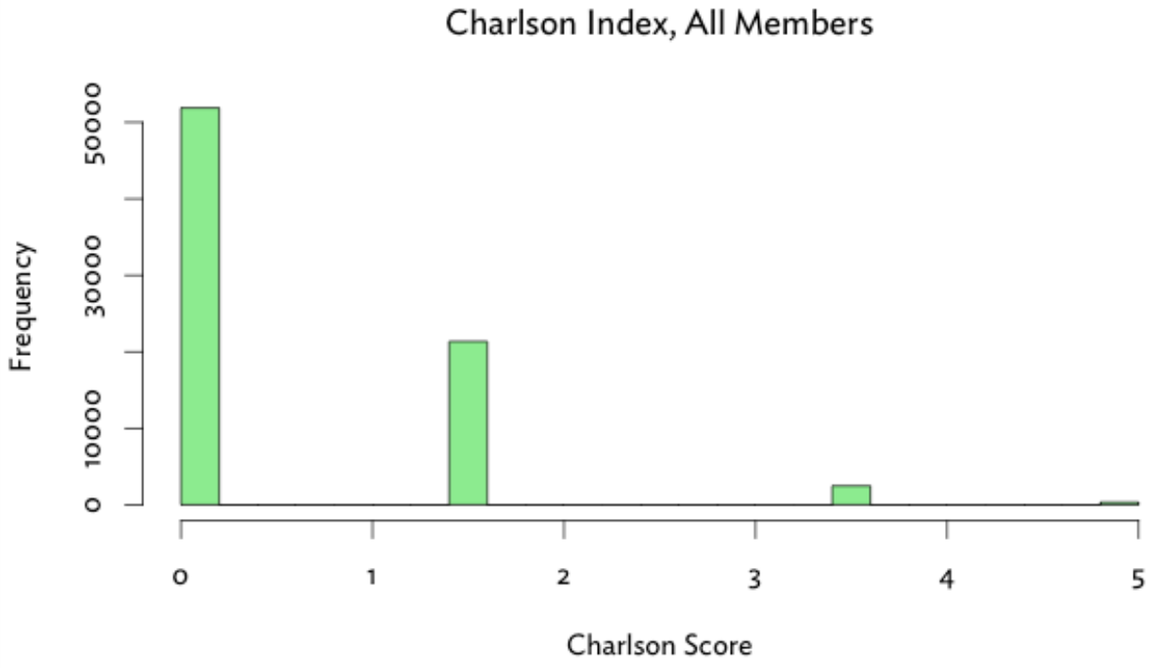
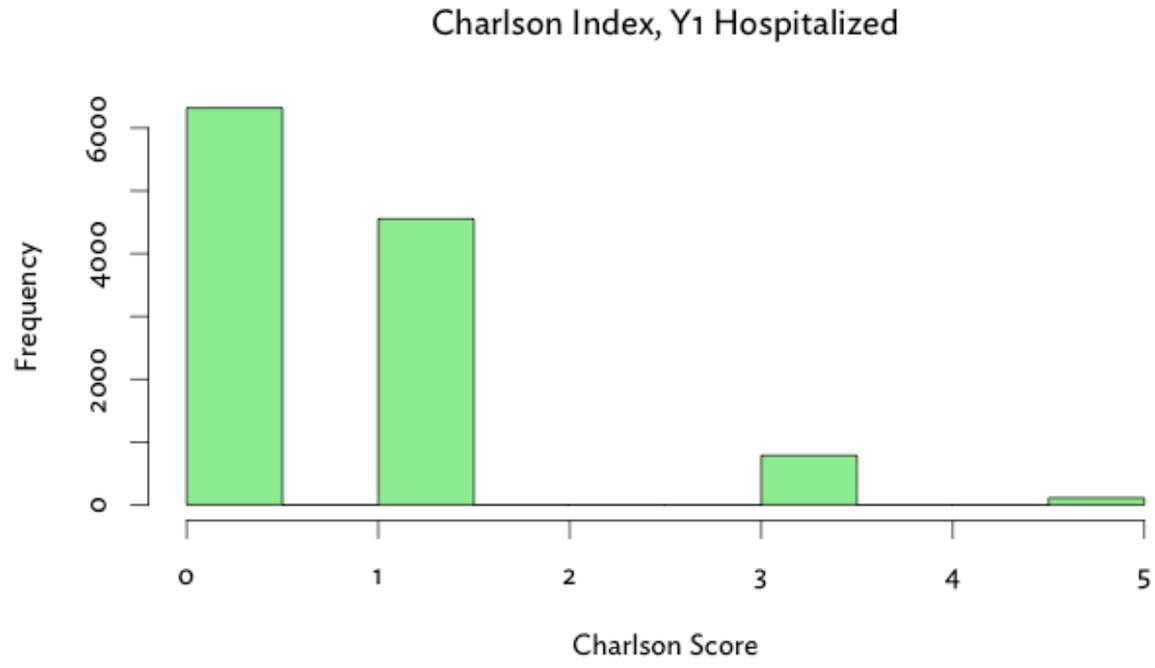
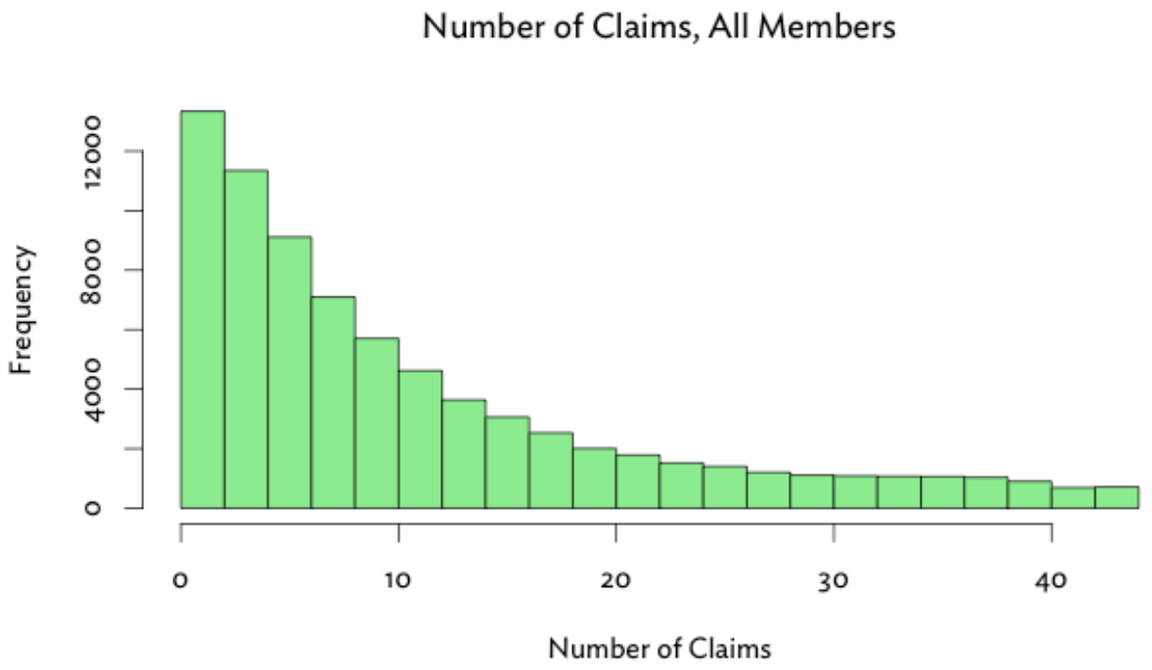
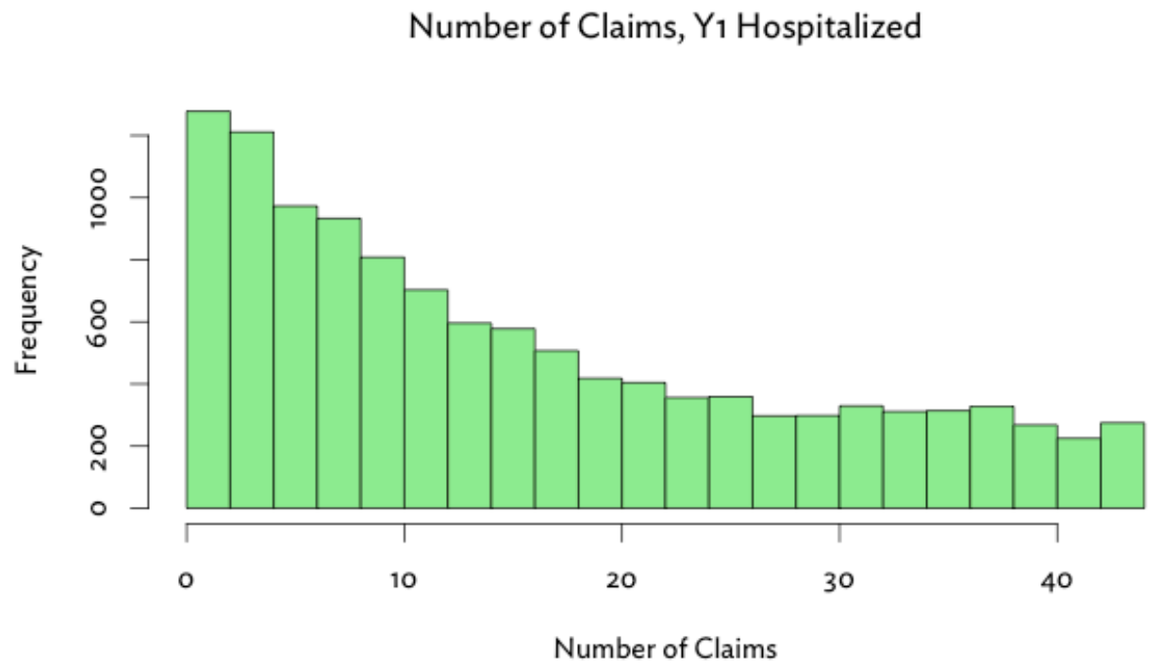








Future Parallelisation

- In June, we applied for a "Academic Partnership" grant with NVidia, and promptly forgot about it.

- In August (the day I flew back), they shipped two Tesla C2070 GPU cards to NYU.

- Each card has 448 CUDA cores (~1 teraflop) and 6GB of RAM.

- Future work in parallelising RDT models on Tesla GPUs will be written in C + CUDA...

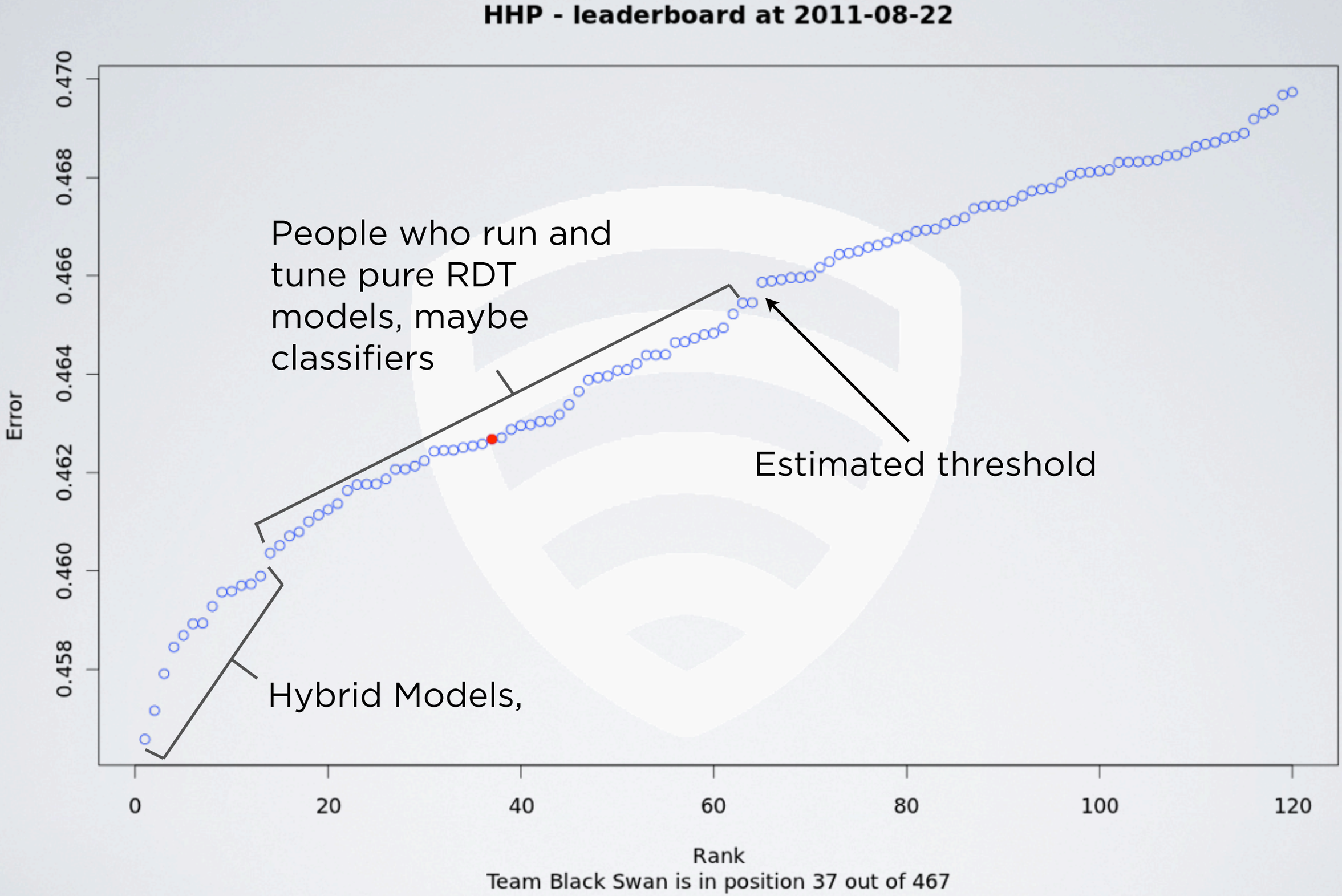
- But will be so much faster with respect to parameter tuning.

Oh well...

After hitting 24th place, I decided to take a break and start:

- Refactoring code
- Writing up the IEEE paper
- Drafting this presentation

After two weeks of no model submissions, I slipped from 24th to 37th.



Things to try

- **Classify first, then regress**
  - Use a kernalised SVM to classify members as either “hospitalised” or “non-hospitalised”,
  - then run an RDT/OLS regression on hospitalised members only, effectively moving the linearisation further.
- **External Datasets**
  - Can we use longitudinal studies on cardiovascular risk and fold relative risk into our hospitalisation model?
- **Merging Teams**
  - Should we merge teams and combine approaches to create a more accurate hybrid model?

Acknowledgments

- Bud Mishra, for advising me on model selection and overall approaches to the HHP.
- Fabian Menges and Giuseppe Narsizi for maintaining Courant Simulation Cluster.
- NYU High Performance Computing Cluster for auxiliary simulations.
- Nvidia for the Tesla GPUs and CUDA support.
- Funding was provided by NYU Courant and NYU Langone Medical Center.