Benchmark Classification for GC Tuning

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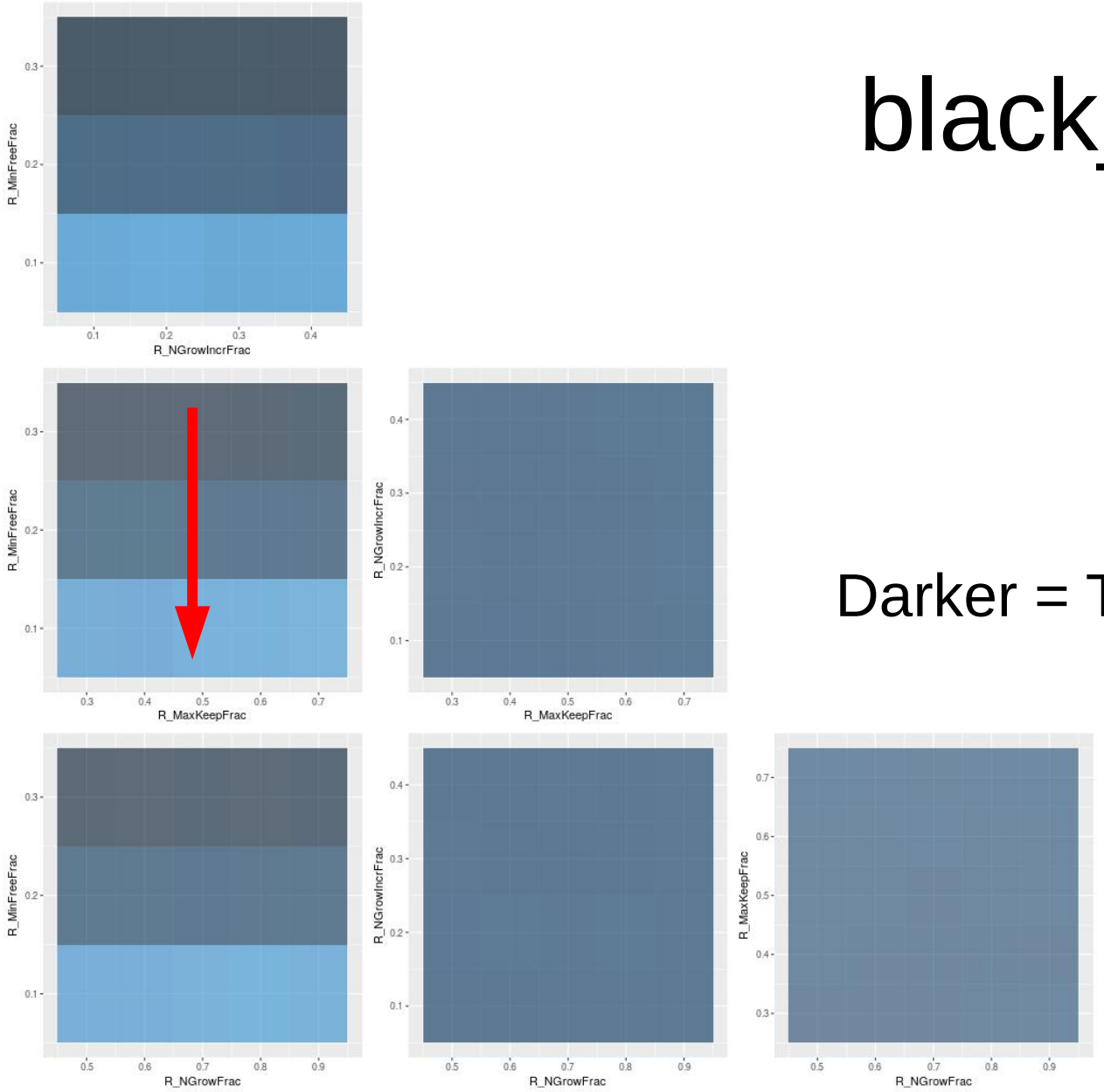
4/9/18

Data Collection

36’000 Runs

Data Collection

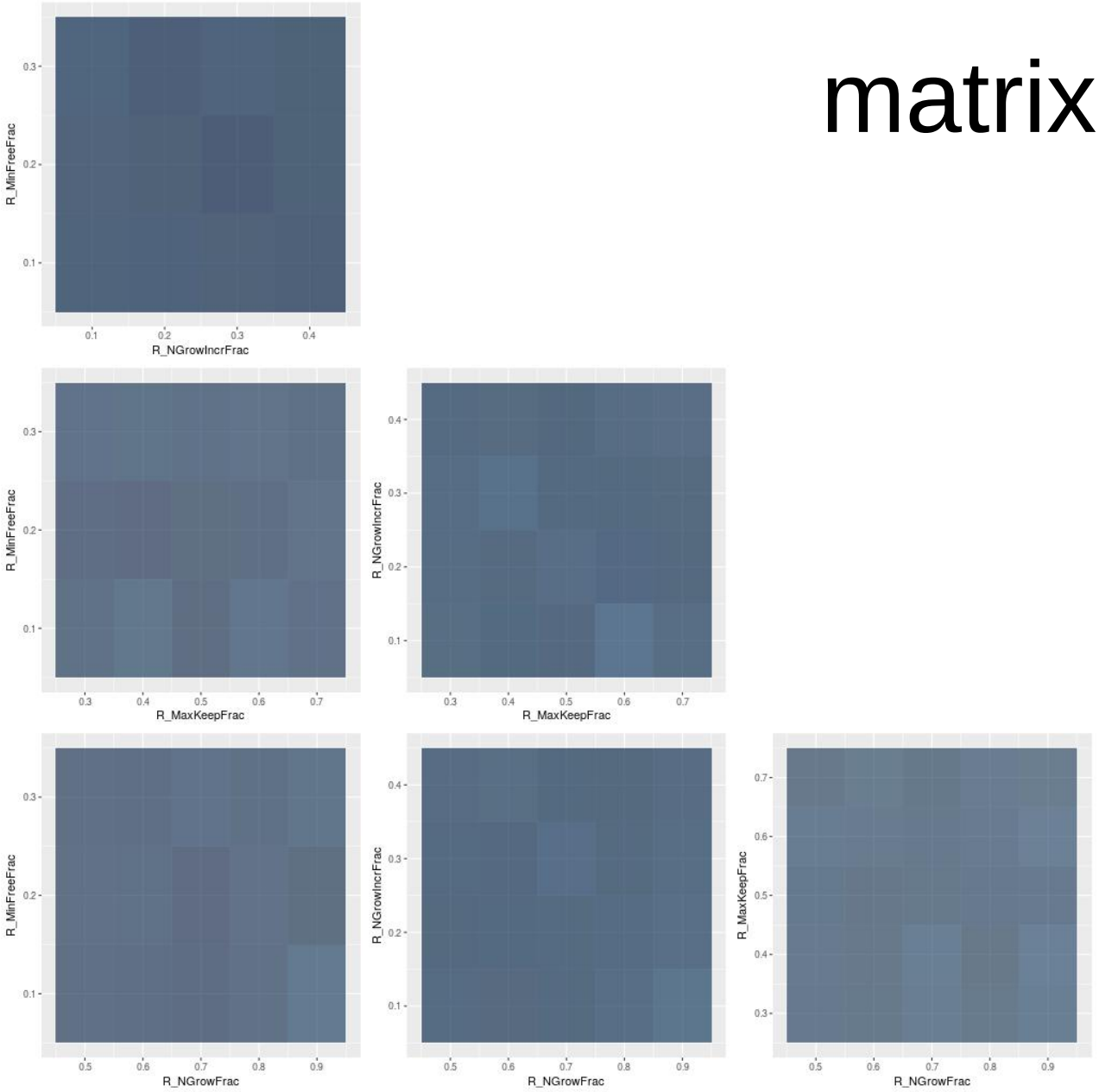
black_scholes



Darker = Takes more Time

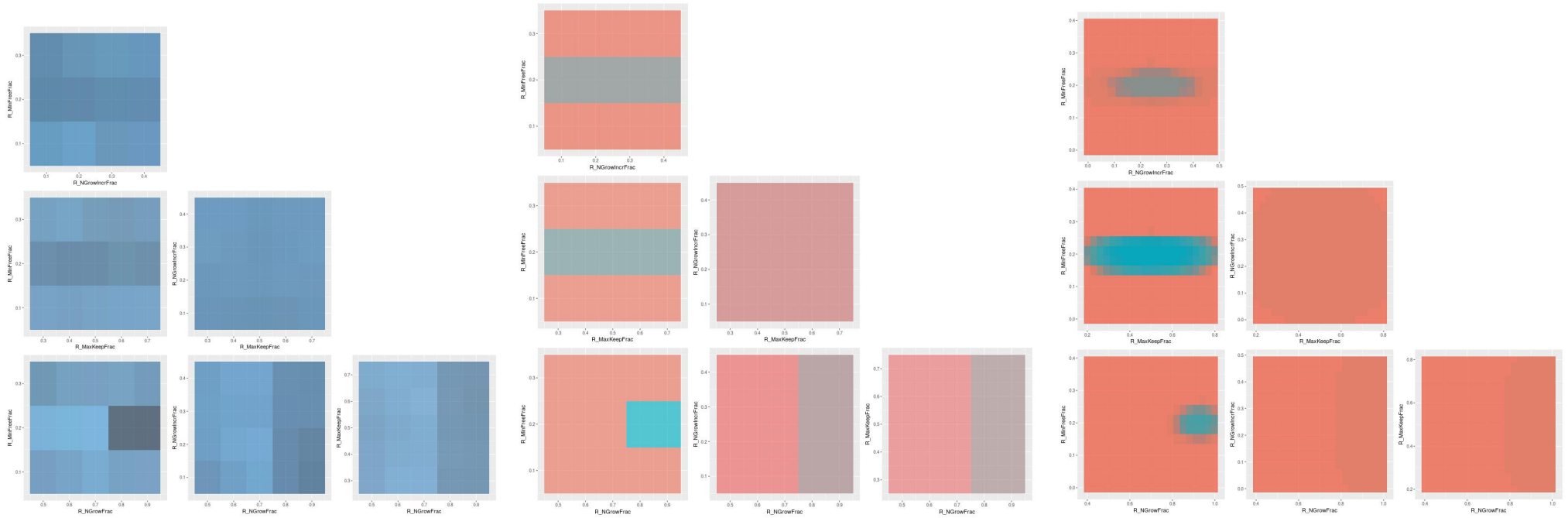
Data Collection

matrix addition



Classification

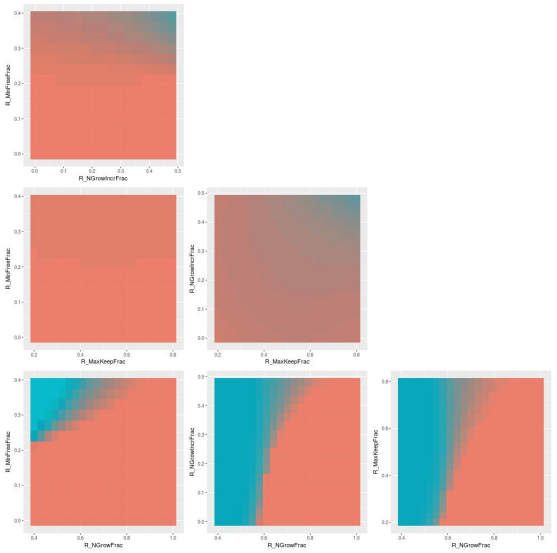
Classification
1. Model Benchmark Response



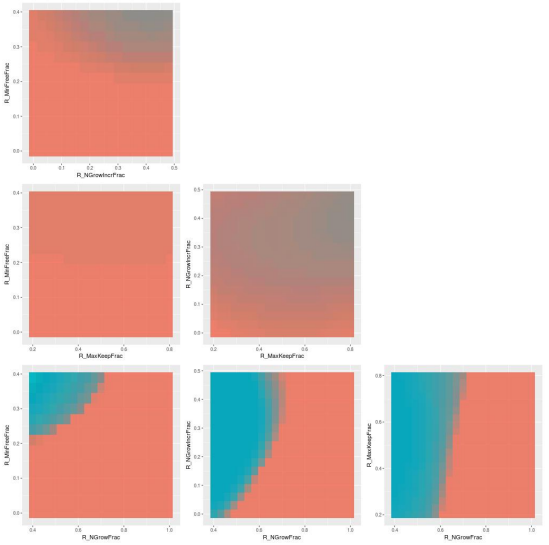
Execution Time → Best Run -3% → SVM Model

Classification
1. Model Benchmark Response
2. K-Means of Model Coefficients

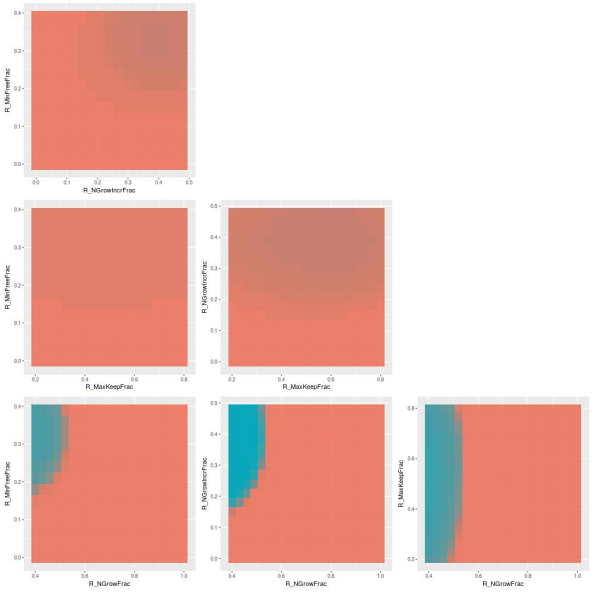
Random Cluster 1



Binary Trees 2



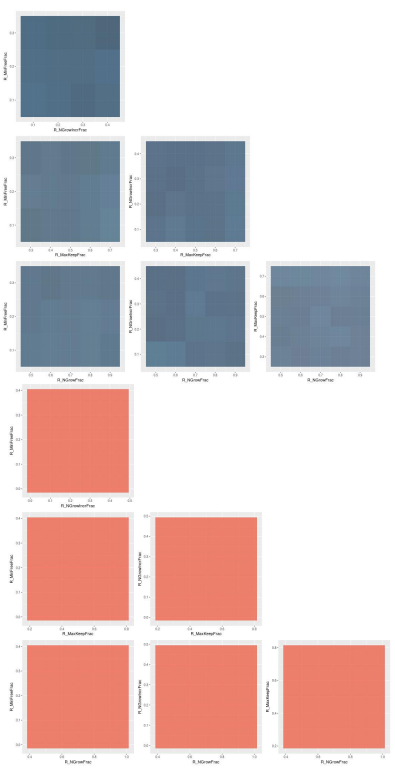
Binary Trees List



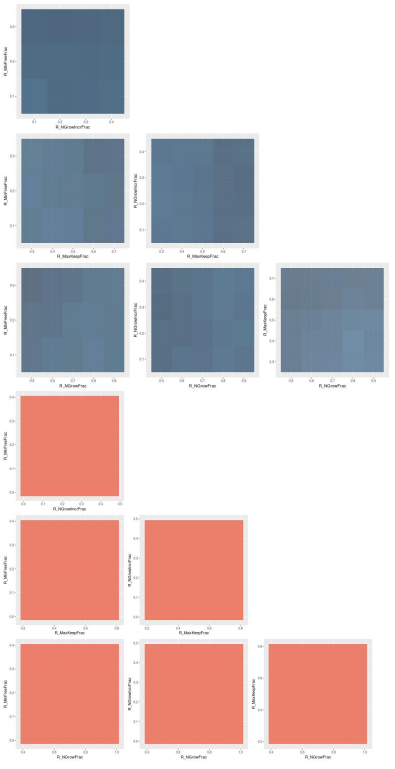
ICA lapply

(not too bad...)

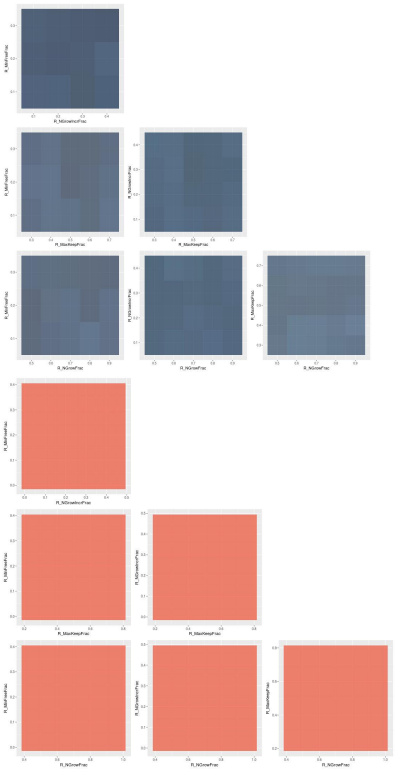
The “Noisy” Cluster



Pidigits



N Body



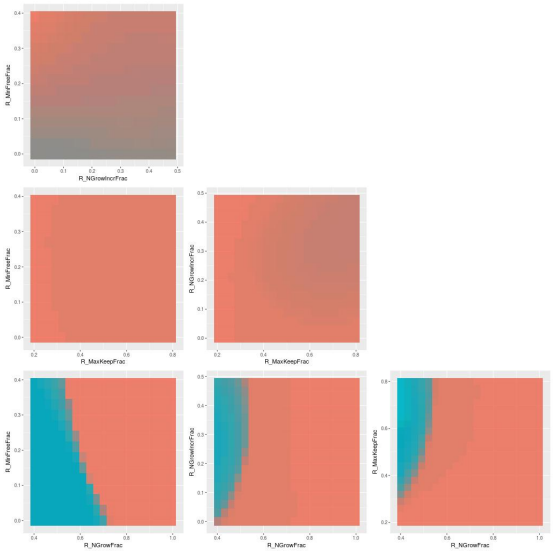
Fasta

… … …

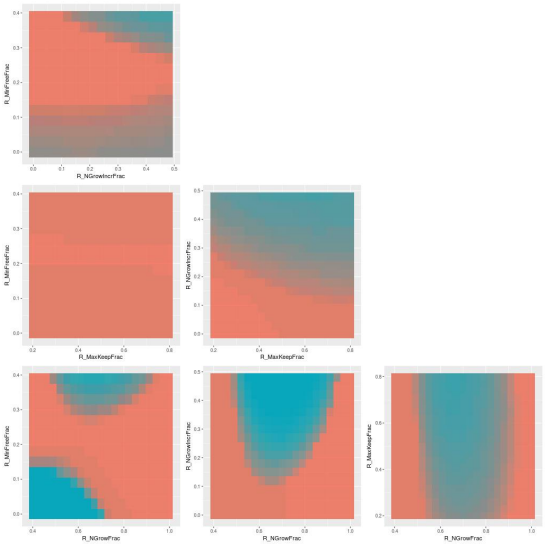
(By far the biggest cluster)

Bad Cluster

k-means badly clusters the k-means benchmarks ;)



k-means 1D



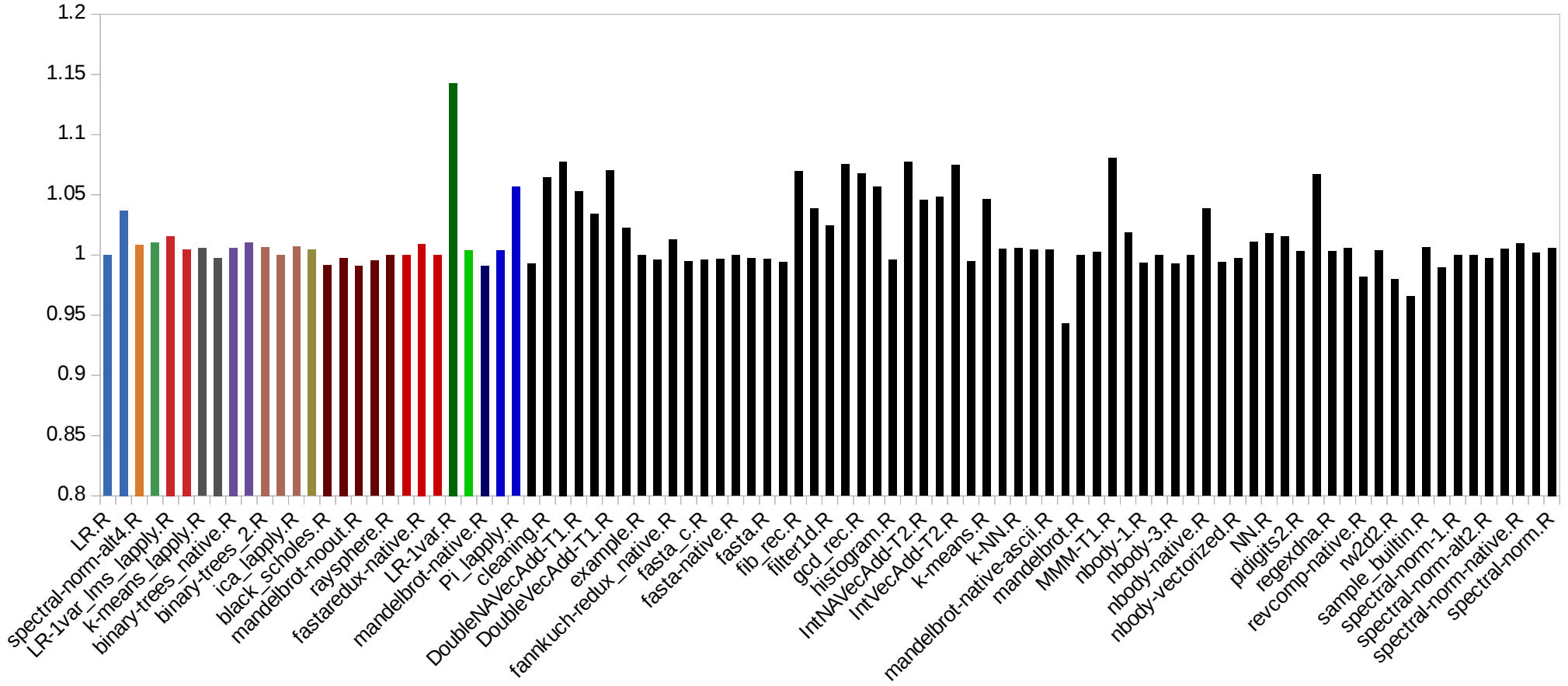
k-means

(even with k=15 the clusters aren’t very homogeneous)

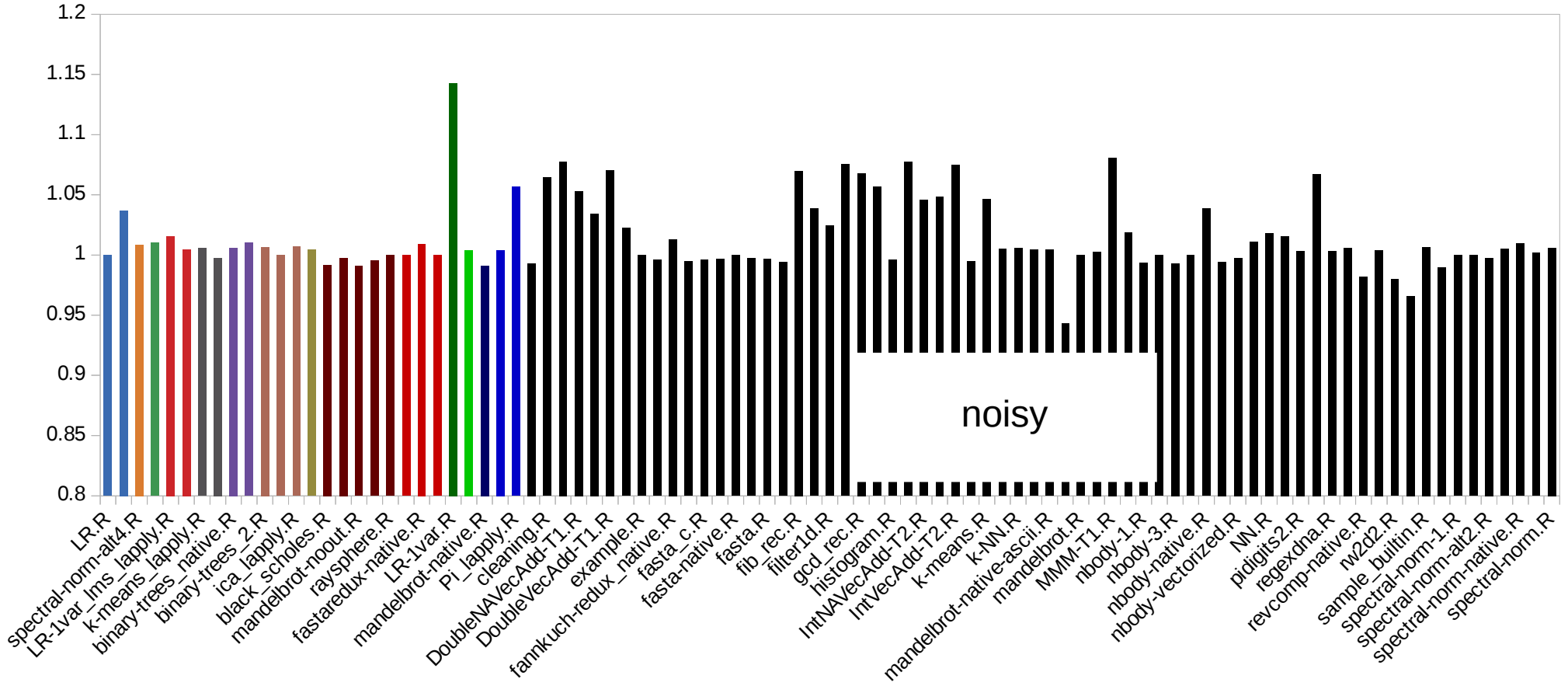
Prediction

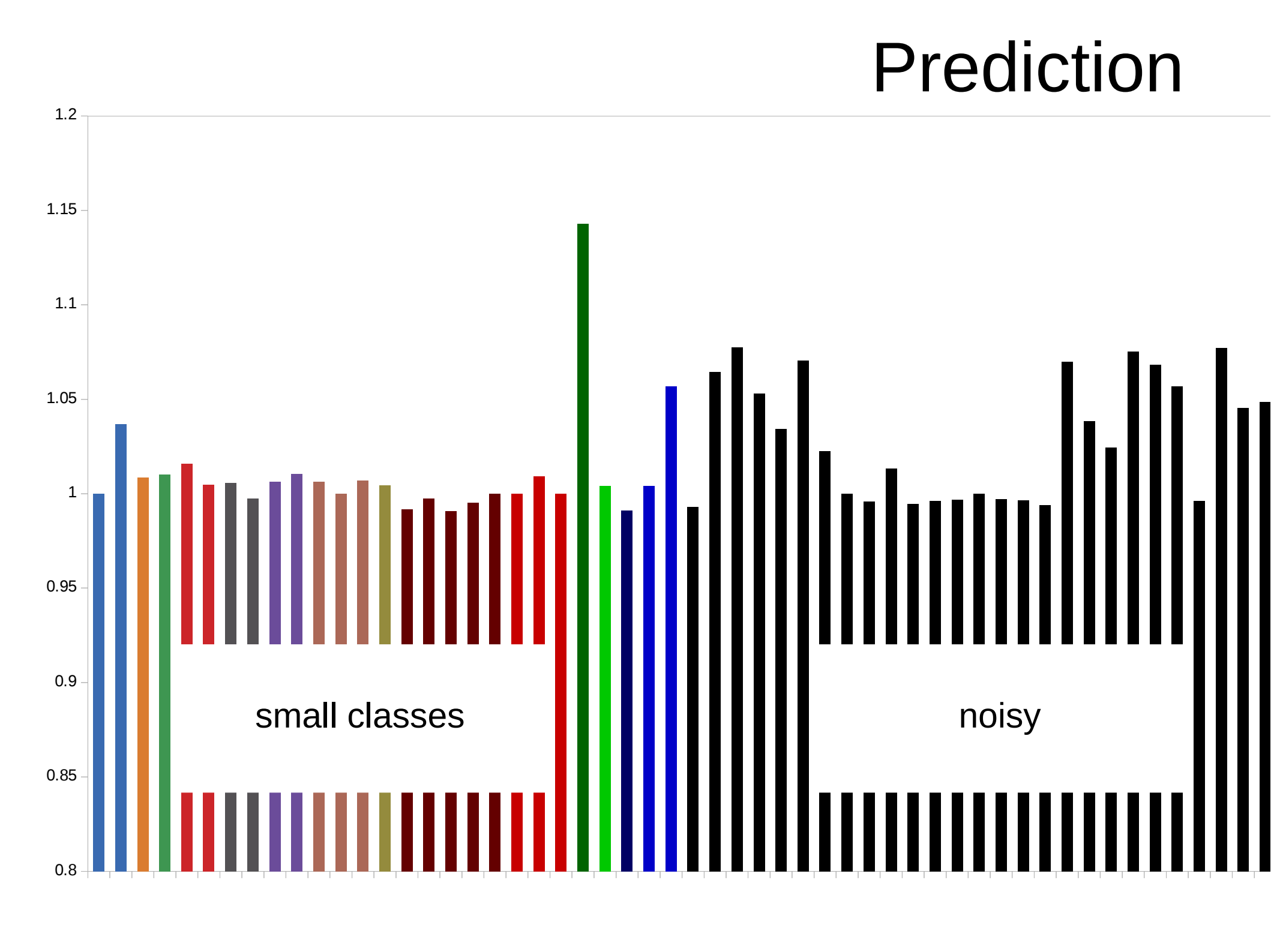
Evaluate the precision against a particular GC Tuning

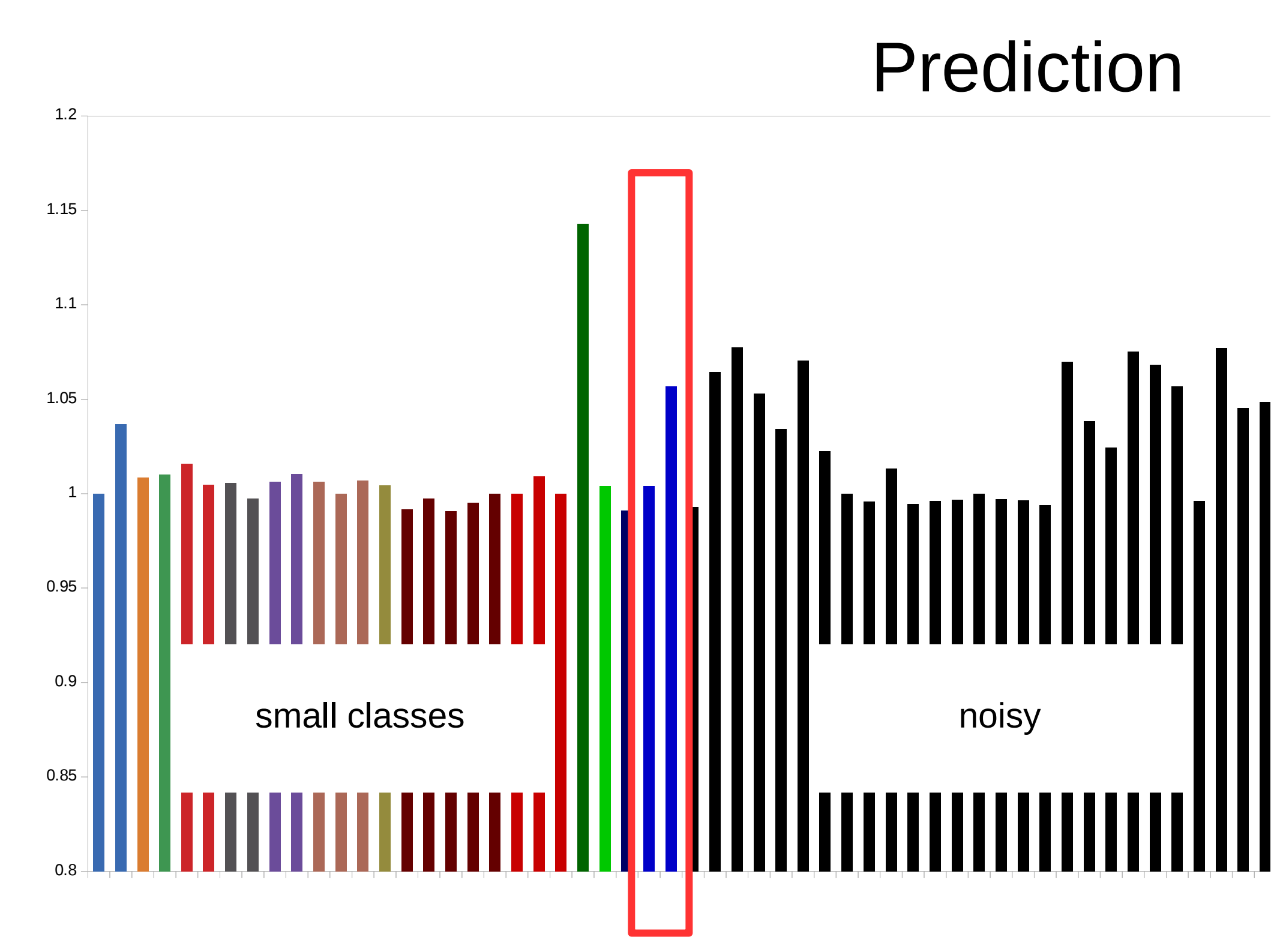
Prediction


1.2
1.15
1.1
1.05
1
0.95
0.9
0.85
0.8
LR.R
spectral-norm-alt4.R
LR-1var_lms_lapply.R
k-means_lapply.R
binary-trees_native.R
binary-trees_2.R
ica_lapply.R
black_scholes.R
mandelbrot-noout.R
raysphere.R
fastaredux-native.R
LR-1var.R
mandelbrot-native.R
Pi_lapply.R
cleaning.R
DoubleNAVecAdd-T1.R
DoubleVecAdd-T1.R
fannkuch-redux_native.R
example.R
fasta_c.R
fasta-native.R
fasta.R
fib_rec.R
filter1d.R
gcd_rec.R
histogram.R
IntNAVecAdd-T2.R
IntVecAdd-T2.R
k-means.R
k-NN.R
mandelbrot-native-ascii.R
mandelbrot.R
MMM-T1.R
nbody-1.R
nbody-3.R
nbody-native.R
nbody-vectorized.R
NN.R
pidigits2.R
regexdna.R
revcomp-native.R
nw2d2.R
sample_builtin.R
spectral-norm-1.R
spectral-norm-alt2.R
spectral-norm-native.R
spectral-norm.R

Prediction

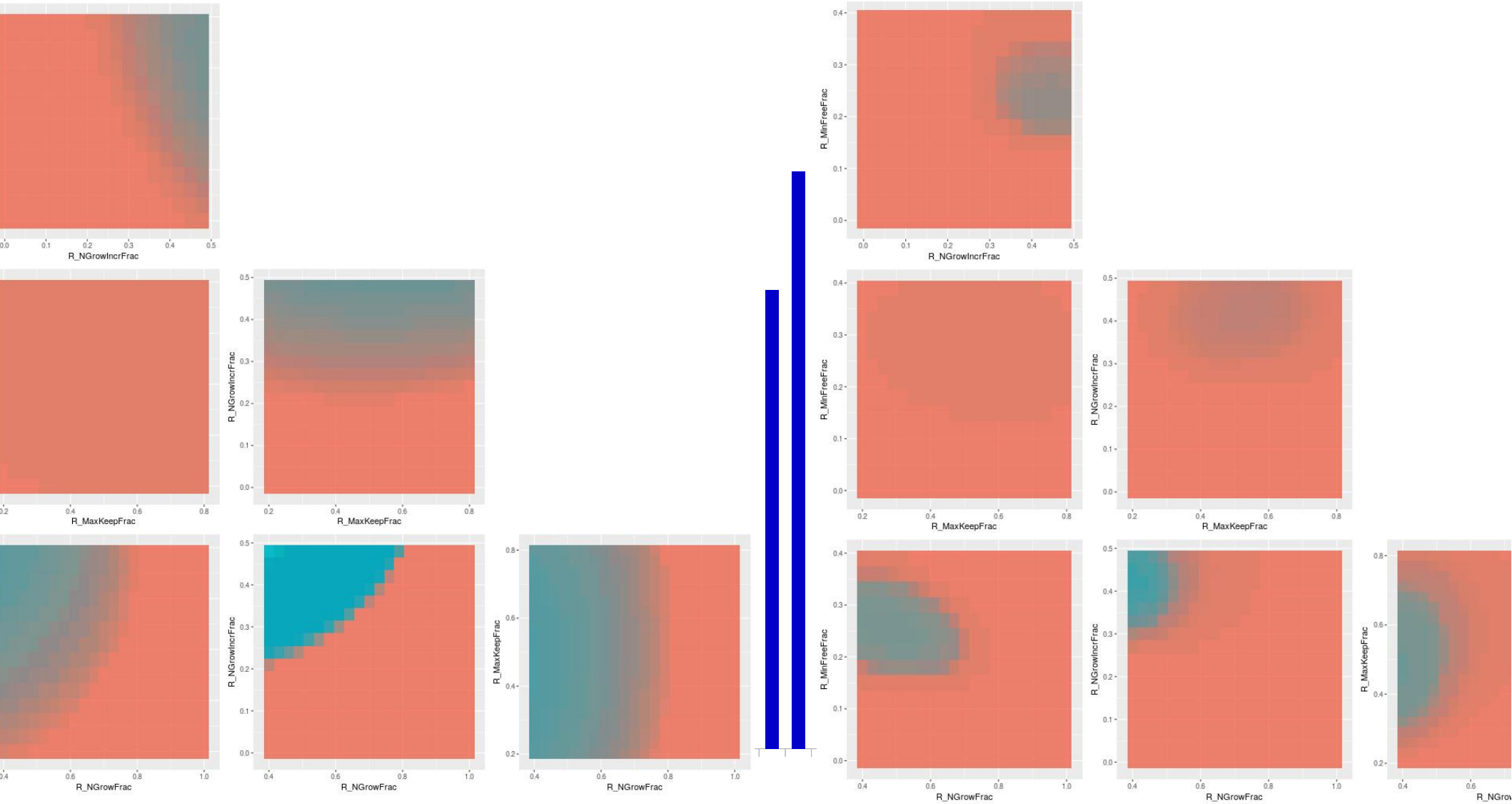

1.2
1.15
1.1
1.05
1
0.95
0.9
0.85
0.8
noisy
LR.R
spectral-norm-alt4.R
LR-1var_lms_lapply.R
k-means_lapply.R
binary-trees_native.R
binary-trees_2.R
ica_lapply.R
black_scholes.R
mandelbrot-noout.R
raysphere.R
fastaredux-native.R
LR-1var.R
mandelbrot-native.R
Pi_lapply.R
cleaning.R
DoubleNAVecAdd-T1.R
DoubleVecAdd-T1.R
fannkuch-redux_native.R
example.R
fasta_c.R
fasta-native.R
fasta.R
fib_rec.R
filter1d.R
gcd_rec.R
histogram.R
IntNAVecAdd-T2.R
IntVecAdd-T2.R
k-means.R
k-NN.R
mandelbrot-native-ascii.R
mandelbrot.R
MMM-T1.R
nbody-1.R
nbody-3.R
nbody-native.R
nbody-vectorized.R
NN.R
pidigits2.R
regexdna.R
revcomp-native.R
nw2d2.R
sample_builtin.R
spectral-norm-1.R
spectral-norm-alt2.R
spectral-norm-native.R
spectral-norm.R


Prediction
1.2
1.15
1.1
1.05
1
0.95
0.9
0.85
0.8
small classes
noisy


Prediction
1.2
1.15
1.1
1.05
1
0.95
0.9
0.85
0.8
small classes
noisy

Prediction

Similar response, but details matter!



Prediction

Similar response, but details matter!

Never Retire a Benchmark