GS01 0163
Analysis of Microarray Data

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Lecture 9: Differential Expression

- Student's t-test
- Simulating nothing
- Family-wise error rate
- Permutation tests
- Is FWER too conservative?
- Beta-uniform mixture model

Class Comparison

Perhaps the most common use of microarrays is to determine which genes are differentially expressed between prespecified classes of samples. In general, we refer to this as the `class comparison` problem. In this lecture, we start looking at the simplest case:

- Given microarray experiments on
  - N_A sample of type A
  - N_B sample of type B
- Decide which of the G genes on the microarray are differentially expressed between the two groups.

Student's t-test

In many cases, we analyze microarrays starting with the "one gene at a time" approach. That is, we first look for a reasonable way to analyze the same problem when we only have one gene, and then figure out how to adapt that method to thousands of genes.

The one-gene version of the class comparison problem with two classes simply asks, "is this gene different in the two classes?" A classic analytical method is Student's t-test. We start by estimating the mean and standard deviation in both classes:

$$\bar{x}_A = \frac{1}{N_A}\sum_{i=1}^{N_A} x_i, \qquad s_A^2 = \frac{1}{N_A - 1}\sum_{i=1}^{N_A}(x_i - \bar{x})^2.$$

Weighted difference in means

Next, we pool the estimates of standard deviation from the two groups:

$$s_P^2 = \frac{(N_A - 1)s_A^2 + (N_B - 1)s_B^2}{N_A + N_B - 2}.$$

The two-sample t-statistic is the difference in means, weighted by the pooled estimate of the standard deviation and the number of samples:

$$t = \frac{\bar{x}_B - \bar{x}_A}{s_P \sqrt{1/N_A + 1/N_B}}.$$

Question: Why not just use the difference in means?

Microarray aside: which scale is best?

Before answering the question, we offer a slight reinterpretation. Most (but not all) analysts believe that microarray data should be transformed by computing logarithms before testing for differential expression. The key mathematical fact supporting this belief is that the logarithm turns multiplication into addition:

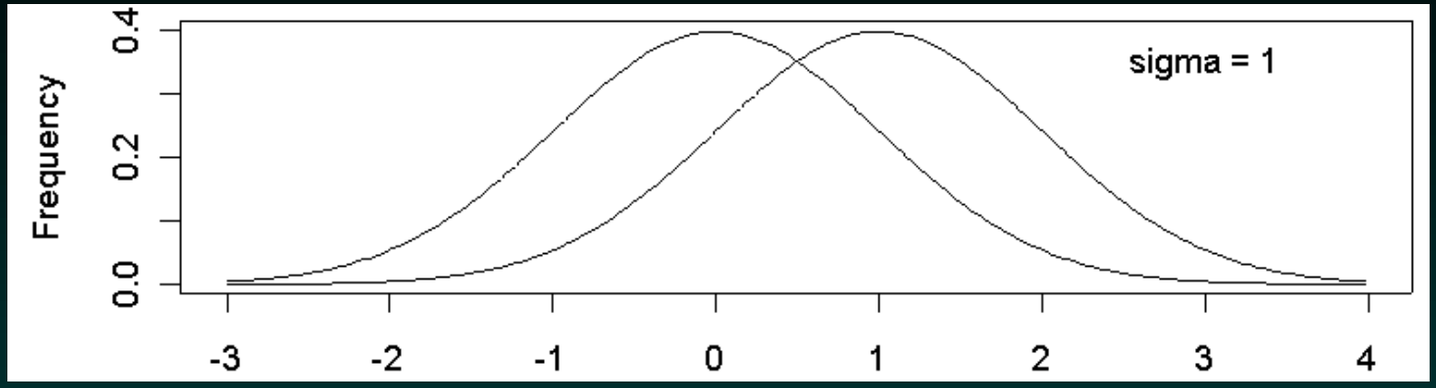
$$\log(xy) = \log(x) + \log(y).$$

In particular

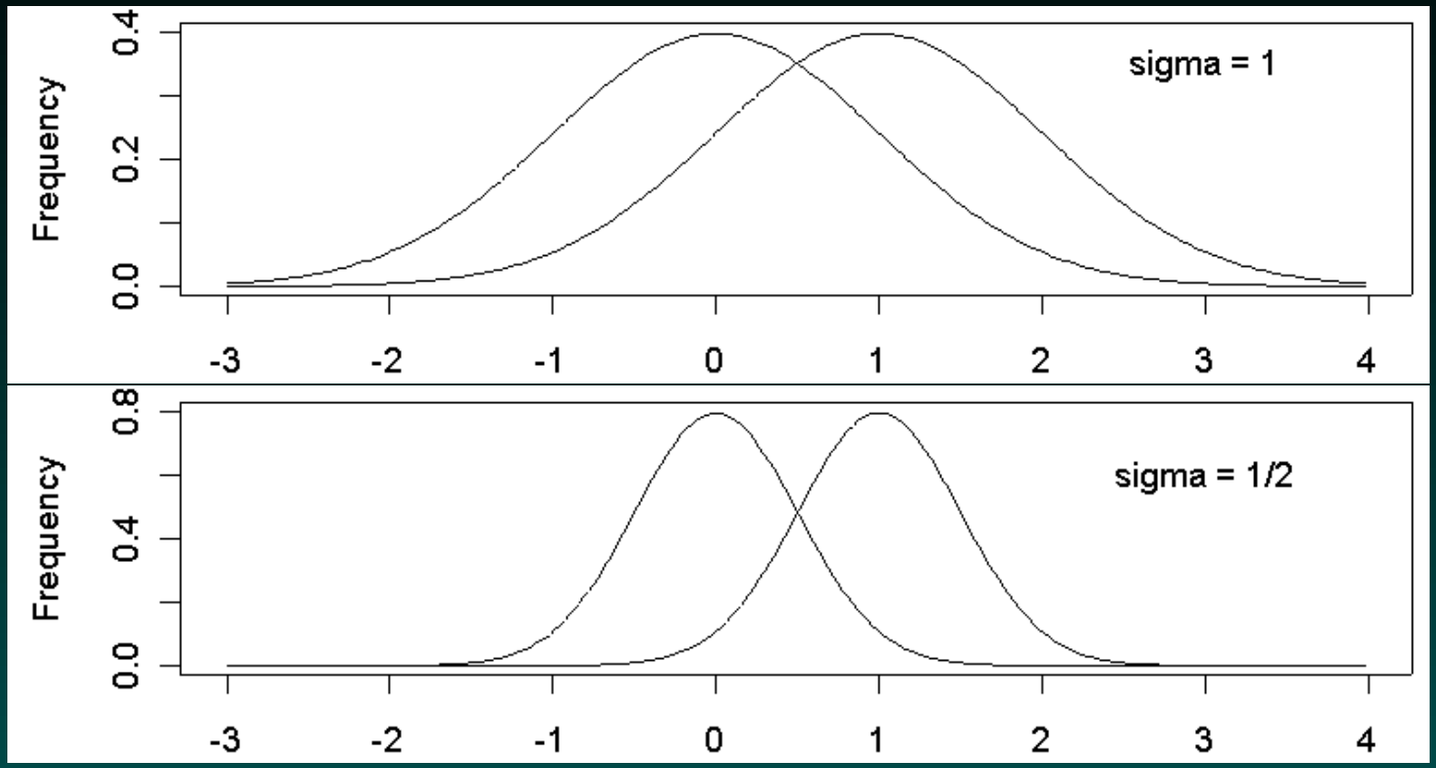
$$\log(2x) = \log(x) + \log(2), \qquad \log(x/2) = \log(x) - \log(2).$$

Differences on the log scale can be interpreted as “fold change” on the original scale of the data. Increases and decreases by the same fold change are treated equally on the log scale.

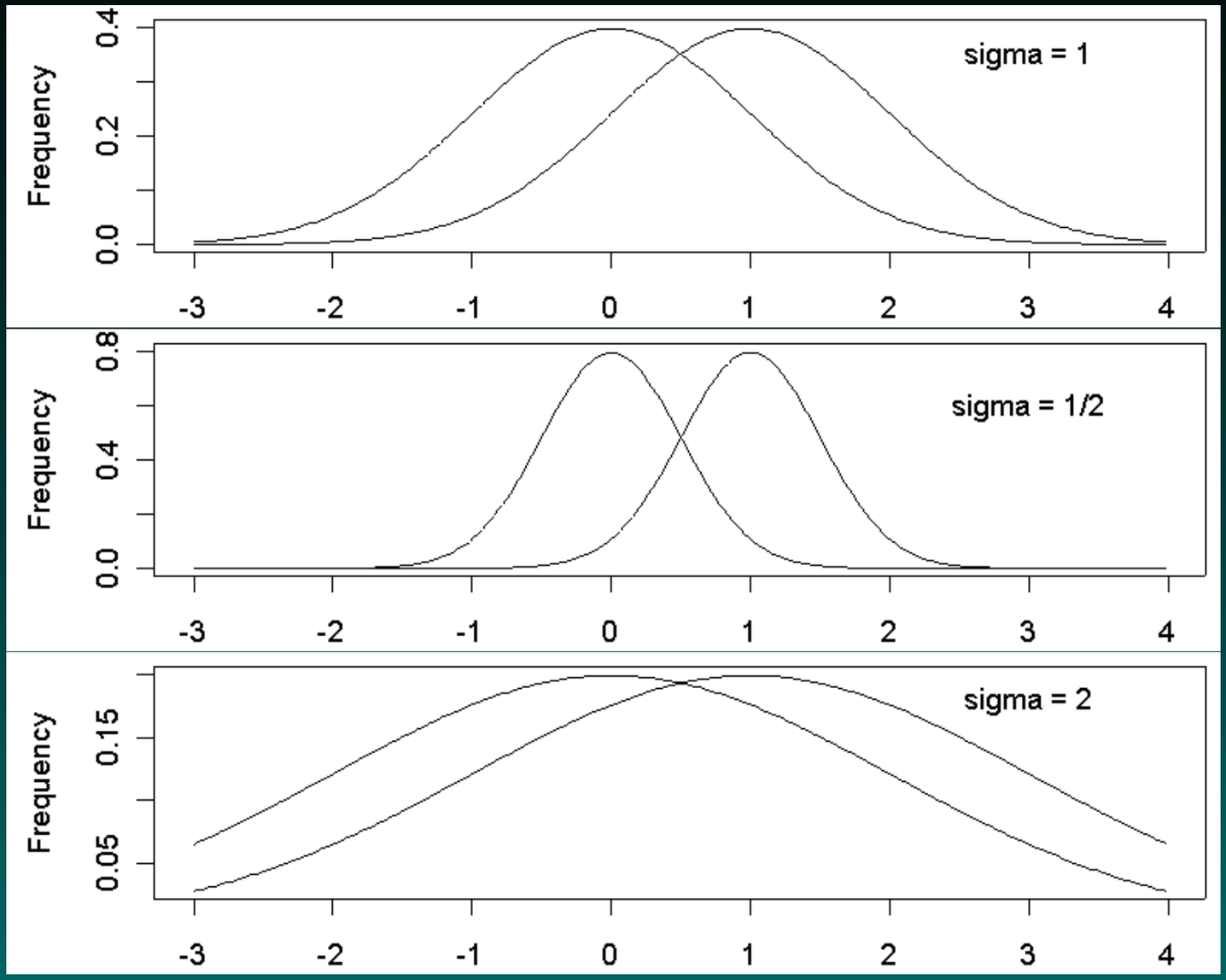
Why the standard deviation matters



Why the standard deviation matters



Why the standard deviation matters



T-statistics

Three ways to get a larger t-statistic:

- Bigger difference in means
- Smaller standard deviation
- More samples

What about p-values?

Null hypothesis: The difference in mean expression between the two groups is zero.

Two-sided alternative hypothesis: The difference in mean expression is non-zero.

P-value = probability of seeing a t-statistic this extreme under the null hypothesis = area in both tails of the distribution.

Interpretation: if you repeat the same experiment many times (with the same number of samples in the two groups), the p-value represents the proportion of times that you would expect to see a t-statistic this large.

BUT: Computing a t-statistic for each gene on a microarray is like performing the same experiment many times.

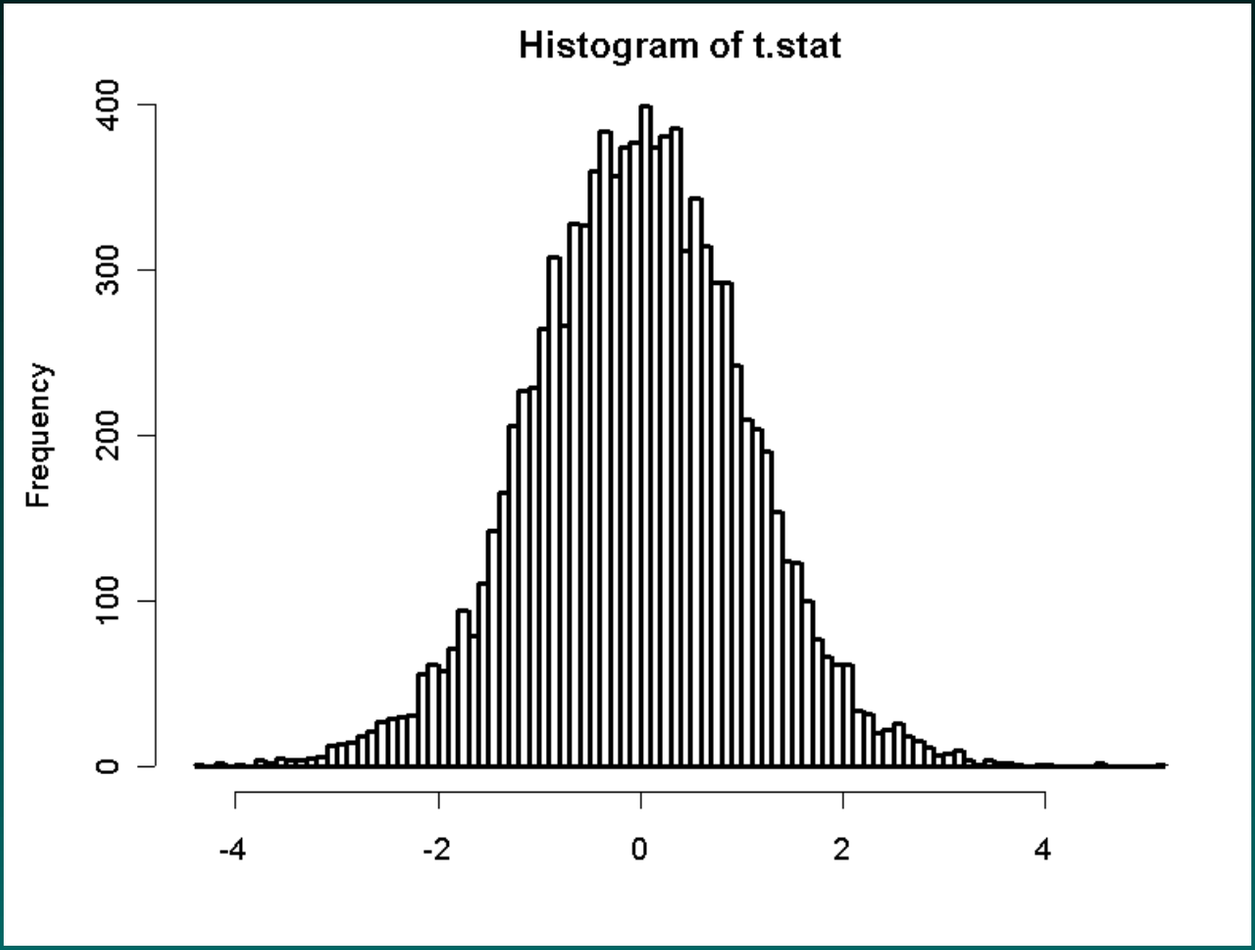
Simulating nothing

We simulated a microarray data set with no differences:

```
n.genes <- 10000
n.samples <- 20
an <- n.samples/2
bn <- n.samples/2
type <- factor(rep(c('A', 'B'), times=c(an, bn)))
data <- matrix(rnorm(n.genes*n.samples),
  nrow=n.genes)
am <- apply(data[, type=='A'], 1, mean)
bm <- apply(data[, type=='B'], 1, mean)
av <- apply(data[, type=='A'], 1, var)
bv <- apply(data[, type=='B'], 1, var)
sp2 <- ((an-1)*av + (bn-1)*bv)/(an+bn-2)
```

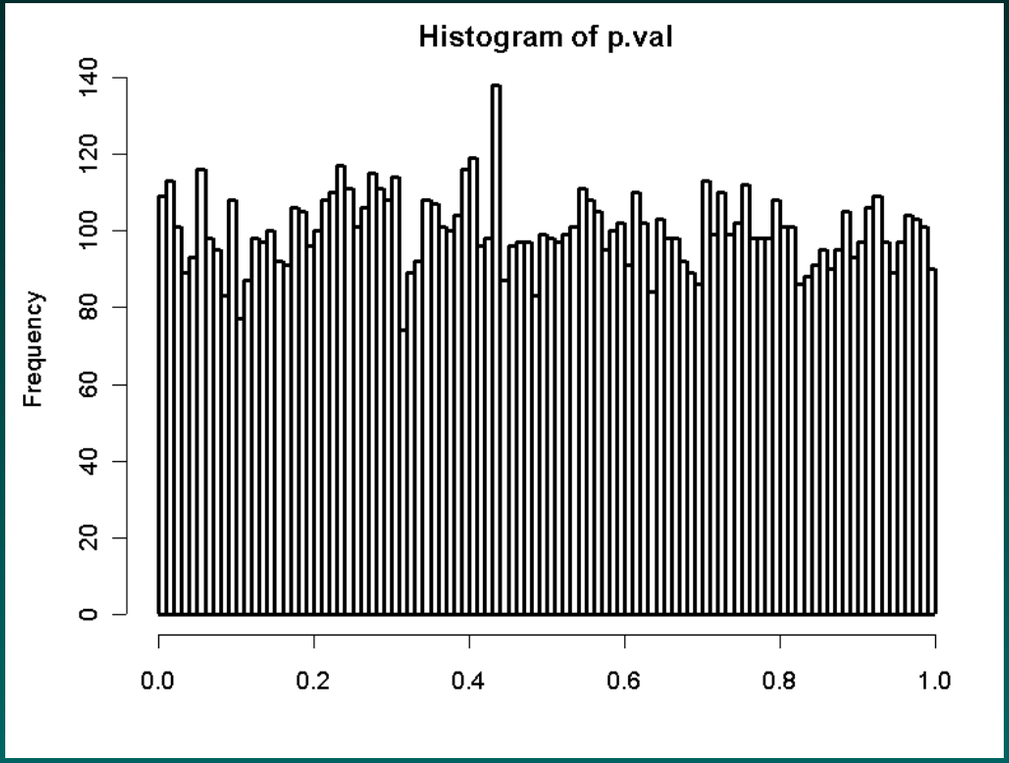
The t distribution

```
t.stat <- (bm - am)/sqrt(sp2)/sqrt(1/an+1/bn)
hist(t.stat, breaks=100, xlab='')
```



P-values are uniformly distributed

```
p.val <- sapply(t.stat, function(tv, df) {
  2*(1-pt(abs(tv), df))
}, an + bn - 2)
hist(p.val, breaks=100, xlab='')
```



How significant is nothing?

```
> sum(p.val < 0.05)
[1] 505
> 0.05 * n.genes
[1] 500
> sum(p.val < 0.01)
[1] 109
> 0.01 * n.genes
[1] 100
```

If there are no real differences, and if we can treat different genes as though they are “replicates” of the same experiment, then

1. Number of genes with $p < \alpha$ is approximately αN.
2. The distribution of p-values is uniform.

Statistical error types

Statisticians (on average) are obsessed with errors. They also tend to use circumlocutions that make it more difficult for non-statisticians to understand them. For example, “rejecting the null hypothesis” means “calling a gene differentially expressed”.

Test Result	Truly Different	Truly Unchanged
Positive	True Positive (TP)	False Positive (FP) Type I Error
Negative	False Negative (FN) Type II Error	True Negative (TN)

P-value = Prob(Type I Error)

To control Type II Errors (FN), you have to increase the sample size to ensure enough power to detect the true differences.

Family-wise error rate (FWER)

$FWER$ = probability of getting at least one FP when performing many statistical test = probability of making at least one mistake

Bonferroni adjustment: To achieve $FWER \leq \alpha$ when looking at G genes, restrict on a per-gene basis to $p \leq \alpha/G$.

```
> bonferroni <- 0.05/n.genes
> bonferroni
[1] 5e-06
> sum(p.val < bonferroni)
[1] 0
```

What happens with real data?

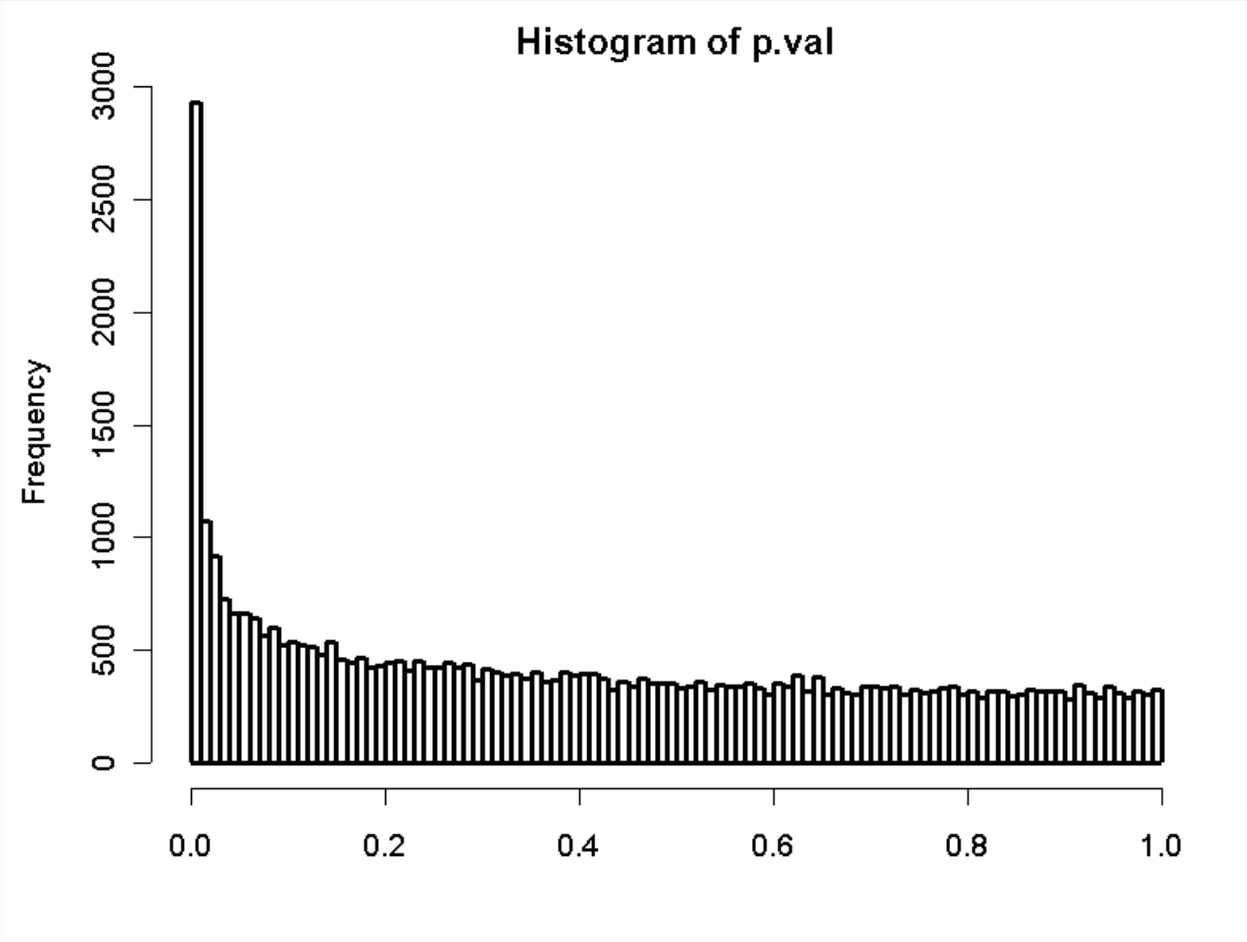
Reference: Lapointe et al. Gene expression profiling identifies clinically relevant subtypes of prostate cancer. *Proc Natl Acad Sci USA*. 2004; **101**: 811–816.

This paper uses two-color microarrays to study prostate cancer. Processed with local background subtraction, loess normalization, then taking log ratios with the reference channel.

- 41 samples of apparently normal prostate
- 62 samples of prostate cancer
- 9 samples of lymph node metastases from prostate cancer

We randomly selected ten samples of normal prostate and ten samples of prostate cancer, and performed two-samples t-tests.

Real p-values



There seems to be an overabundance of small p-values, causing the distribution to differ considerably from uniform.

```
> n.genes <- nrow(data)
> n.genes
[1] 42129
> sum(p.val < 0.05)  # observed
[1] 6316
> 0.05 * n.genes     # expected
[1] 2106.45
> sum(p.val < 0.01)  # observed
[1] 2931
> 0.01 * n.genes     # expected
[1] 421.29
> bonferroni <- 0.05/n.genes
> bonferroni
[1] 1.186831e-06
> sum(p.val < bonferroni)
[1] 42
```

Simulating something

We also simulated two data sets with differences:

1. Data Set I
   - 10 arrays per group, 2000 genes per array
   - Gene expressions in each group are independent, $N(\mu, 1)$.
   - In group A, take all $\mu_A = 0$.
   - 50 genes are different, with $|\mu_A - \mu_B| \sim 5 * Beta(2, 8)$.
2. Data Set II
   - 10 arrays per group, $10,000$ genes per array
   - Mean expression $\mu_A \sim Exp(1/20)$.
   - 100 genes are different, with $\mu_A/\mu_B \sim 1 + 9 * Beta(3, 7)$.

Bonferroni Correction: Results

- Data Set I (normal model)
  - Truth: 50 genes differ out of 2000
  - With $\alpha = 0.05$, makes 21 positive calls, 21 correct.
- Data Set II (exponential + noise)
  - Truth: 100 genes differ out of $10,000$
  - With $\alpha = 0.05$, makes 25 positive calls, 25 correct.

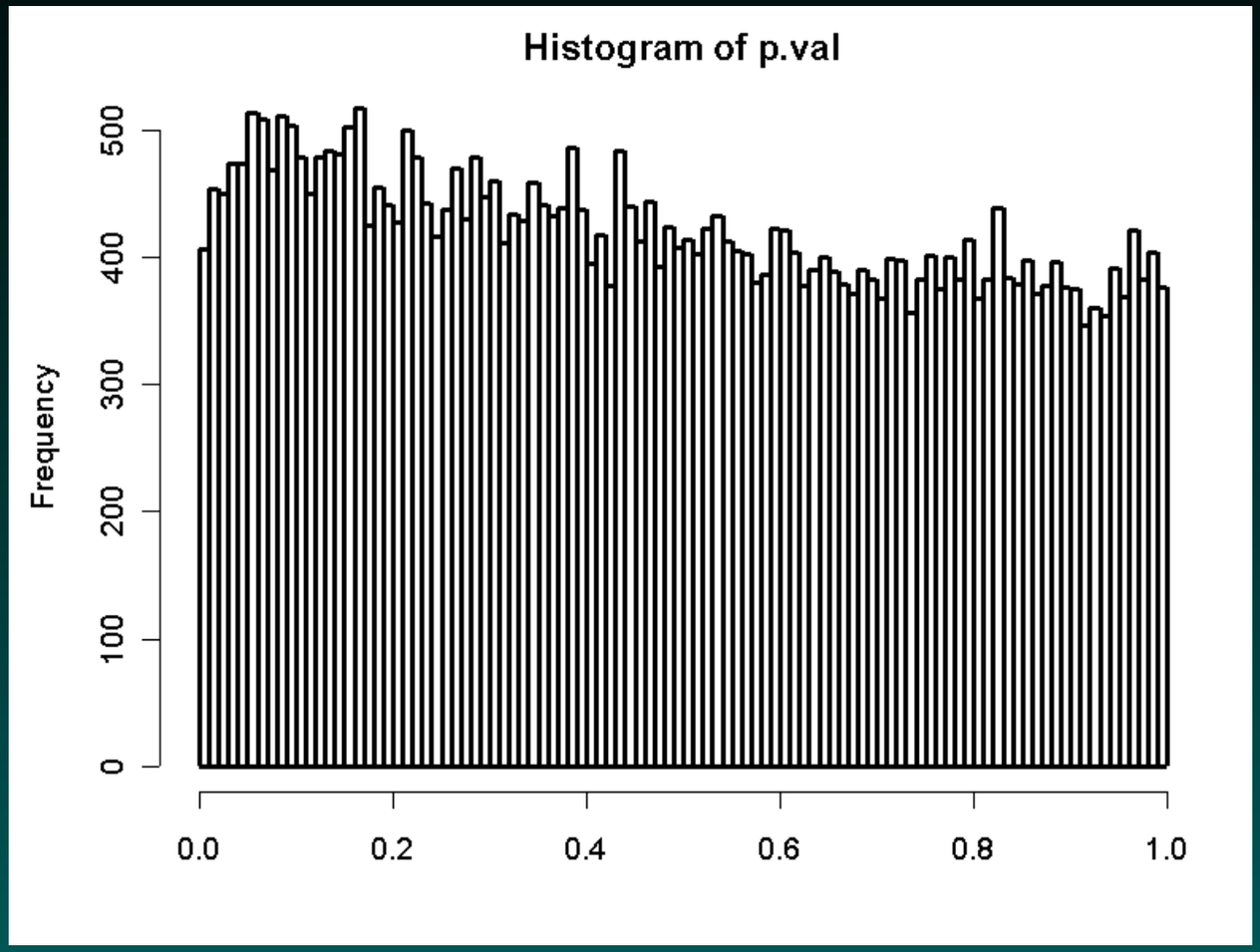
Begining to assess the model

A key assumption of the Bonferroni approach is that a uniform distribution adequately describes the p-values when there are no differntially expressed genes present.

We can start testing how good the uniform model is by performing a permutation test. In this case, we simply scramble the labels on the samples.

In the prostate example, we have ten normal and ten cancer samples. We choose ten samples at random to call “normal”, and call the other ten “cancer”, and we repeat the analysis with the two-sample t-test.

P-values for scrambled sample labels



Nearly uniform, with a slight bulge near $p = 0.01$. This might be attributable to an imbalance of “truth” in the permuted groups.

Scrambled data is insignificant

```
> sum(p.val < 0.05)  # observed
[1] 2257
> 0.05 * n.genes     # expected
[1] 2106.45
> sum(p.val < 0.01)  # observed
[1] 406
> 0.01 * n.genes     # expected
[1] 421.29
> sum(p.val < bonferroni)
[1] 0
```

Should we believe the p-values?

There is another potential difficulty with using the Bonferroni approach: in order to get a significant gene, we need extremely small p-values. That means we have to very accurately estimate the tails of the distribution, which is a fairly difficult thing to do unless one of two fairly unlikely things happens:

1. The number of samples is extremely large, or

2. The distribution of expression values is almost perfectly described by a normal distribution.

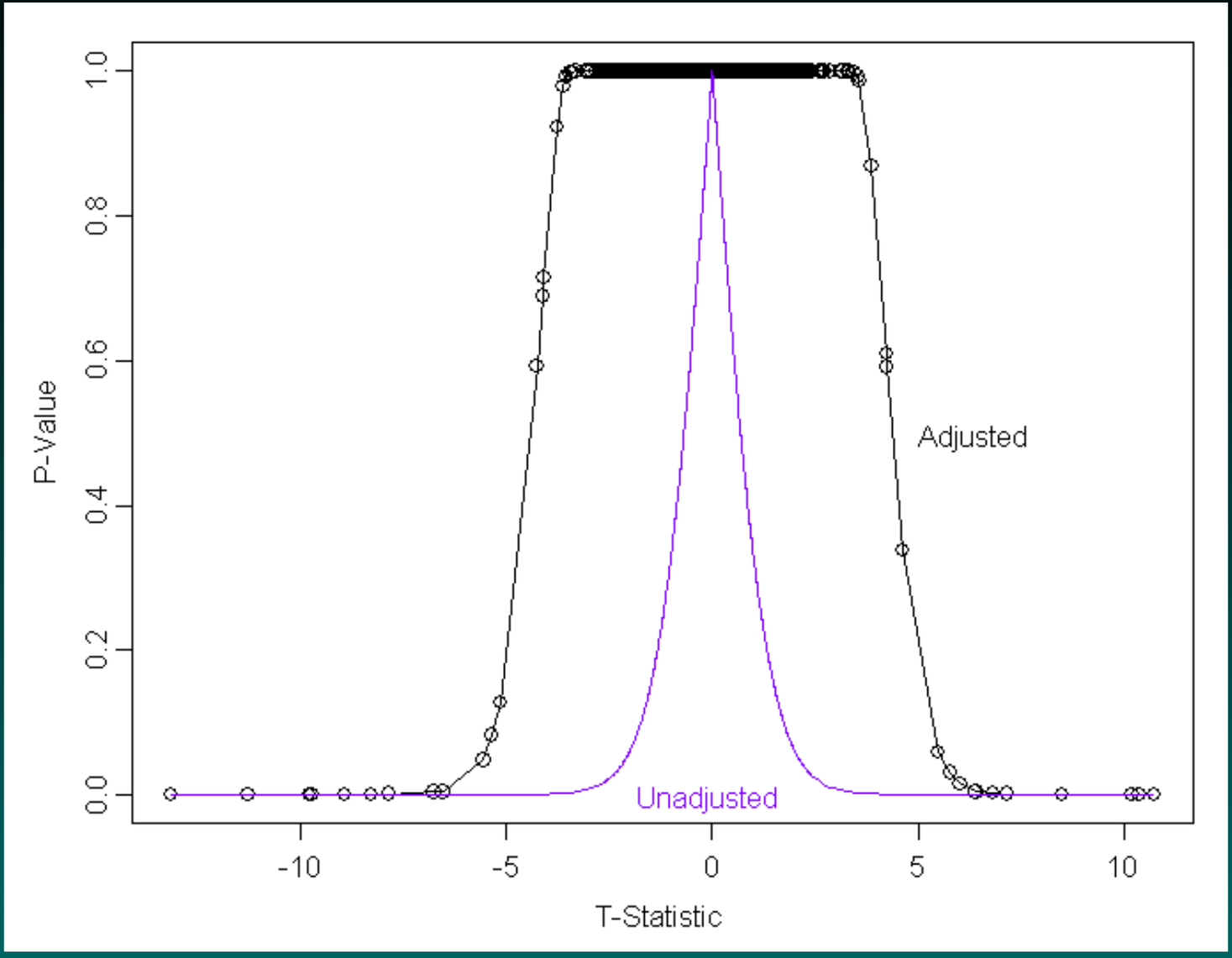
We can use permutations to get around the second problem, but that only makes the first problem worse.

Dudoit's permutation p-values

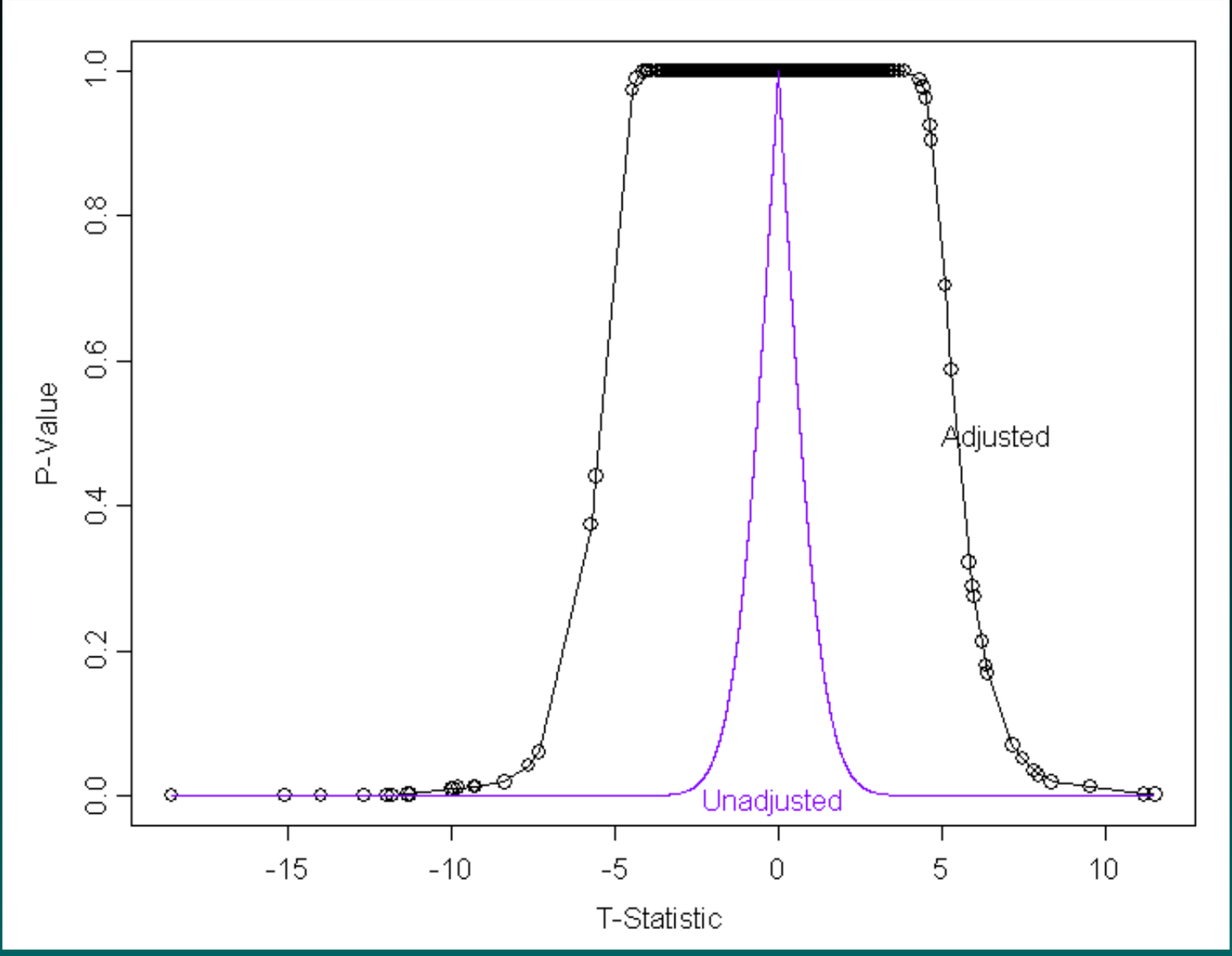
Reference: Dudoit et al. Statistical methods for identifying differentially expressed genes in replicated cDNA microarray experiments. *Statistica Sinica*, 2004; **12**: 111-139.

- Perform t-test for each gene g and sort the absolute t-statistics, $|t_g|$.
- Repeat many times:
  - Randomly permute sample labels.
  - Compute new t-statistics
- Adjust p-values based on empirical joint distribution of t-statistics to control $FWER$.

Adjusted p-values, Data Set I



Adjusted p-values, Data Set II



Dudoits Method: Results

- Data Set I (normal model)
  - Truth: 50 genes differ, out of 2000.
  - With $\alpha = 0.05$, makes 21 positive calls, 21 correct.
- Data Set II (exponential + noise)
  - Truth: 100 genes differ, out of $10,000$
  - With $\alpha = 0.05$, makes 21 positive calls, 21 correct.

Is FWER too conservative?

1. In the prostate data set, Bonferroni with $FWER \leq 5\%$ flagged 42 genes.

2. With an uncorrected $p \leq 1\%$, the model underlying the Bonferroni correction predicts only 421 genes, but we actually observe 2931.

3. With an uncorrected $p \leq 5\%$, the model underlying the Bonferroni correction predicts only 2106 genes, but we actually observe 6316.

Are there only 42 differentially expressed genes among the $42,129$ spots on this array, or are there $2510 = 2931 - 421$? Or maybe even $4210 = 6316 - 2106$?

Opportunity cost

The Bonferroni correction only considers Type I Errors. Microarray experiments, however, are often used for discovery. Findings are usually confirmed by performing additional experiments (typically, real-time PCR). In some cases, the "opportunity cost" of missing out on a discovery (by making a Type II Error) is greater than the "validation cost" of finding some false positives (Type I Errors) in your list of genes.

Like anything else, there are trade-offs. By choosing a smaller significance cutoff for the p-values, you get fewer false positives but more false negatives. By choosing a larger cutoff, you get more false positives and fewer false negatives.

The false discovery rate

$FDR = FP/(TP + FP) =$ fraction of false positives among all genes called differentially expressed by the test. Here is a crude way to estimate FDR: Assume the uniform model for p-values holds under the null hypothesis. The the expected number of false discoveries at a given p-value cutoff is pG. If the total number of discoveries is V, then we can estimate $FDR = pG/V$. In the prostate cancer example, this gives

- When $p = 0.05$, $FDR = 0.3334 = 2106/6316$.
- When $p = 0.01$, $FDR = 0.1436 = 421/2931$.

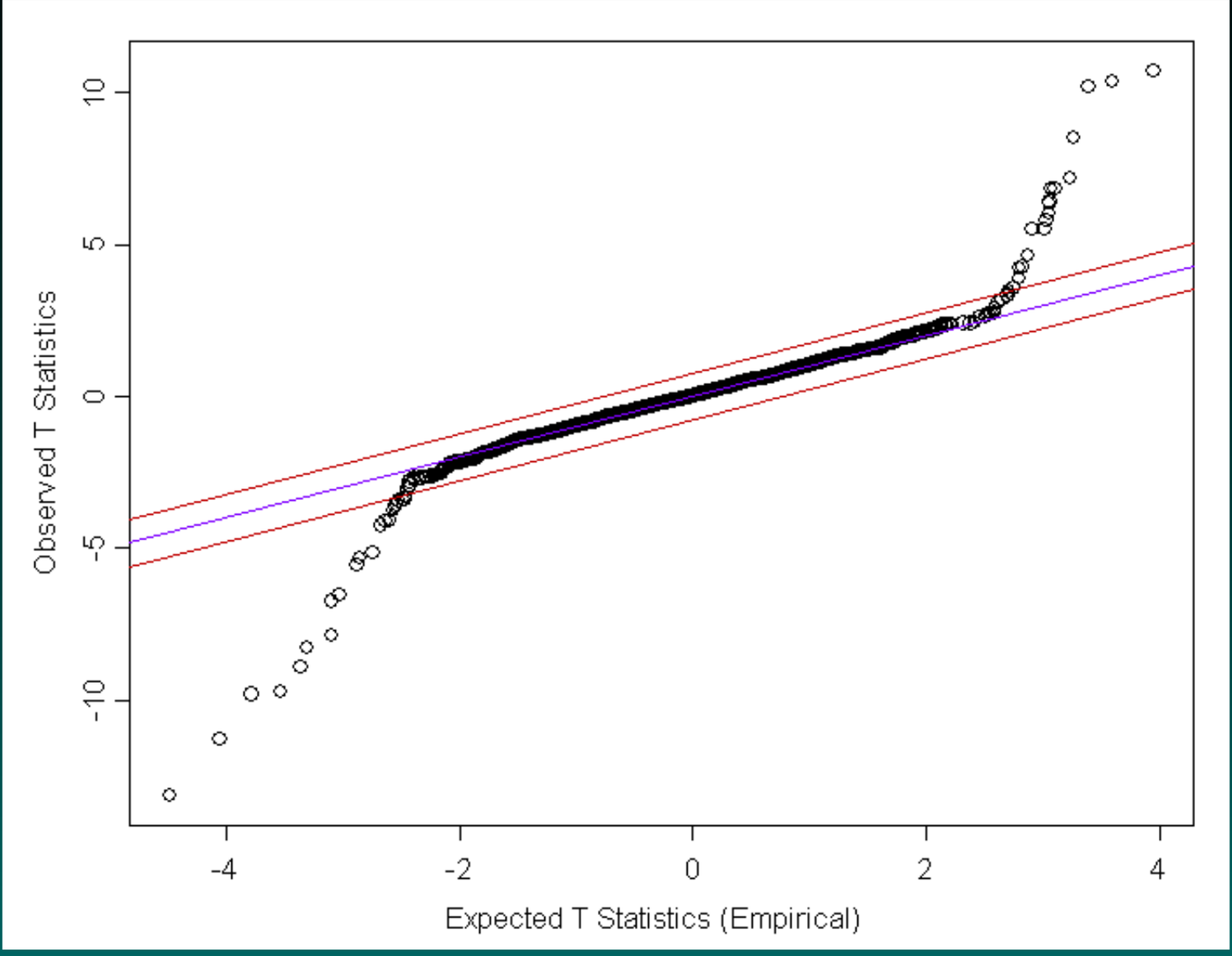
This estimate is not very good; it overestimates the number of errors by not accounting for the fact that there seem to be some true discoveries.

Significance analysis of microarrays (SAM)

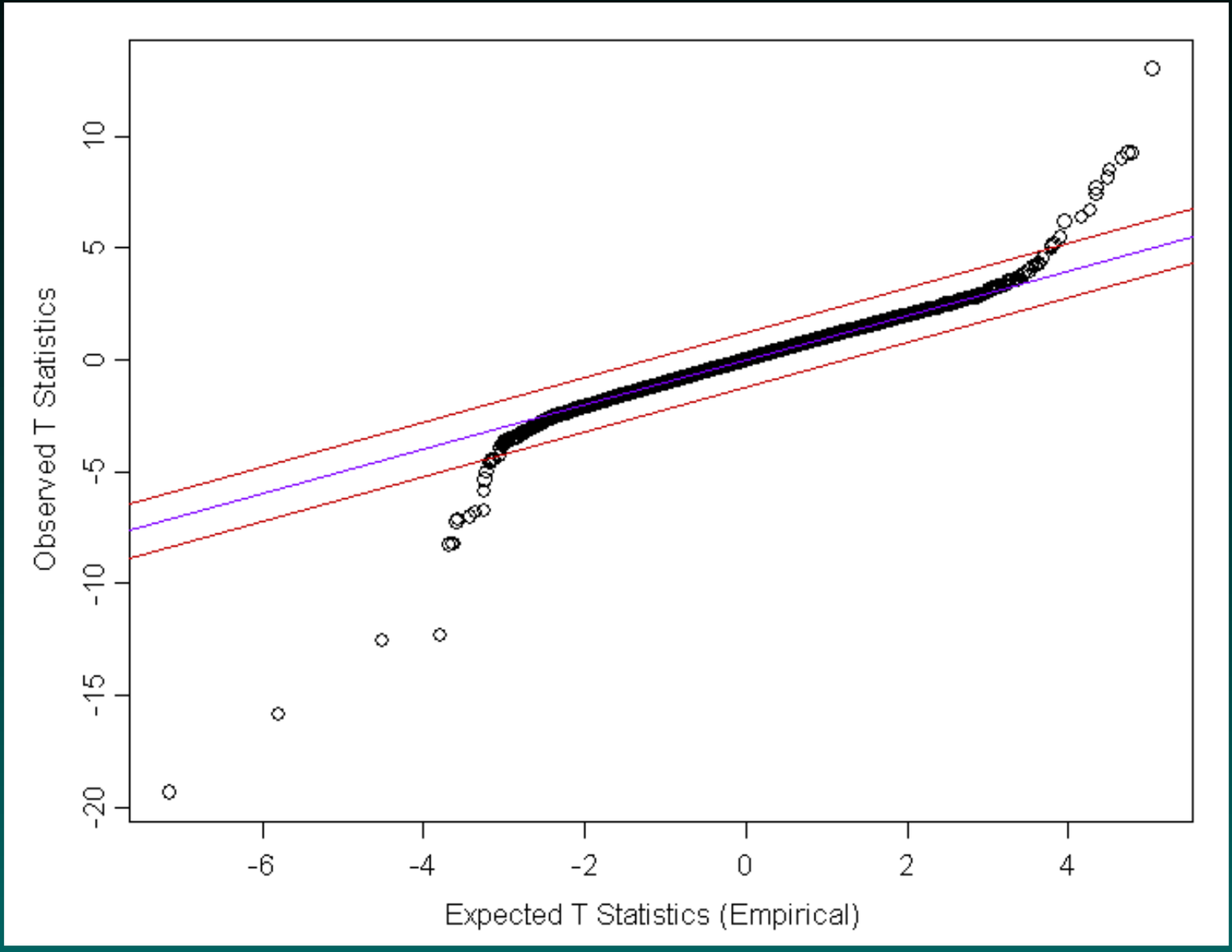
Reference: Tusher et al. Significance analysis of microarrays applied to the ionizing radiation response. *PNAS*, 2001; **98**: 5116–5121.

- Compute modified t-statistics (increase σ to minimize coefficient of variation across the array).
- Recompute t-statistics based on balanced permutations (each group equally represented) of the sample labels.
- Decide on significance cutoff based on quantile-quantile plot of observed versus expected t-statistics.
- Estimate FDR from the permutations.

SAM, Data Set I



SAM, Data Set II



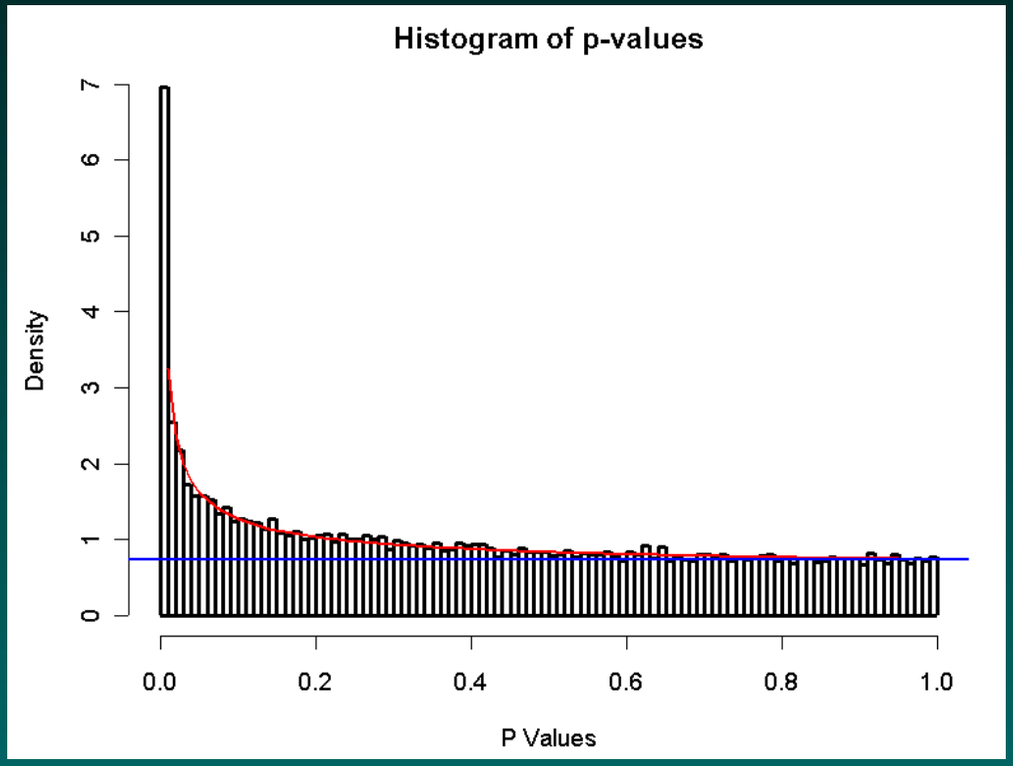
SAM: Results

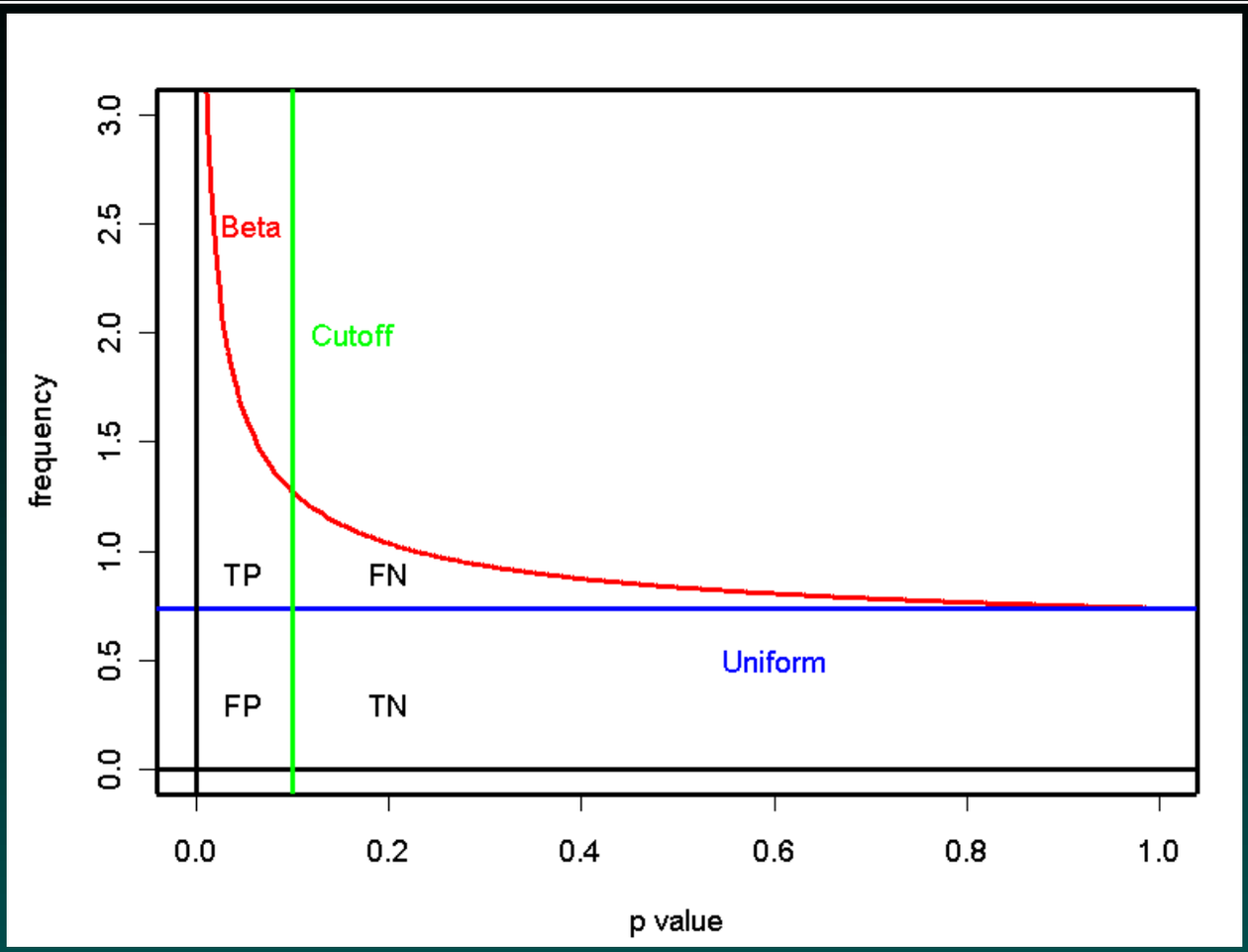
- Data Set I (normal model)
  - Truth: 50 genes differ, out of 2000.
  - With $FDR = 0.10$, makes 32 positive calls, 30 correct.
- Data Set II (exponential + noise)
  - Truth: 100 genes differ, out of $10,000$
  - With $FDR = 0.10$, makes 41 positive calls, 37 correct.

Detects more true positives in simulated data than Bonferroni or Dudoit, at some cost in false positives. Like Dudoit's method, it is computationally intensive.

Beta-uniform mixture model (BUM)

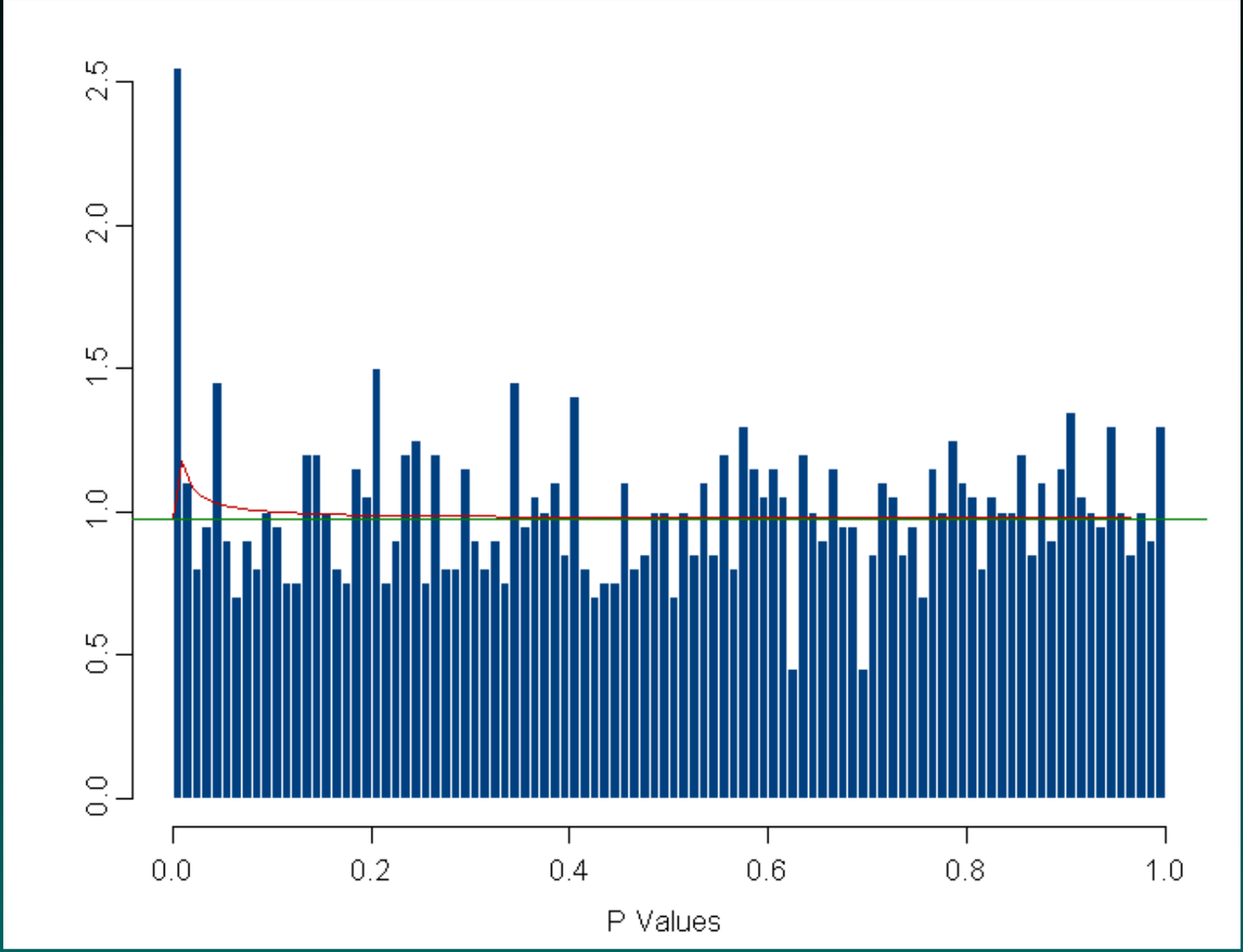
Reference: Pounds and Morris. Estimating the occurrence of false positives and false negatives in microarray studies by approximating and partitioning the empirical distribution of p-values. *Bioinformatics*, 2003; **19**: 1236–1242.



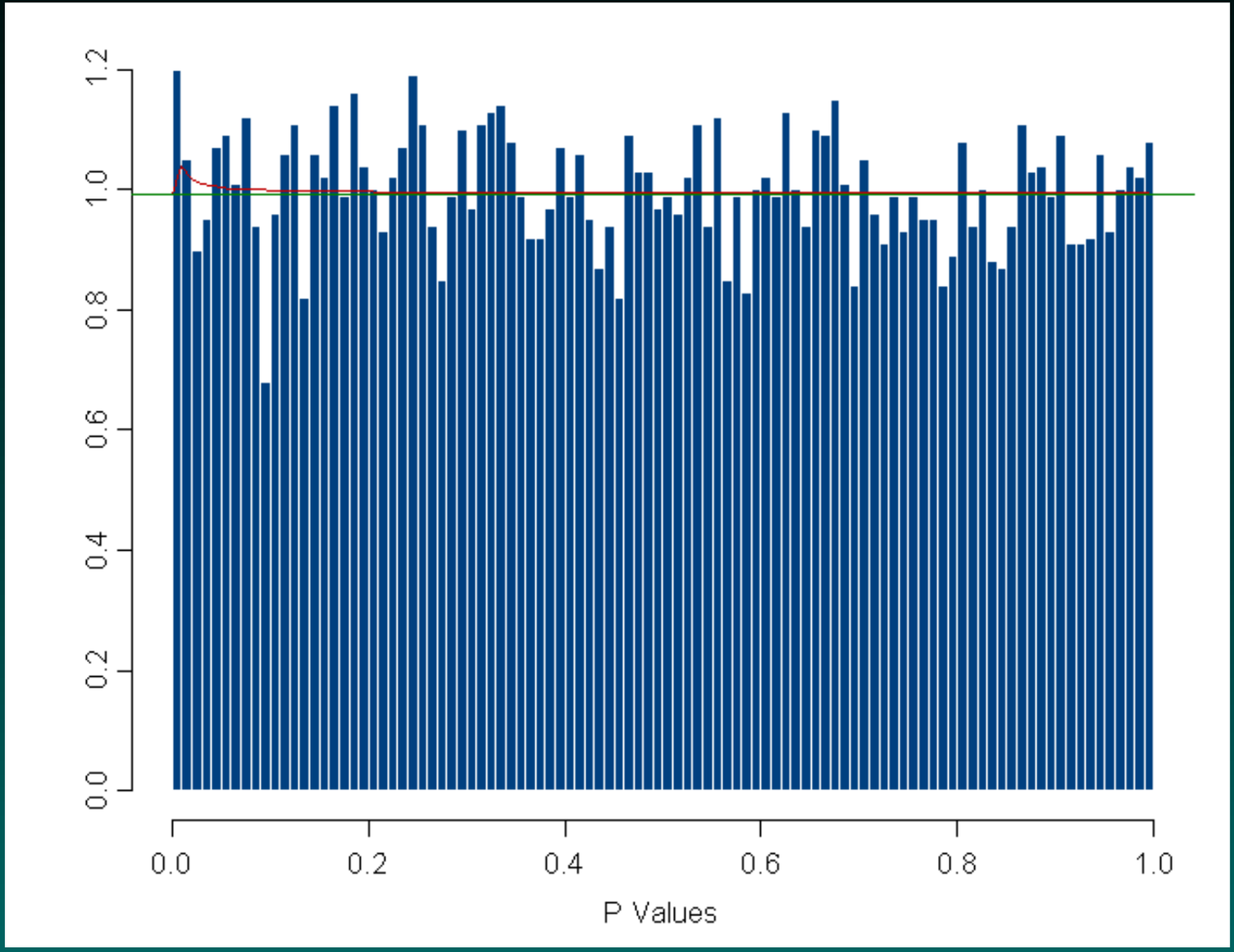


Idea: Model the p-values as a mixture of a uniform distribution and a beta distribution. Estimate mixture parameters. Obtain estimates of TP, FP, FN, TN as a function of significance cutoff.

BUM, Data Set I



BUM, Data Set II



BUM: Results

- Data Set I (normal model)
  - Truth: 50 genes differ, out of 2000.
  - With $FDR = 0.10$, makes 33 positive calls, 31 correct.
  - Estimates that 2.8% of genes are different (truth = 2.5%)
- Data Set II (exponential + noise)
  - Truth: 100 genes differ, out of $10,000$
  - With $FDR = 0.10$, makes 40 positive calls, 37 correct.
  - Estimates that 0.7% of genes are different (truth = 1.0%)

Results equivalent to SAM, with much less computation.

BUM results on prostate data

We have already seen the histogram, and the fit of the beta-uniform mixture.

- With $FDR < 0.01$, calls 427 genes differentially expressed.
- With $FDR < 0.05$, calls 1513 genes differentially expressed.
- With $FDR < 0.10$, calls 2727 genes differentially expressed.

Overall, BUM estimates that 26% of the genes are differentially expressed at some level. (That's more than $10,000$ genes!)