

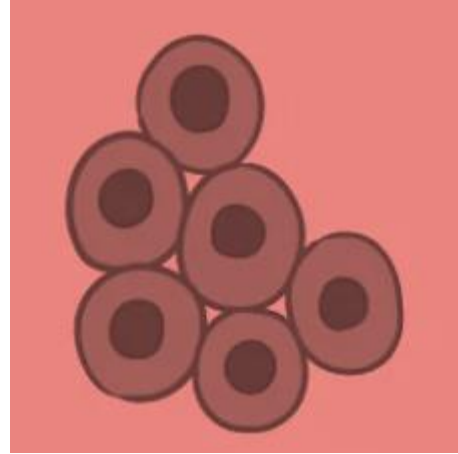
PSY810: Tumor Cell Classification by Nuclear Morphology

Christian D'Andrea

June 3 2020

Research
Question:

How can we separate
benign tumor cells
from **malignant** tumor
cells based on
morphology of the
nucleus?

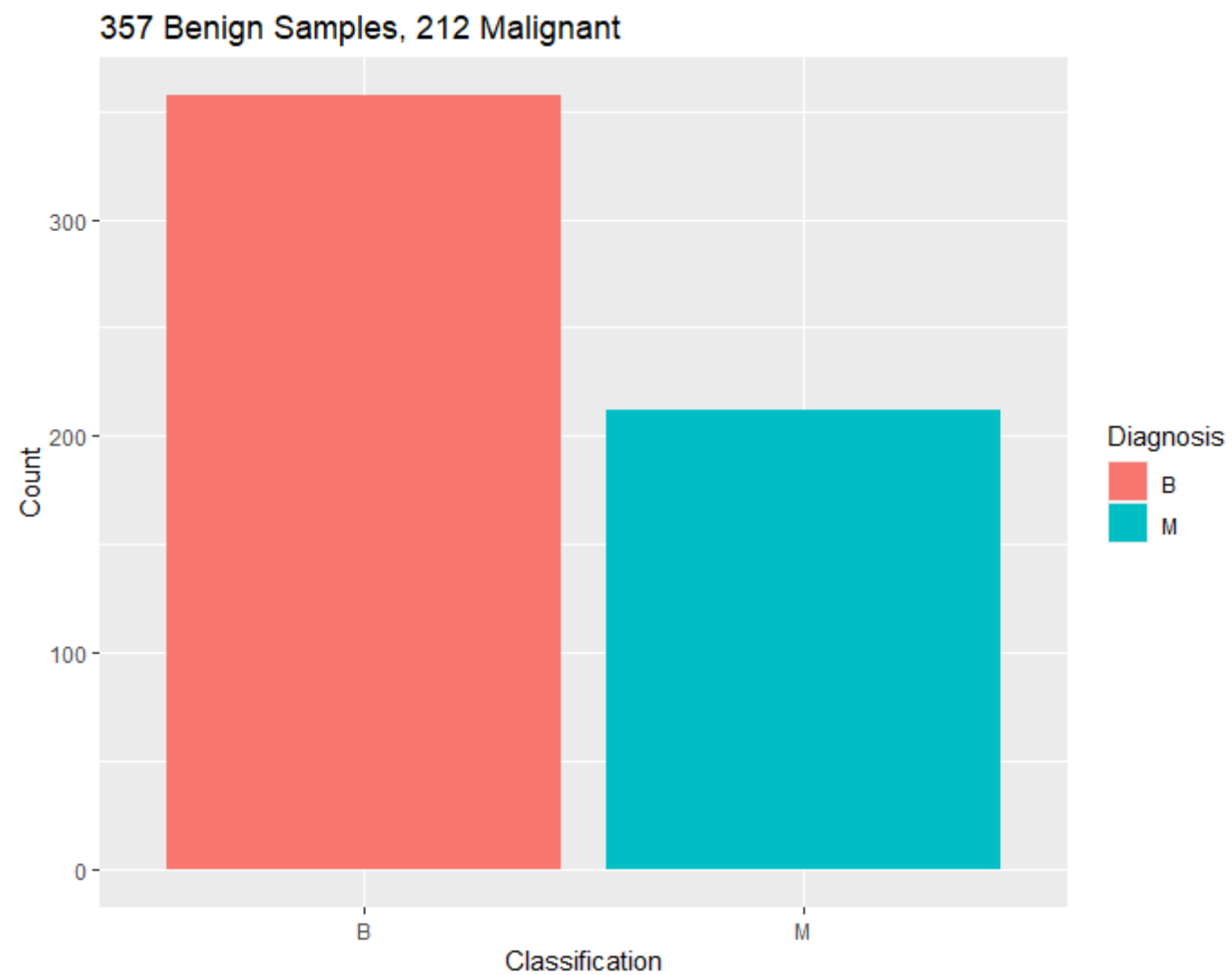


“Histological Samples”

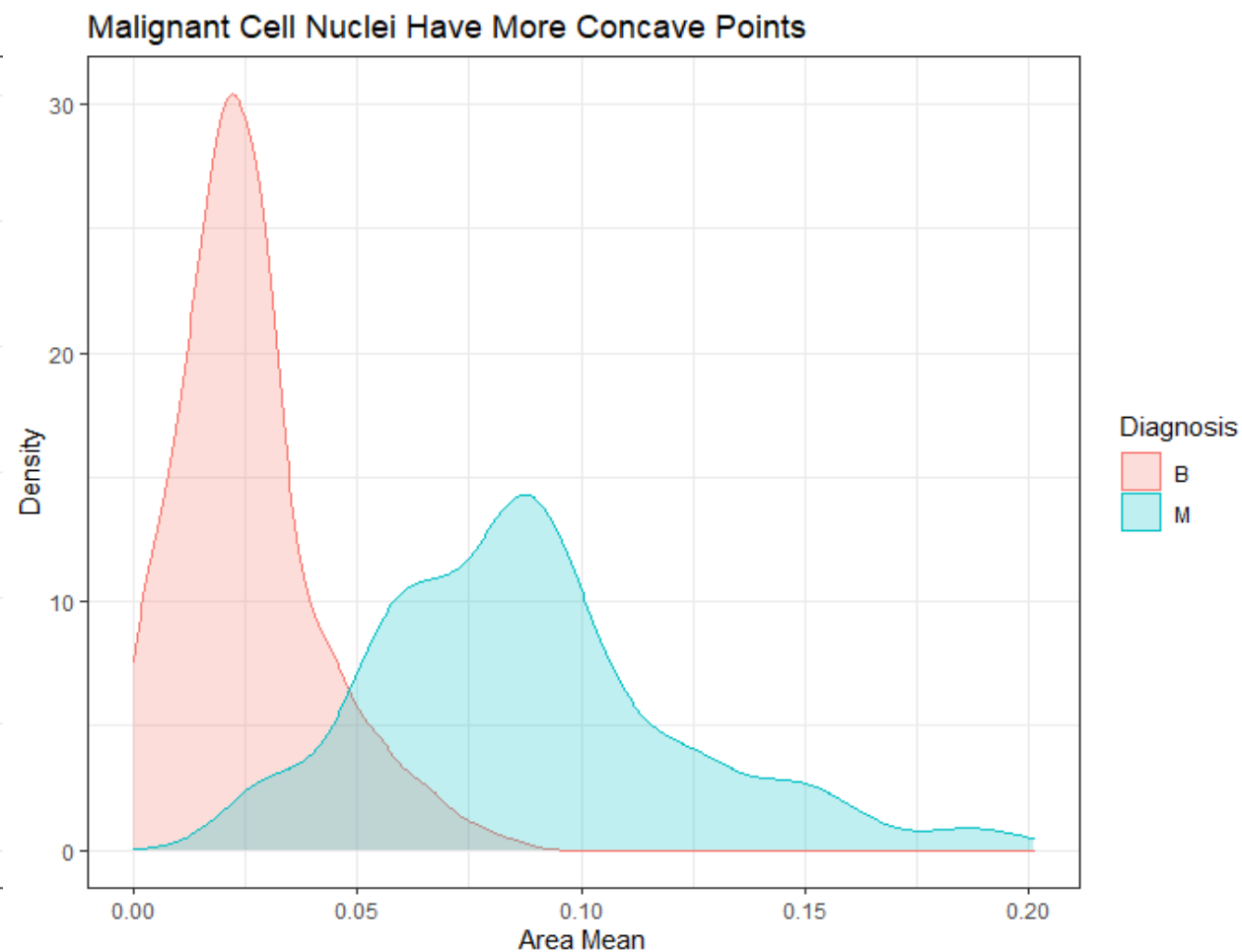
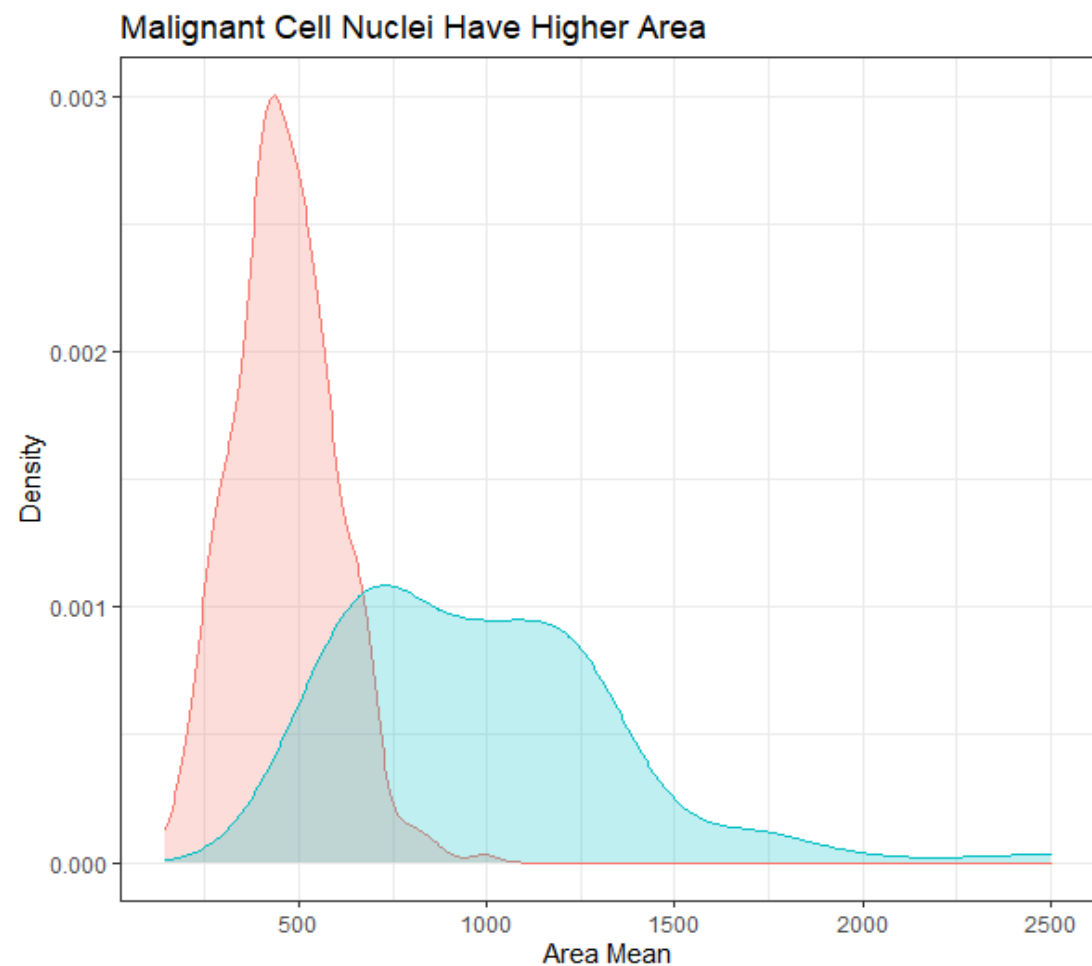
Predictors (mean, max, SE of):

- a) radius (mean of distances from center to points on the perimeter)
- b) texture (standard deviation of gray-scale values)
- c) perimeter
- d) area
- e) smoothness (local variation in radius lengths)
- f) compactness ($\text{perimeter}^2 / \text{area} - 1.0$)
- g) concavity (severity of concave portions of the contour)
- h) concave points (number of concave portions of the contour)
- i) symmetry (long axis/short axis)
- j) fractal dimension ("coastline approximation" – describes complexity of border pattern with respect to scale of measurement)

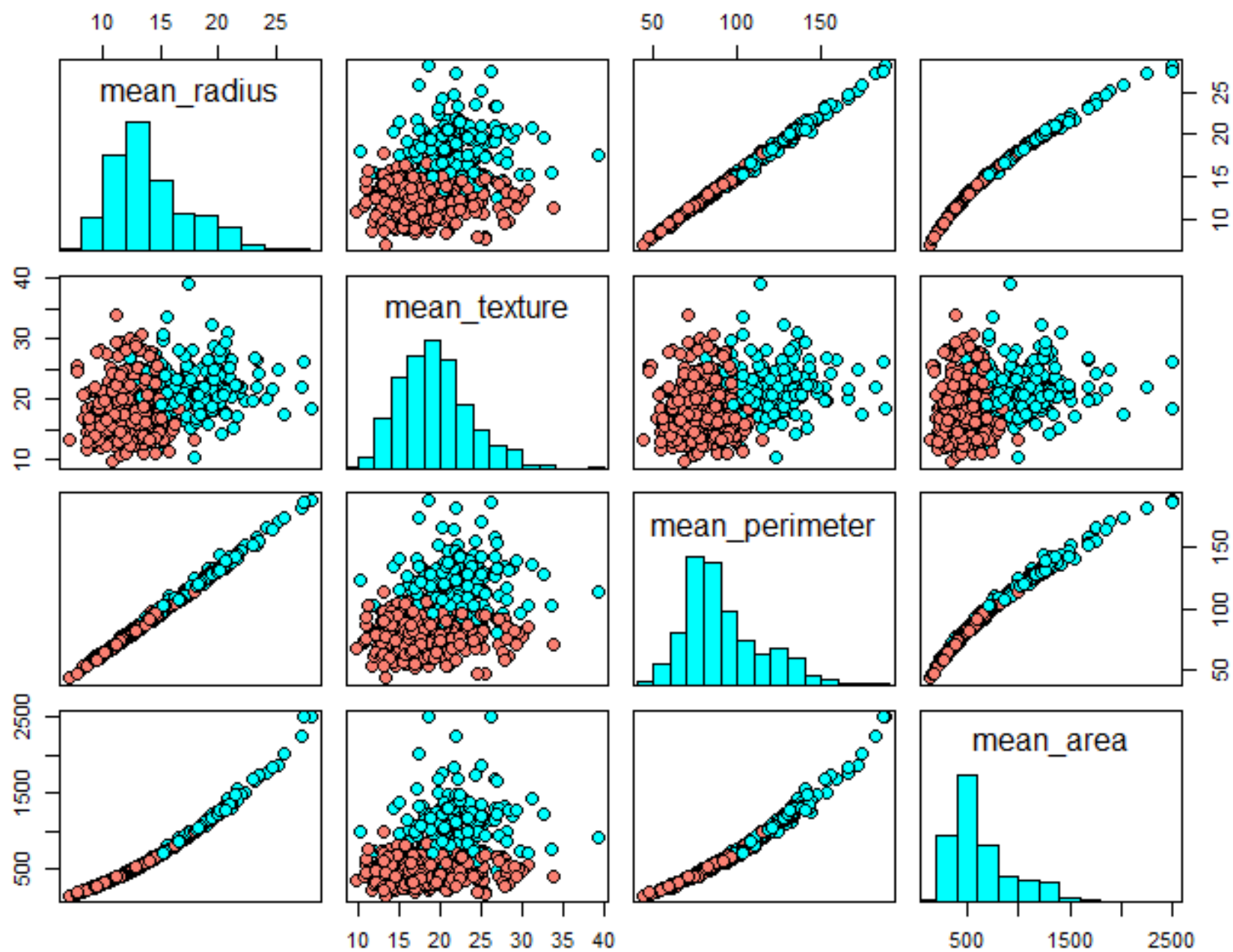
569 Samples



Fairly distinct distribution
across predictors

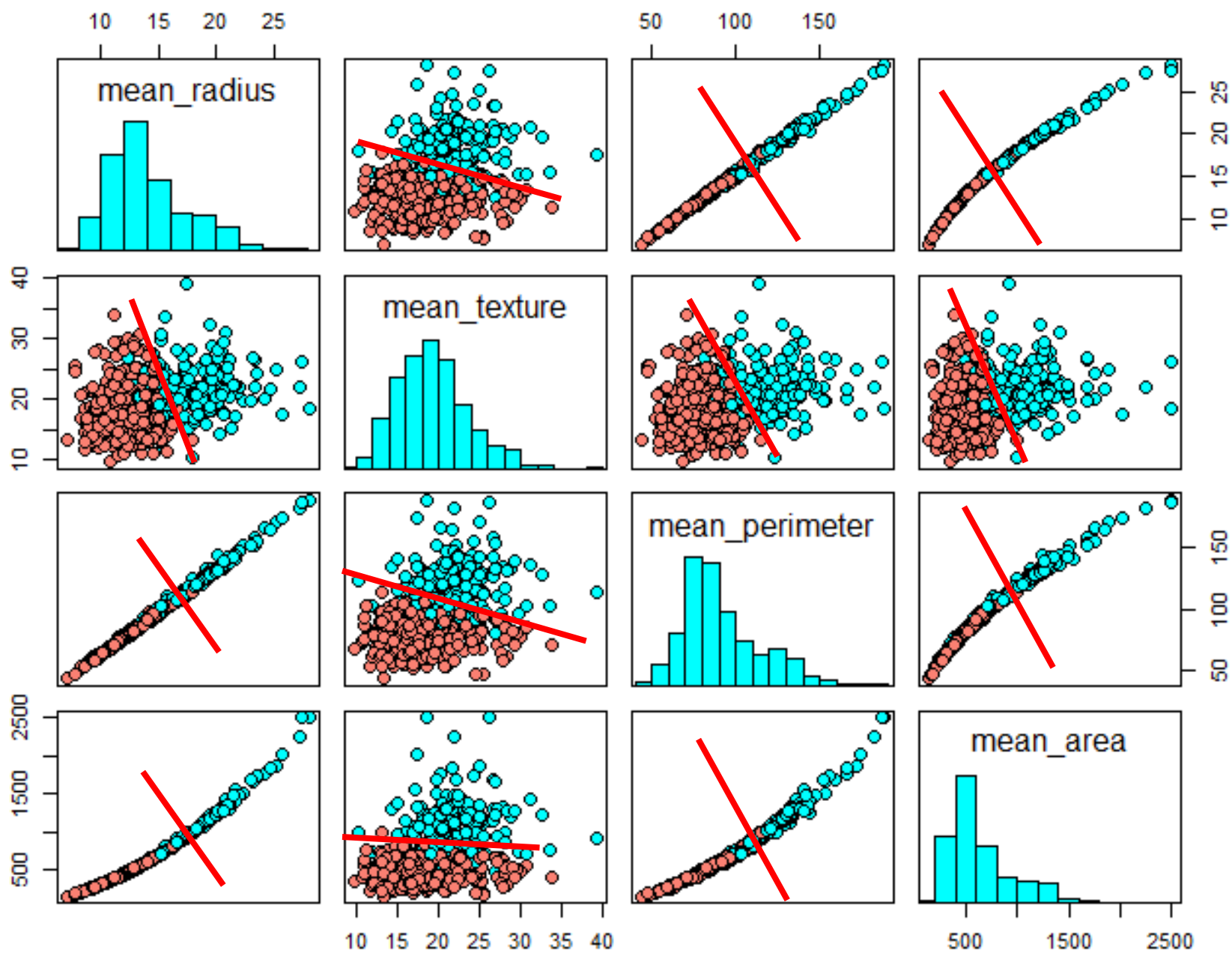


How do the
decision
boundaries
look?



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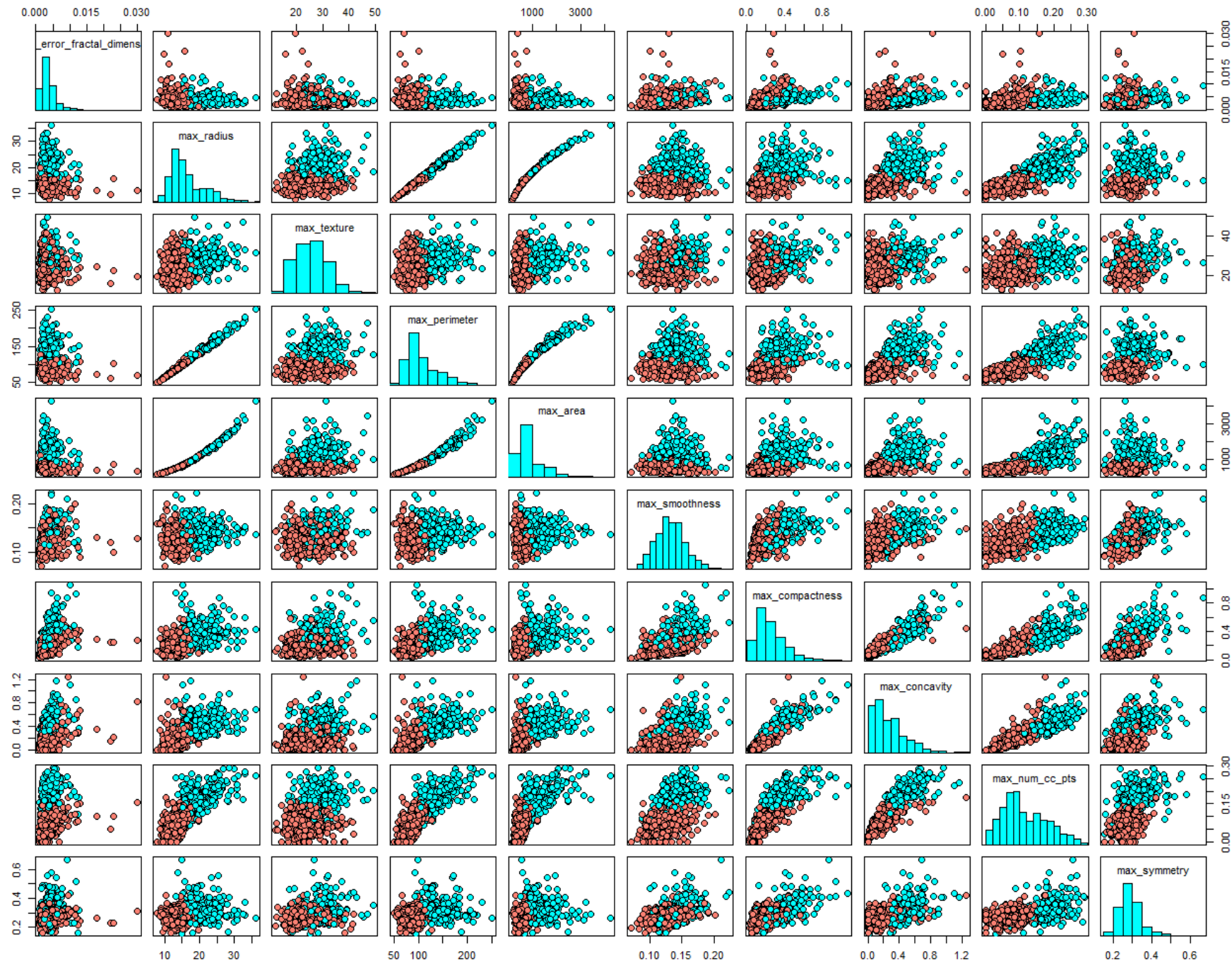
At first glance,
all boundaries
seem close to
linear, nothing
resembling
radial



How do the
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look?

At first glance,
All boundaries
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Same for all
predictors



Some Possible Methods:

Linear Regression

Logistic Regression

LDA

QDA

Linear SVM

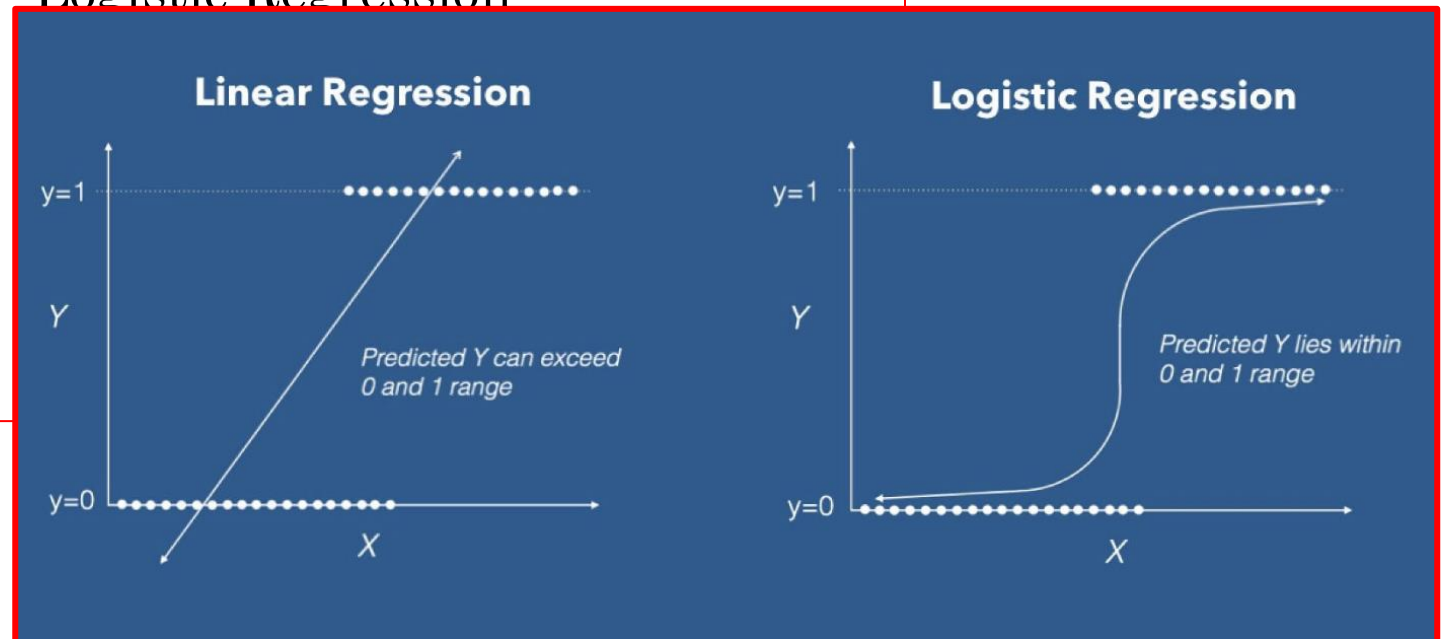
Radial SVM

Random Forest

Some Possible Methods:

~~Linear Regression~~
Logistic Regression

Not suitable for
binary
classification



Strong 1st option
(Zoe's suggestion),
commonly used
for binary
classification [1]

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Not as suitable as
LR for binary
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May work,
assumptions must
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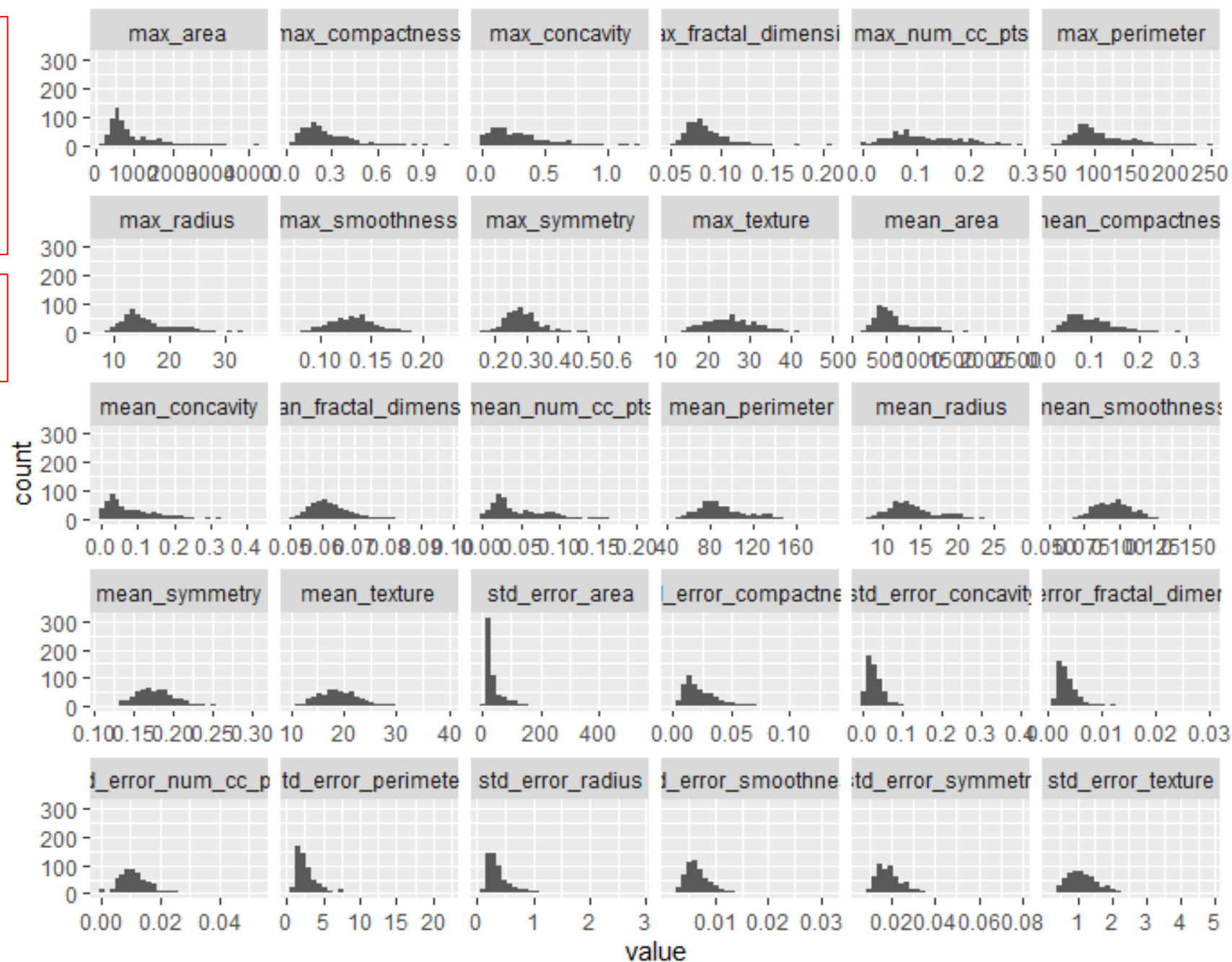
Random Forest

Not as suitable as
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Variable distributions are loosely normal

LDA and QDA may work well



Variable
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LDA and QDA
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But variance is
probably not
common, so the
LDA assumption
of common
variance is
violated

```
> min(colVariance)
[1] 7.001692e-06
> max(colVariance)
[1] 324167.4
> mean(colVariance)
[1] 15063.22
> sd(colVariance) #....no shot for LDA
[1] 62593.55
```

Strong 1st option
(Zoe's suggestion),
commonly used
for binary
classification [ref]

May work,
assumption must
be met to beat LR

May provide
better fit with
decreased
interpretability

Some Possible Methods:

~~Linear Regression~~

Logistic Regression

~~LDA~~

QDA

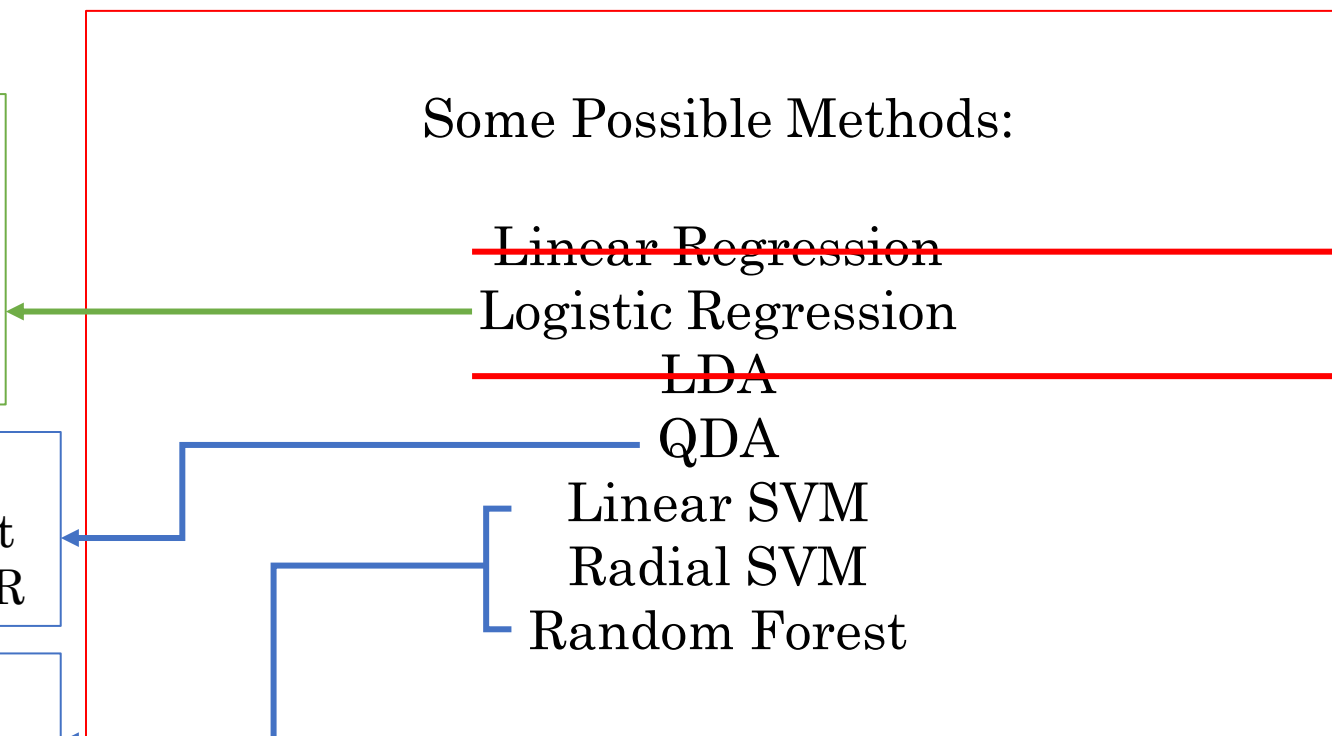
Linear SVM

Radial SVM

Random Forest

Not as suitable as
LR for binary
classification

Variance
assumption not
met



Logistic Regression

vs

QDA,
Linear SVM,
Radial SVM, and
Random Forest

LR with all 30 predictors did fit the data, but $z=0$ indicates perfect separation, can't assess $\beta \pm SE$

Hmm...
Let's get rid of variables causing perfect separation

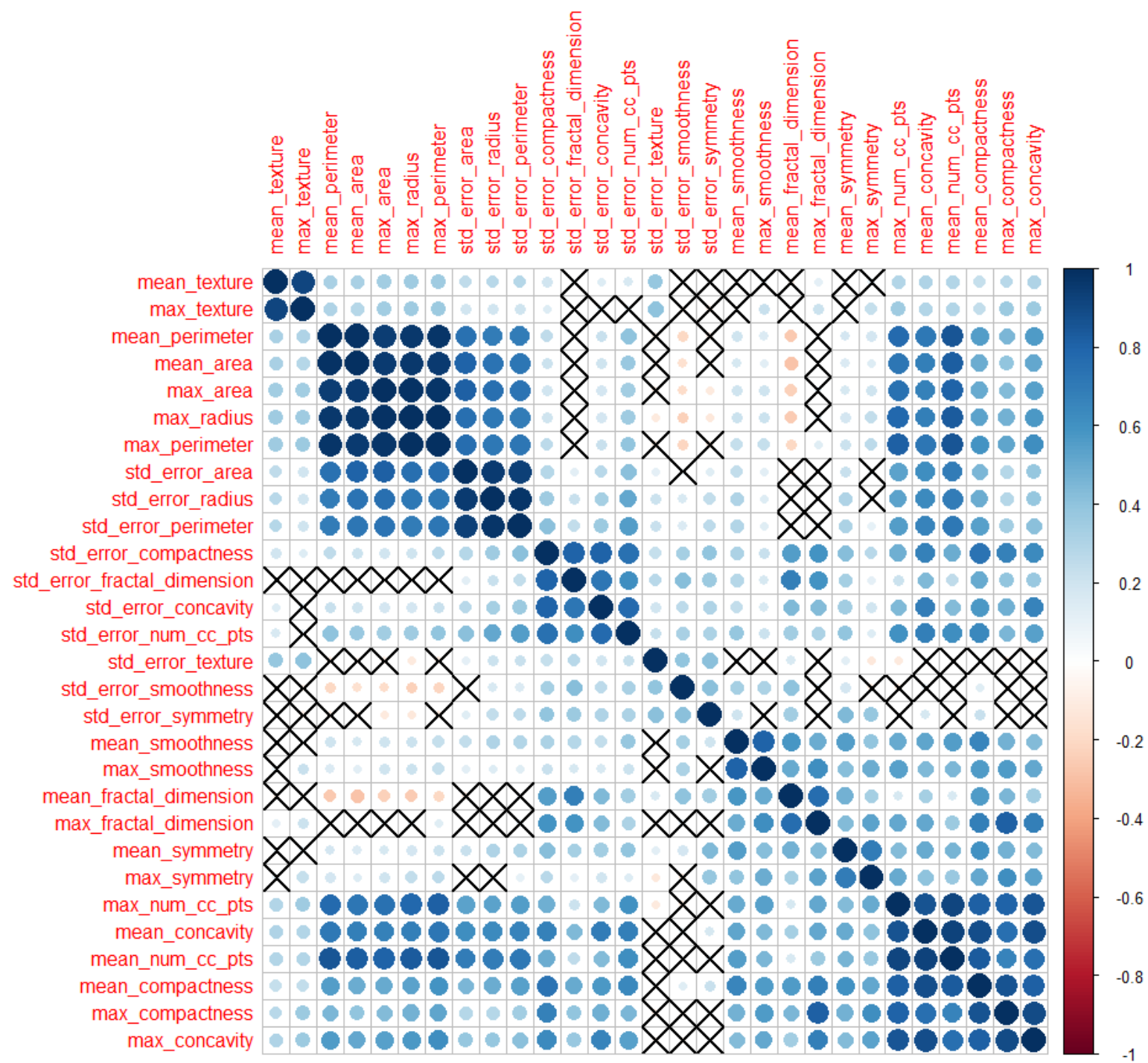
Check for collinear variables (two highly correlated independent variables)

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-9.543e+02	6.974e+06	0.000	1
mean_radius	-1.043e+03	7.462e+06	0.000	1
mean_texture	1.890e-01	1.612e+05	0.000	1
mean_perimeter	4.712e+01	9.022e+05	0.000	1
mean_area	6.262e+00	2.636e+04	0.000	1
mean_smoothness	1.318e+04	6.640e+07	0.000	1
mean_compactness	-9.352e+03	3.028e+07	0.000	1
mean_concavity	1.418e+02	2.537e+07	0.000	1
mean_num_cc_pts	7.873e+03	3.732e+07	0.000	1
mean_symmetry	5.506e+02	2.851e+07	0.000	1
mean_fractal_dimension	-5.957e+03	5.436e+07	0.000	1

Large SEs, Wald's test failed, normally should reject variables

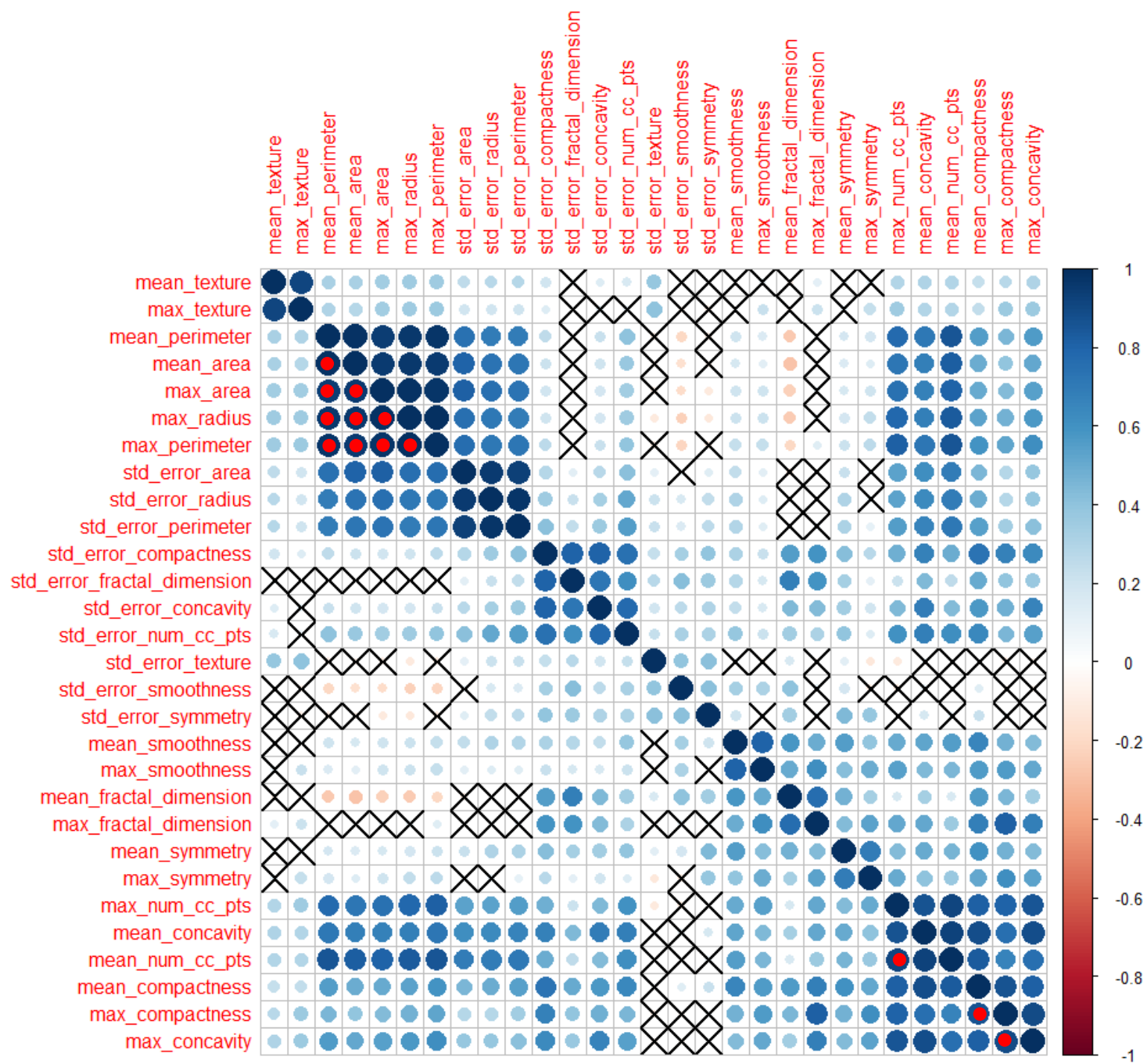
Collinearity?



Collinearity?

Yes •

Obscures the
attribution of
predictive power

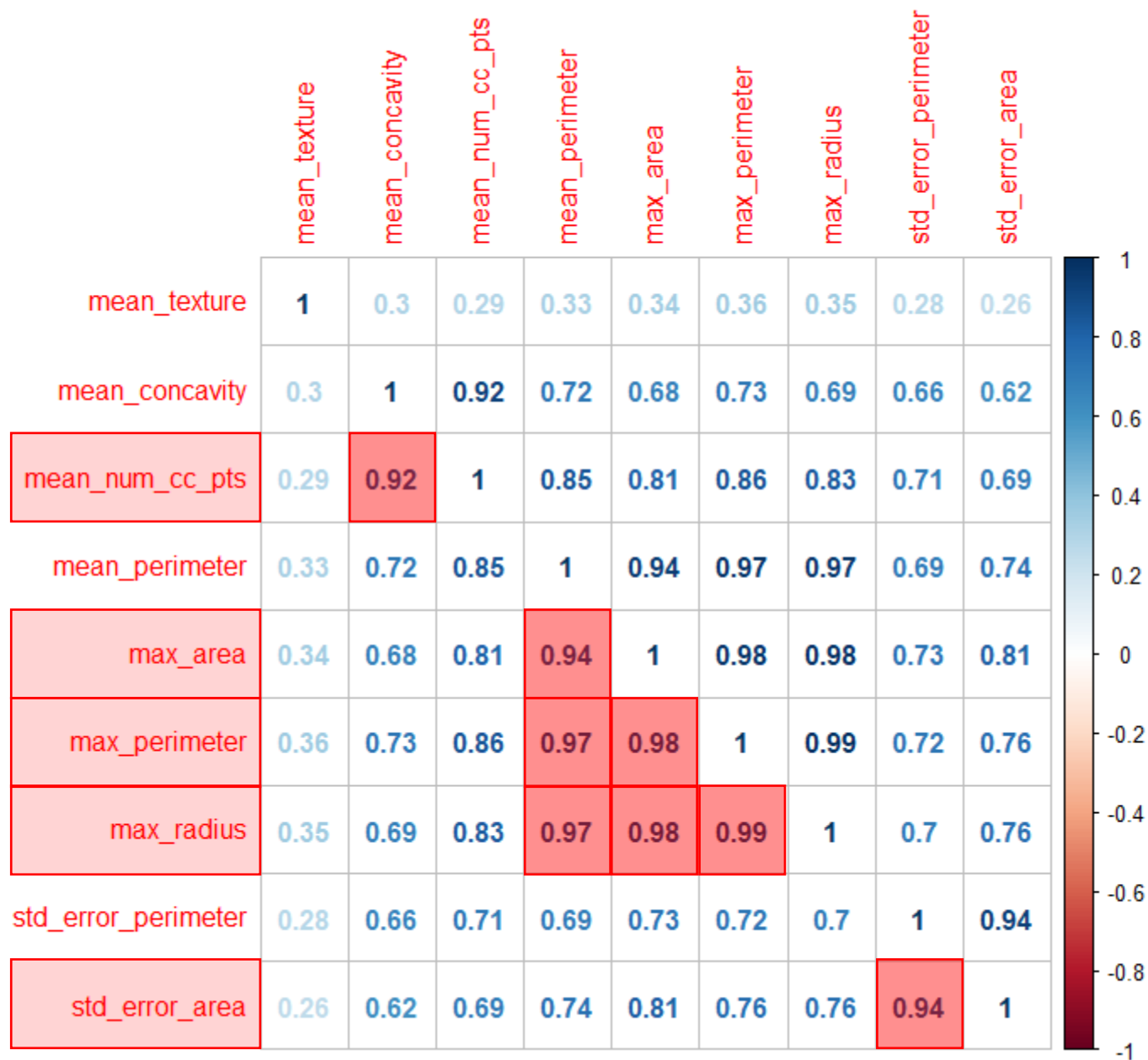


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Remove 1/2 variables with $R^2 > 0.9$



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Seems to have fixed the issue

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-5.988e+01	5.753e+01	-1.041	0.2979
mean_radius	-3.389e+01	2.408e+01	-1.407	0.1593
mean_texture	-5.206e-01	7.217e-01	-0.721	0.4707
mean_perimeter	4.174e+00	3.345e+00	1.248	0.2121
mean_area	9.365e-02	8.365e-02	1.120	0.2629
mean_smoothness	3.800e+02	2.472e+02	1.537	0.1242
mean_compactness	-2.193e+02	1.777e+02	-1.234	0.2171
mean_concavity	1.153e+02	7.464e+01	1.544	0.1225
mean_symmetry	-1.210e+02	8.925e+01	-1.356	0.1752
mean_fractal_dimension	3.500e+00	4.015e+02	0.009	0.9930
std_error_radius	1.132e+02	5.888e+01	1.922	0.0546 .
std_error_texture	-5.939e+00	3.963e+00	-1.499	0.1339
std_error_perimeter	-9.945e+00	6.602e+00	-1.506	0.1319
std_error_smoothness	1.118e+03	8.795e+02	1.271	0.2036
std_error_compactness	9.409e+02	4.750e+02	1.981	0.0476 *
std_error_concavity	-3.565e+02	1.757e+02	-2.029	0.0425 *
std_error_num_cc_pts	7.813e+02	6.566e+02	1.190	0.2341
std_error_symmetry	-6.131e+02	3.439e+02	-1.783	0.0746 .
std_error_fractal_dimension	-8.216e+03	4.134e+03	-1.987	0.0469 *
max_texture	1.247e+00	7.610e-01	1.638	0.1013
max_smoothness	-1.902e+02	1.597e+02	-1.191	0.2338
max_compactness	-1.210e+02	6.749e+01	-1.793	0.0730 .
max_concavity	3.620e+01	2.872e+01	1.261	0.2074
max_num_cc_pts	1.287e+02	1.042e+02	1.235	0.2168
max_symmetry	1.172e+02	5.815e+01	2.016	0.0438 *
max_fractal_dimension	8.600e+02	4.060e+02	2.118	0.0341 *

signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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log odds of M Intercept β Variable

β of 941 means $\ln\left(\frac{p}{1-p}\right) = -599 + (941 * SE_{compactness})$

and let $L = -599 + (941 * SE_{compactness})$

So the effect on probability is $p = \frac{\exp(L)}{\exp(L)+1}$

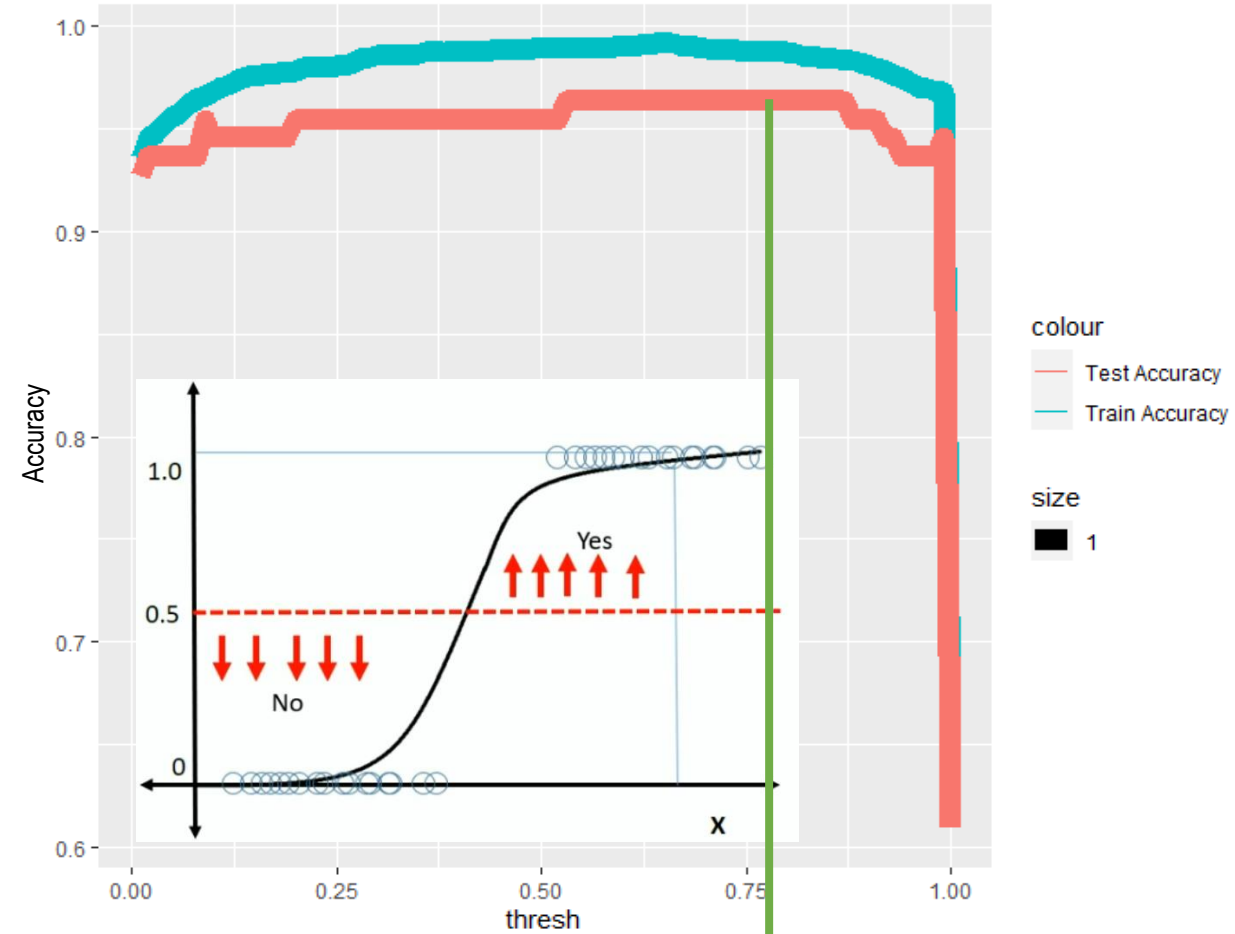
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(Intercept)

std_error_compactness

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Threshold optimization

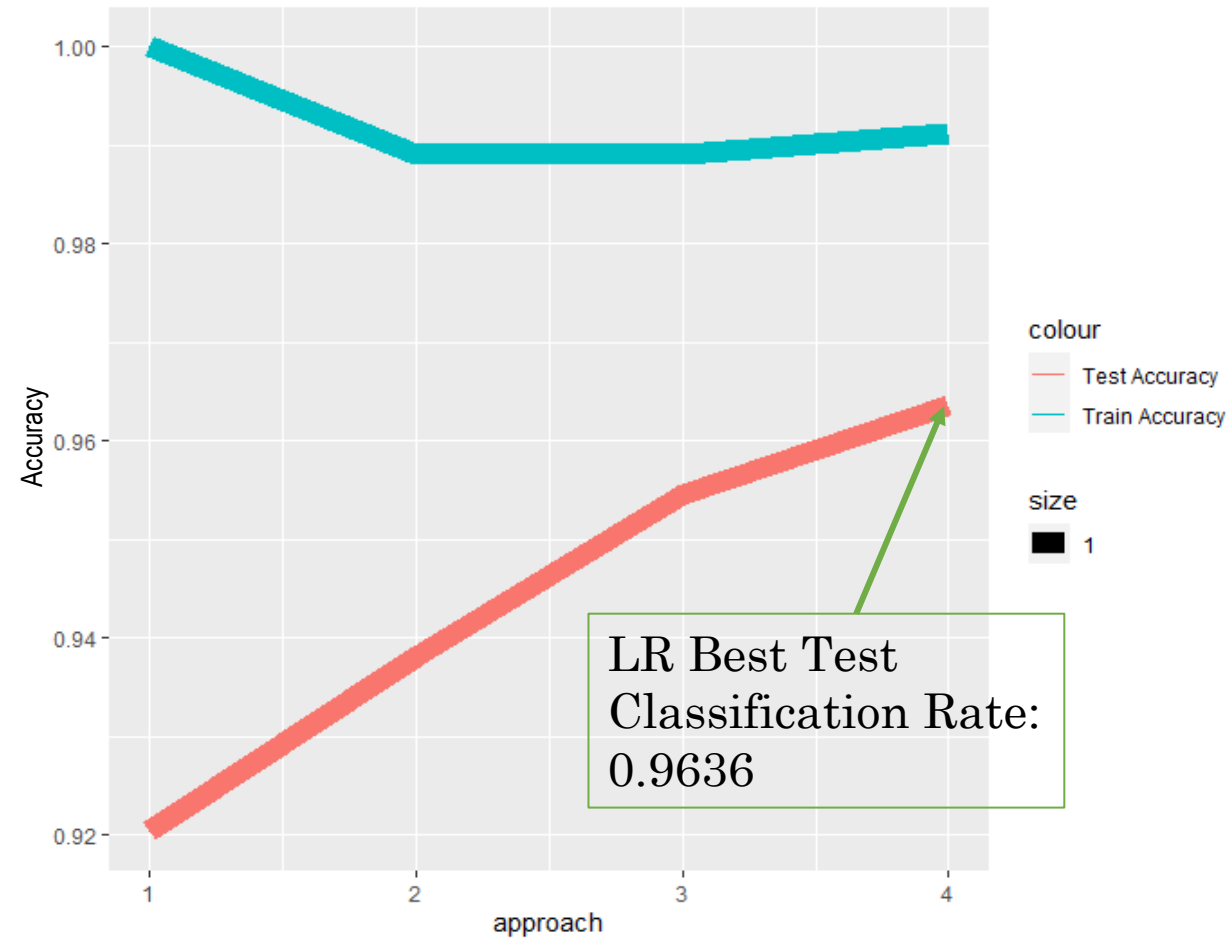


$$T_{\text{optimized}} = 0.77$$

Logistic Regression Results

Approaches:

1. 30 predictors, no CV, $T = 0.5$
2. 1, sans $\frac{1}{2}$ collinear predictors
3. 2, with 10-fold CV
4. 3, with $T_{\text{optimized}} = 0.77$



SVM Results

Accuracy of *tuned* linear and radial SVMs over costs and gammas range with 10-fold CV

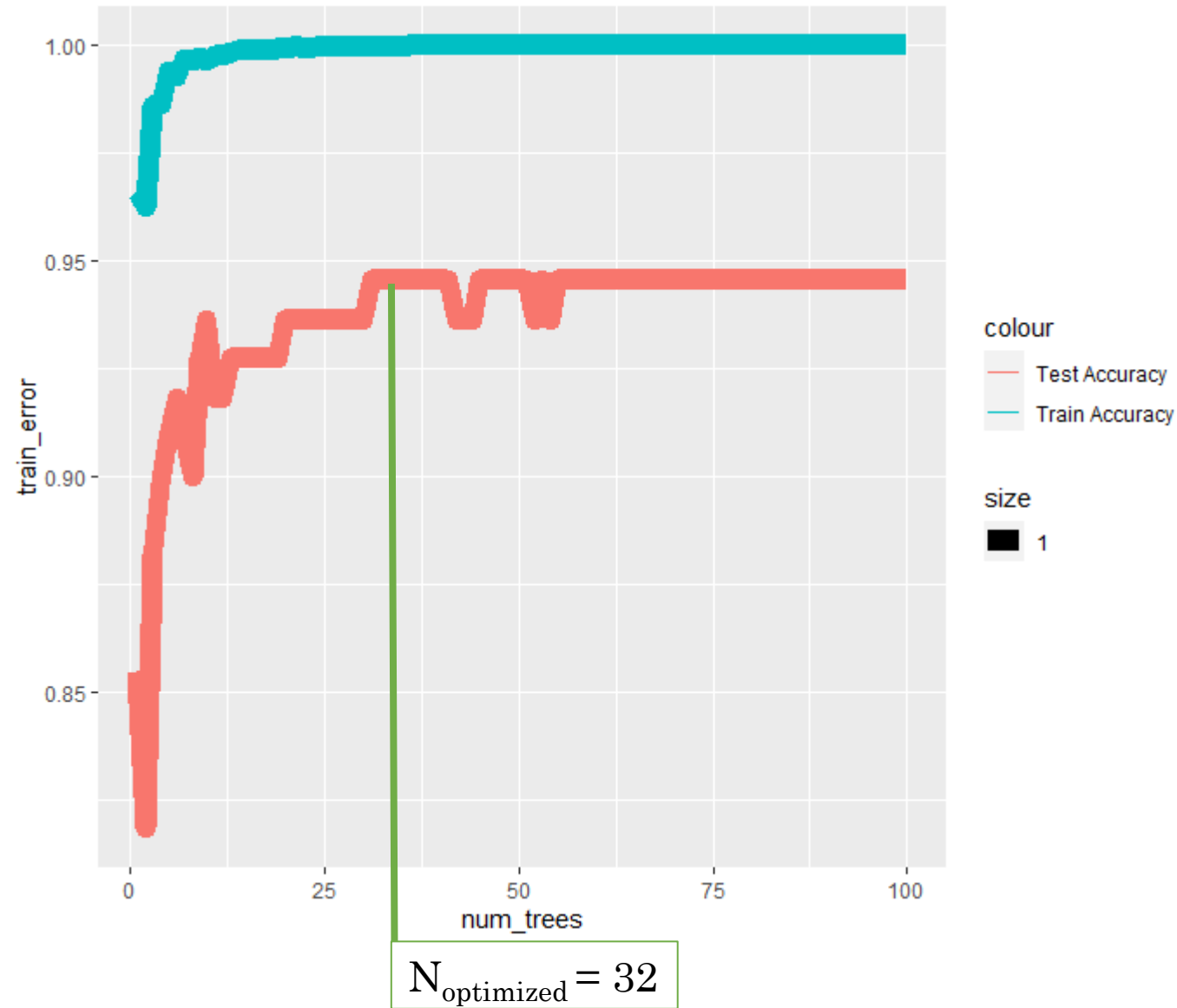
Linear SVM: **0.930** with cost=0.1 and gamma = 1e-5

Radial SVM: **0.960** with cost = 10 and gamma = 0.1

Random Forest
Results:
10-fold CV and
 N_{trees} optimization

Input data is
reduced dataset
after removal of
collinear
variables

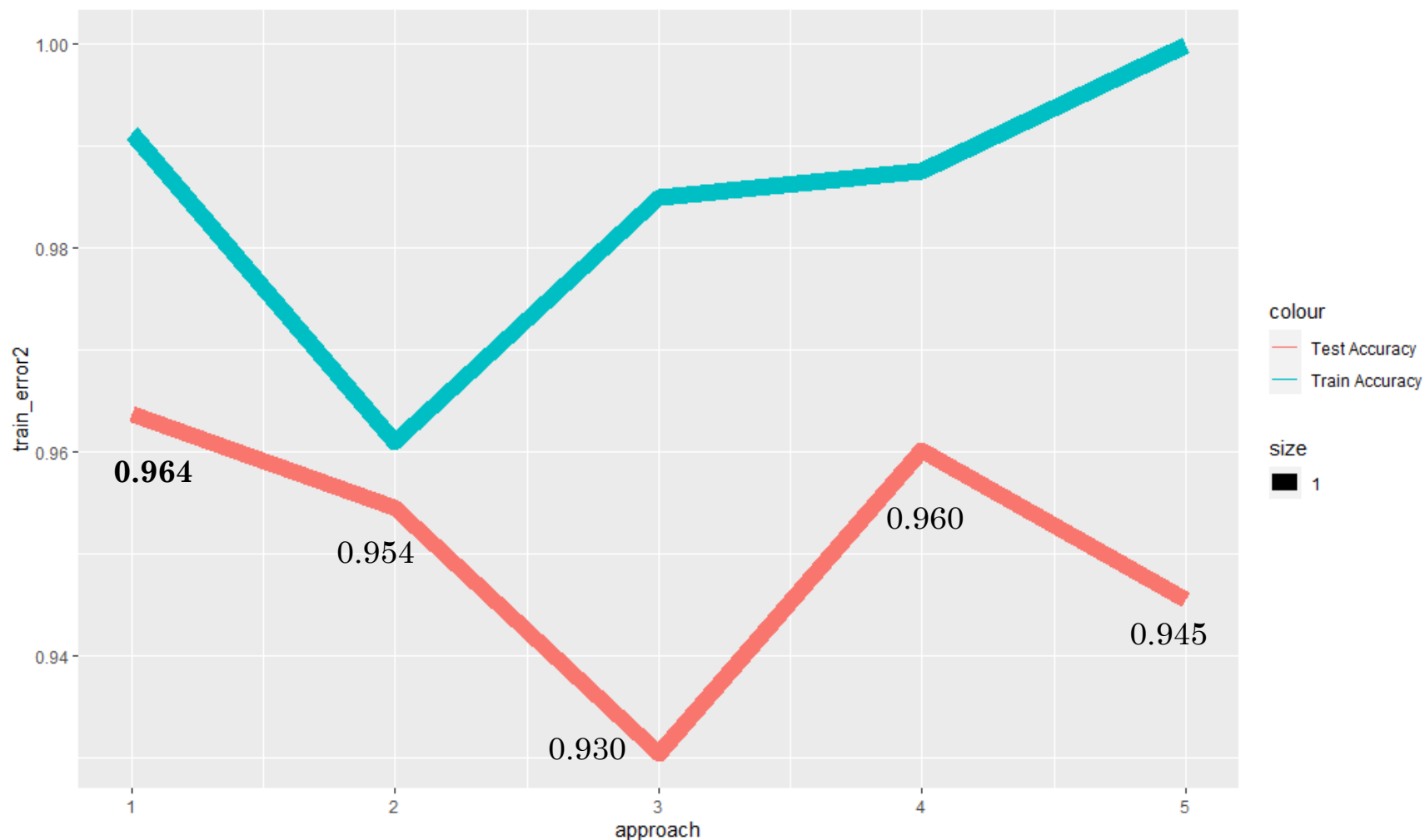
Classification
accuracy with
optimization was
0.945



All Approaches Comparison

Approaches:

1. Logistic Regression
2. QDA
3. Linear SVM
4. Radial SVM
5. Random Forest



With another month,

- Consider penalties/regularization for logistic regression to further reduce overfitting
- Normalize scales of all independent variables
 - Most are currently within about one order of magnitude, but normalizing all to one scale will give better results of coefficient interpretation
- Correlate to other aspects relating to breast cancer detection such as *ESR1* gene which, when expression is low, indicates poor survival outcomes.