

# Inclusion Frequencies in Null Setting and Preliminary TF Discovery Results

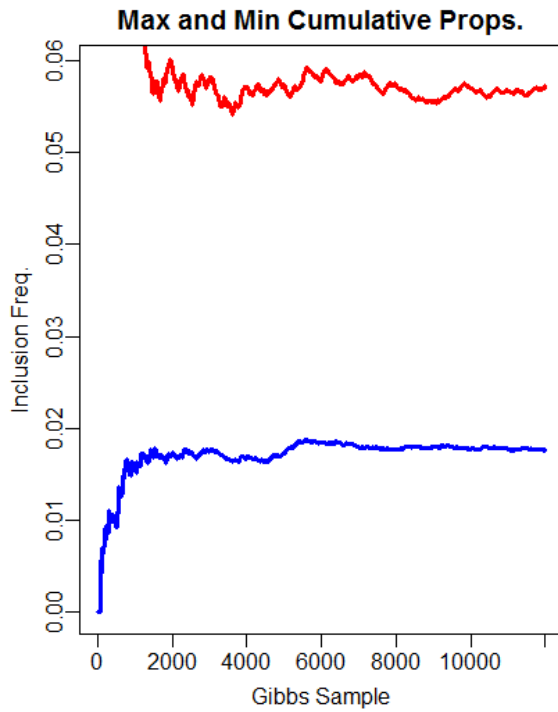
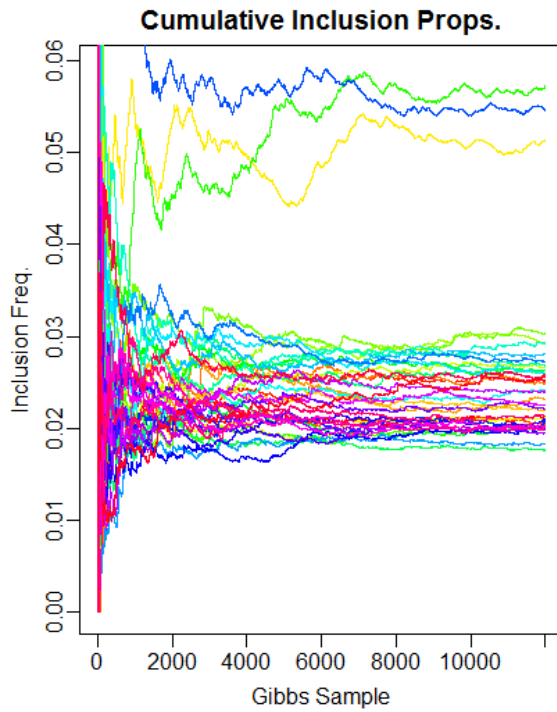
November 15, 2012

For the following simulations,  $y_i \stackrel{iid}{\sim} \mathcal{N}(0, \sigma^2)$  and  $\mathbf{X}$  consists of entries that are all  $x_{ij} \stackrel{iid}{\sim} \mathcal{N}(0, 1)$ . Shown below are the cumulative inclusion probabilities. The burn-in is purposely excluded to see the behavior of an entire Gibbs chain. 12000 Gibbs samples were generated with no thinning.

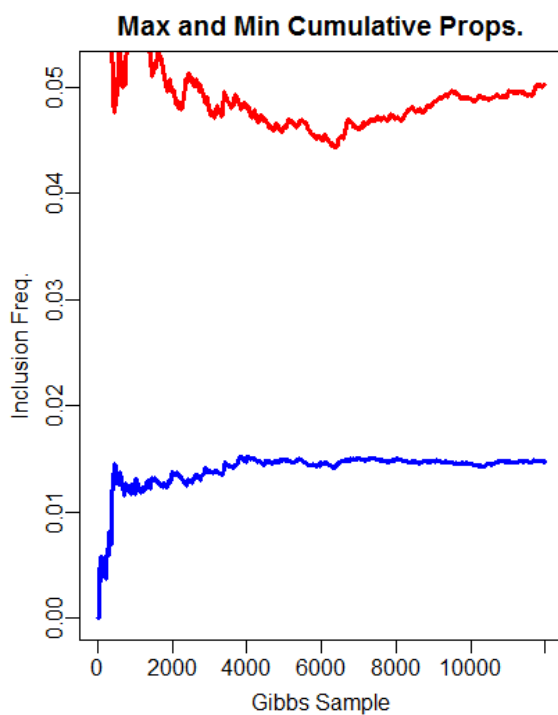
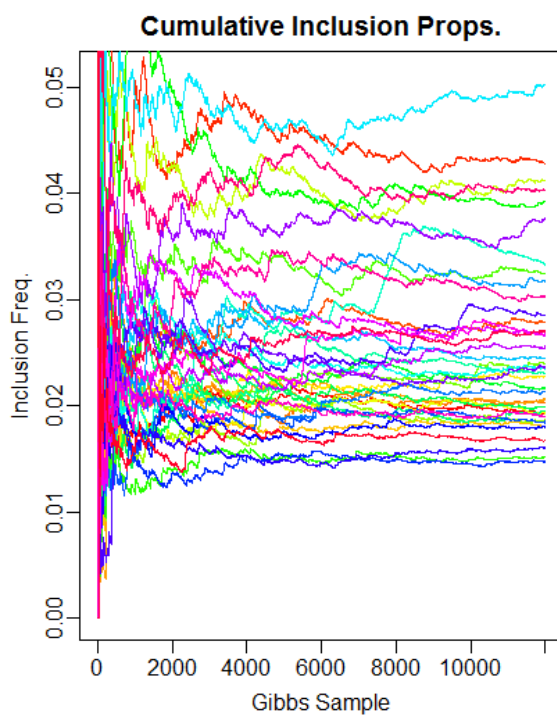
A number of different settings for  $\sigma$  and  $n$  will be included. The number of covariates is 39, which is the same as the number of TFs in the real data. Hence, the expectation might be that inclusion frequencies would converge to .0256.

1  $\sigma=.1$

N=250

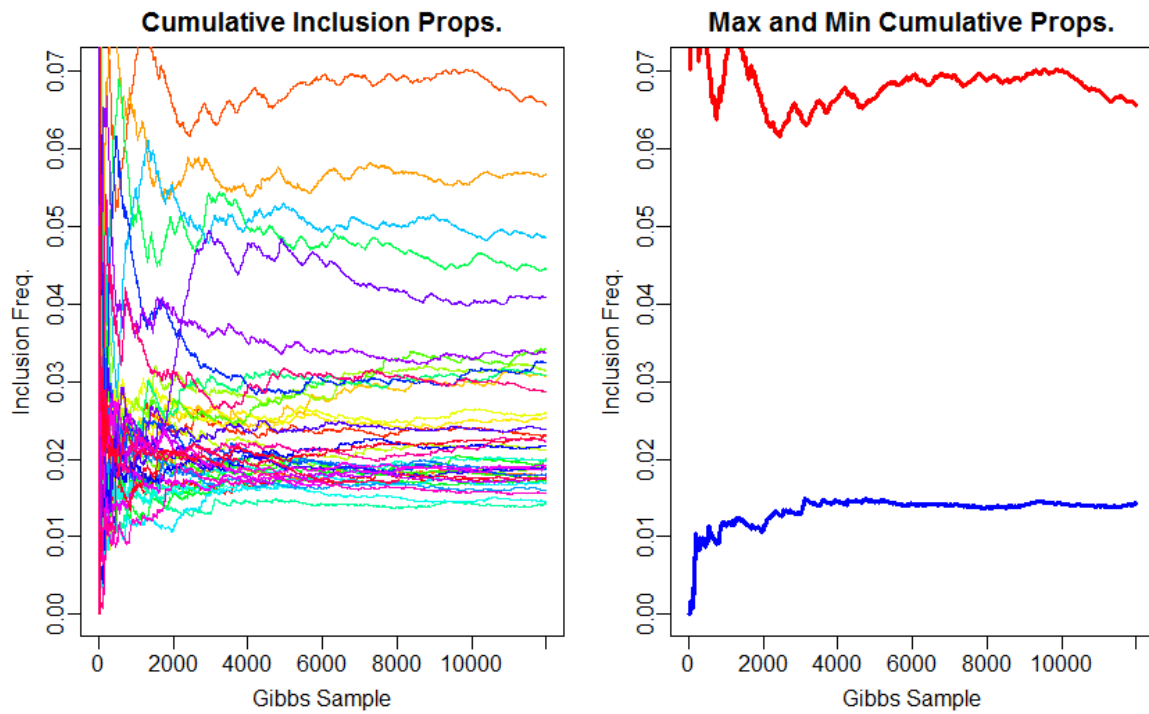


N=1000

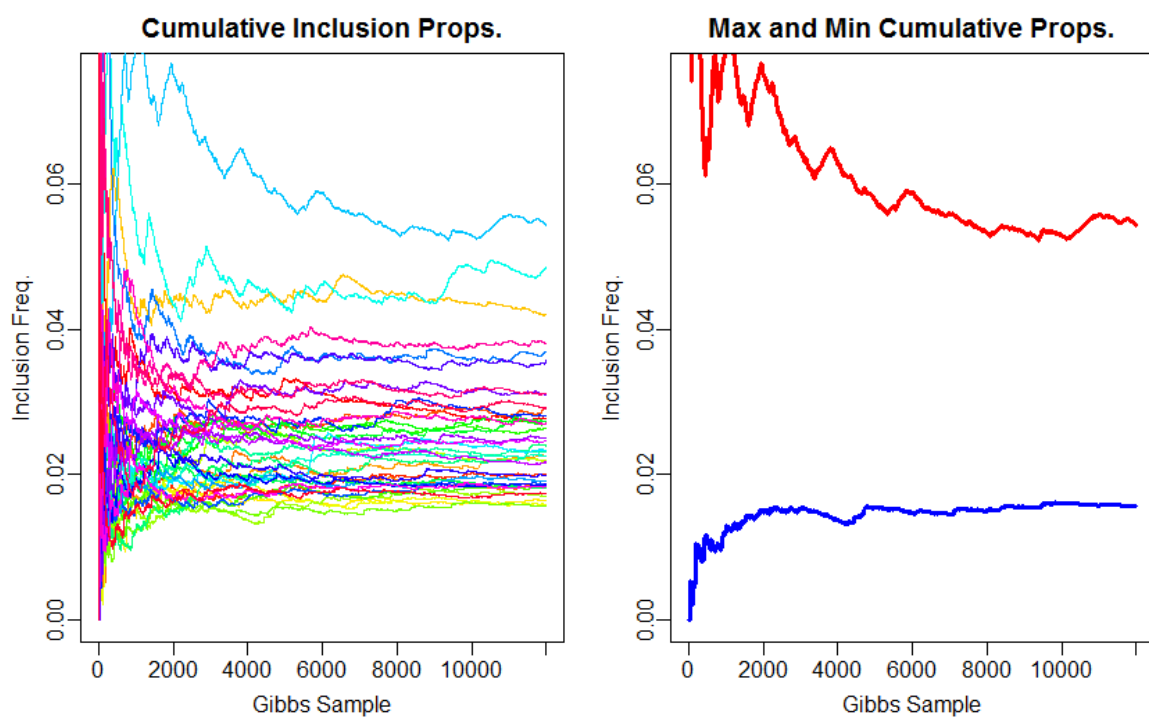


2  $\sigma=1$

N=250

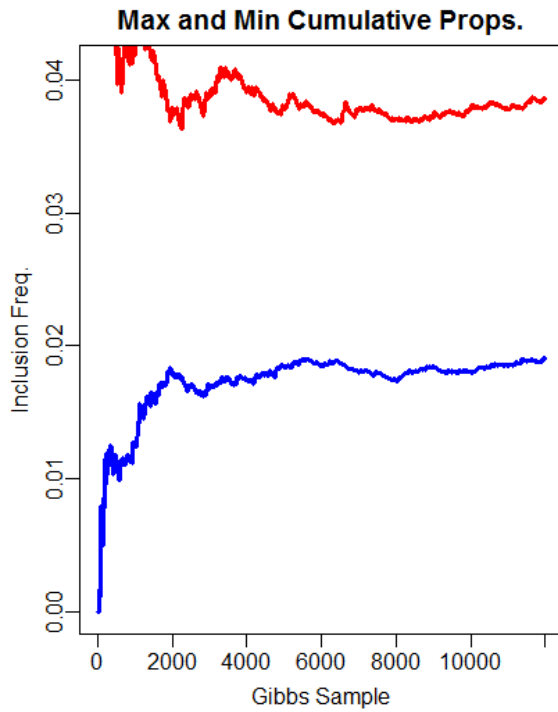
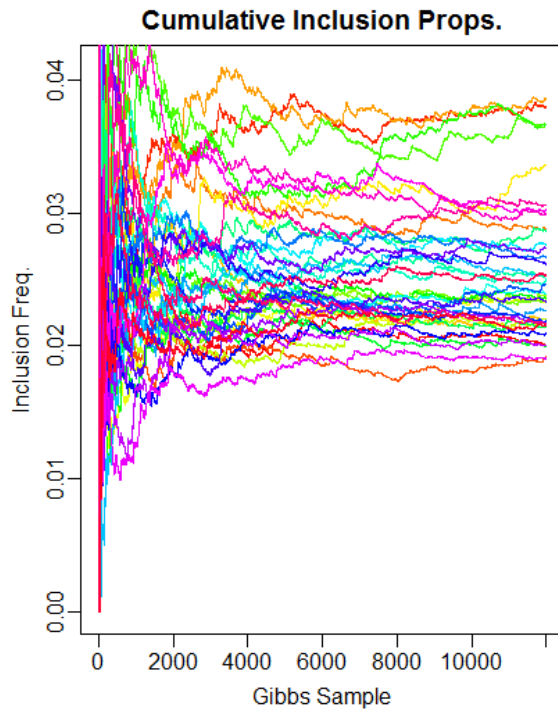


N=1000

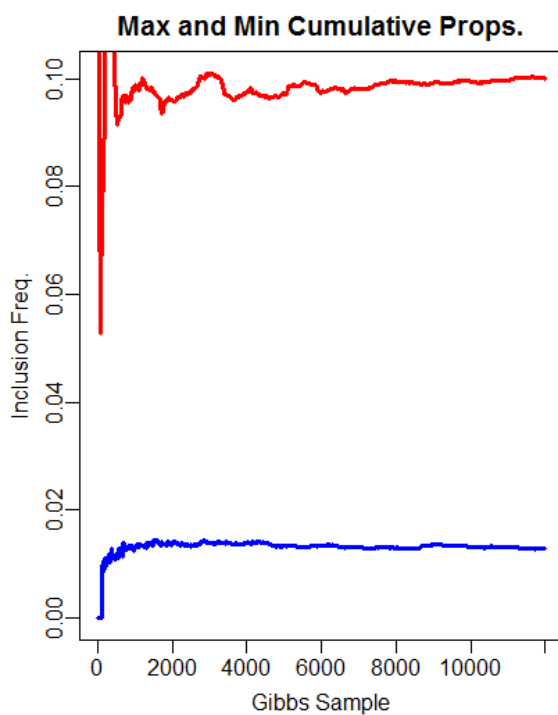
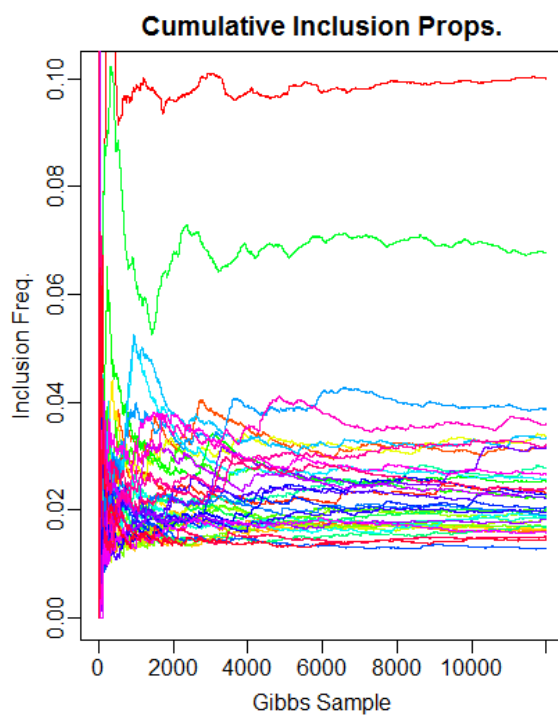


3  $\sigma=2$

N=250

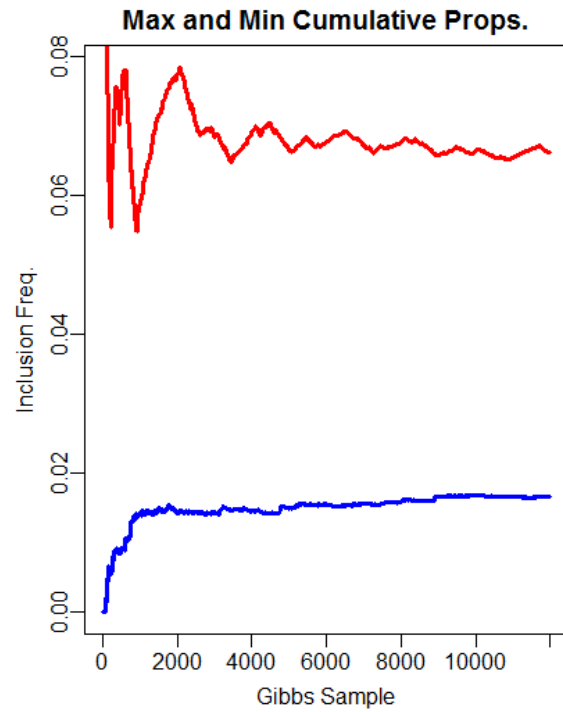
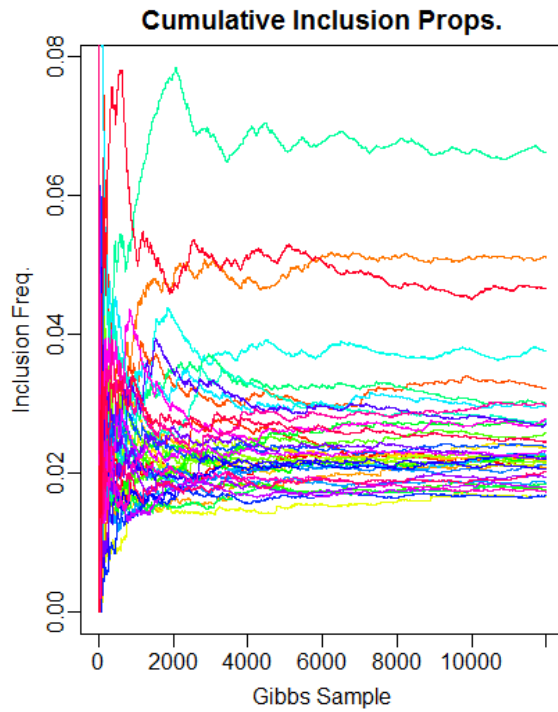


N=1000

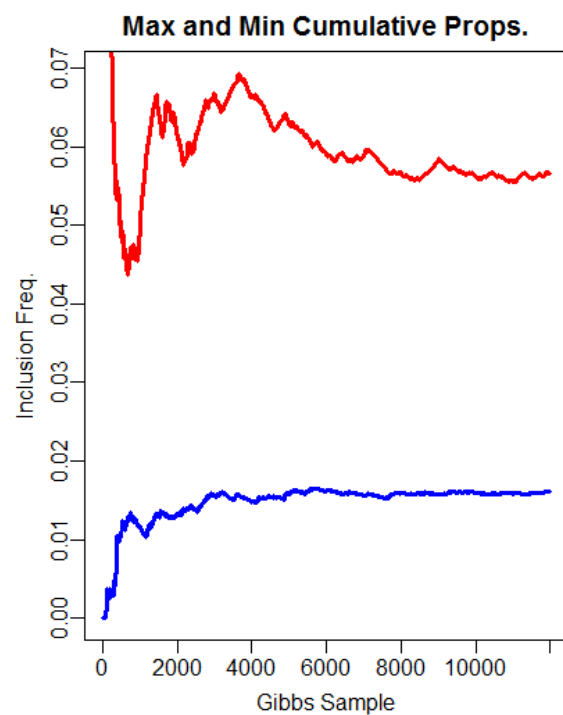
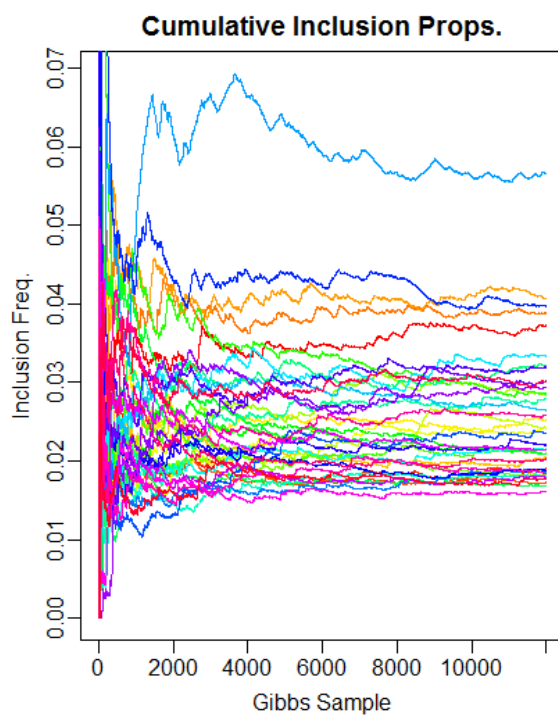


4  $\sigma=8$

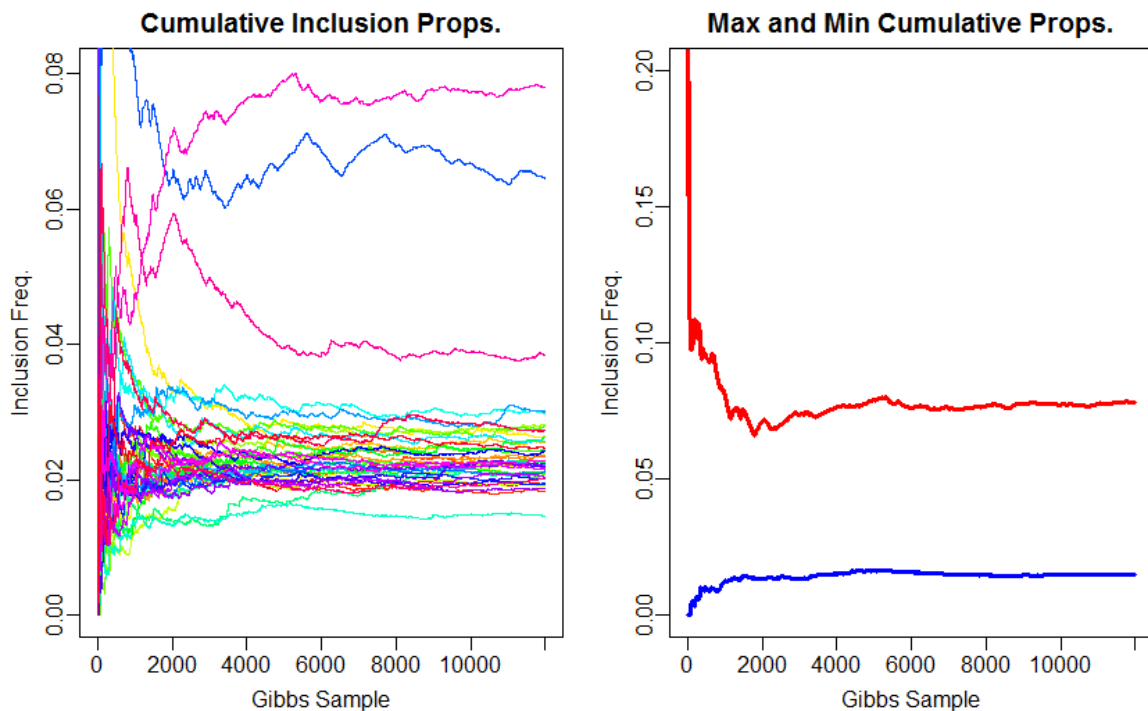
N=250



N=1000



## 5 4 Aggregated Chains-Multiple Starting Points

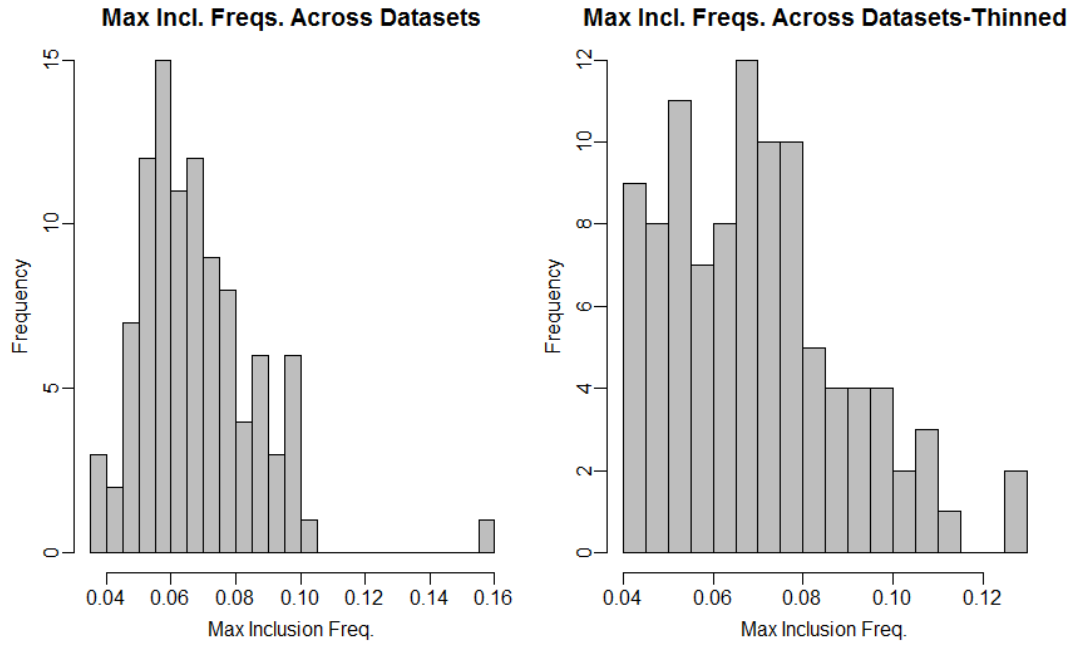


**Hypothesis:** From the above plots as well as the attempt to use multiple chains, it seems that autocorrelation is not necessarily the root of the problem. The issue seems to be more linked to the existence of posterior modes that BART is discovering. These modes tend to move around from dataset to dataset, but nonetheless, the posterior probability surface doesn't seem to be flat enough to allow the algorithm to wander randomly and create a uniform distribution on the splitting rules.

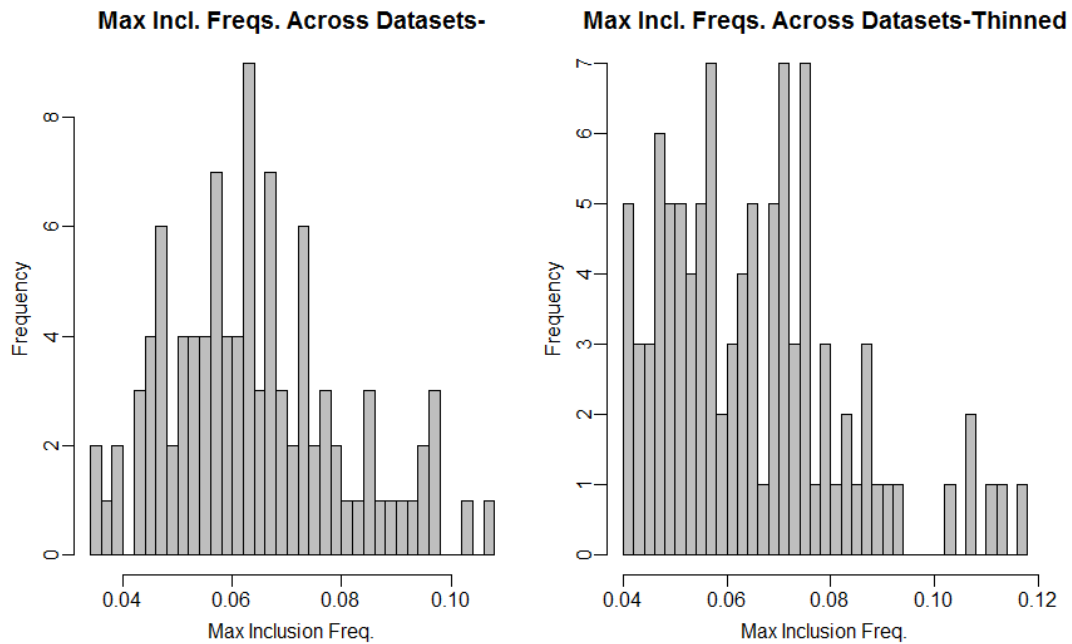
## 6 Maximum Inclusion Frequencies Across Datasets (N=100)

2000 Burn-in and 5000 posterior samples. 10 Trees. Different  $\mathbf{y}$  vector for each of 100 iterations. Thinning is by 25.

$$\sigma = 1$$



$$\sigma = 8$$



## 7 TF Discoveries-500 Genes

1000 Burn-in and 2000 posterior samples at 10 trees with no thinning. 100 bootstrap iterations for null setting. Algorithm ran in 2 hours on 20 cores.

Shown below are the various proportions of times a TF was “discovered” in the 500 genes examined.

### No Simultaneous Coverage

ABF1	ACE2	BAS1	CAD1	CBF1	FKH1	FKH2	GAL4	GCN4	GCR1	GCR2
0.148	0.072	0.250	0.260	0.176	0.150	0.180	0.102	0.316	0.122	0.158
HAP2	HAP3	HAP4	HSF1	INO2	LEU3	MBP1	MCM1	MET31	MSN4	NDD1
0.074	0.222	0.118	0.308	0.176	0.152	0.184	0.136	0.158	0.298	0.098
PDR1	PHO4	PUT3	RAP1	RCS1	REB1	RLM1	RME1	ROX1	SKN7	SMP1
0.146	0.104	0.076	0.284	0.056	0.174	0.074	0.178	0.070	0.262	0.108
STB1	STE12	SWI4	SWI5	SWI6	YAP1					
0.148	0.166	0.130	0.162	0.170	0.286					

### Simultaneous Coverage Bands

ABF1	ACE2	BAS1	CAD1	CBF1	FKH1	FKH2	GAL4	GCN4	GCR1	GCR2
0.038	0.006	0.072	0.056	0.026	0.024	0.014	0.008	0.116	0.008	0.022
HAP2	HAP3	HAP4	HSF1	INO2	LEU3	MBP1	MCM1	MET31	MSN4	NDD1
0.008	0.054	0.014	0.070	0.022	0.016	0.046	0.008	0.008	0.060	0.006
PDR1	PHO4	PUT3	RAP1	RCS1	REB1	RLM1	RME1	ROX1	SKN7	SMP1
0.010	0.010	0.006	0.066	0.004	0.022	0.002	0.028	0.006	0.058	0.004
STB1	STE12	SWI4	SWI5	SWI6	YAP1					
0.024	0.024	0.020	0.044	0.030	0.064					

The maximum cut-off method is omitted, but similar to the simultaneous coverage scenario, which is clearly too restrictive. There is some inherent Type I error control build into this model as there is a constraint on the total budget on inclusion frequencies.