

SUCCOTASH vs Methods in Mengyin’s Code when all Null

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Abstract

Here, I compare SUCCOTASH’s lfdr to the lfdr’s provided in all of the methods in Mengyin’s code. I then compare SUCCOTASH’s estimation performance to those of CATE, SVA, LEAPP, RUV, and OLS. These are all under the data generation process that Mengyin coded up using the GTEX data where all genes are null.

1 Competitors

For each of procedure in Mengyin’s code, I performed the following two-step procedure:

1. Estimate $\hat{\beta}_{[2,i]}$ and it’s corresponding standard error \hat{s}_i .
2. Run ASH on $\hat{\beta}_{[2,i]}$ and \hat{s}_i .

The methods available in Mengyin’s code to get $\hat{\beta}_{[2,i]}$ and \hat{s}_i were

- VOOM [Law et al., 2014].
- RUVseq [Risso et al., 2014] followed by VOOM [Law et al., 2014] with the estimated confounding factors. Half of the factors were used as control genes.
- SVASEq [Leek, 2014] followed by VOOM [Law et al., 2014] with the estimated confounding factors.
- RUVseq + quasi-binomial glm.
- SVASEq + quasi-binomial glm.
- MYRNA, which is just a quasi-binomial glm using the 75th percentile of the samples’ counts as covariates [Langmead et al., 2010].
- MYRNA offset, which is just a quasi-binomial glm using the 75th percentile of the samples’ counts as offsets [Langmead et al., 2010].
- EdgeR [Robinson et al., 2010].
- DESeq2glm [Love et al., 2014].

Note that “VOOM” means using VOOM [Law et al., 2014] to find weights for each observations, then fitting a linear model using LIMMA [Smyth, 2005].

I also compared the estimation performance of SUCCOTASH with

- LEAPP [Sun et al., 2012].
- The robust regression version of CATE [Wang et al., 2015].
- SVA [Leek and Storey, 2007] with the number of confounders estimated using the method of Bai et al. [2012].

- RUV4 [Gagnon-Bartsch et al., 2013] with 50% of the observations being control genes with the number of confounders estimated using the method of Bai et al. [2012].
- The ordinary least squares (OLS) estimator.

The factor analysis part of SUCCOTASH was done with the quasi-mle approach of Bai et al. [2012] with the number of hidden confounders using the methods of Buja and Eyuboglu [1992] implemented in the `num.sv()` function in the `sva` package in R.

2 Simulation Study

I ran through 100 repetitions of generating the data using Mengyin’s code with

- $n = 200$,
- $p = 1000$.

That is, 1000 genes are chosen at random from the GTEX lung data and 200 samples are chosen at random. One hundred of these samples are randomly given the “treatment” label 1, the other one hundred given the “treatment” label 0. Since the assignments are random, the true effect is 0 for all genes.

For SUCCOTASH, CATE, LEAPP, SVA, RUV, and OLS I merely applied a log transformation to the counts with a 1 offset before applying each method.

I calculated the sum of squared errors (SSE’s) for SUCCOTASH, LEAPP, CATE, RUV, SVA, and OLS on the $\log(\text{counts} + 1)$ data. Since all effects are null, this is just the sum of squares for each method’s estimates. I didn’t look at the SSE of the other methods because they have different data normalization procedures.

I also compared the local false discovery rates (lfdr’s) of SUCCOTASH, VROOM, RUVseq + VROOM, SVASEq + VROOM, RUVseq + quasi-binomial glm, SVASEq + quasi-binomial glm, MYRNA, MYRNA offset, EdgeR, and DESeq2. Specifically, I calculated the mean of the lfdr’s at each iteration for all methods. The higher the mean lfdr’s the better as all genes are null.

3 Results

SUCCOTASH performed the best in terms of MSE against the other confounder adjustment methods (Figure 1).

The results for lfdr are less clear (Figure 2). There are many methods that beat SUCCOTASH a majority of the time, but SUCCOTASH’s average performance is not much worse than the best average performance. No method stands out.

Note that for these data sets, some of the quasi-binomial glm methods were unable to provide lfdr’s. For each of the 100 trials, the number of times each method failed to provide lfdr’s is provided in Table ???. The labels in Table ??? are the same as in Figure 2.

```
## Error in is.data.frame(x): object 'lfdr_mat' not found
## Error in xtable(fail_mat, caption = paste0("Number of times each method failed to
provide lfdrs out of ", : object 'fail_mat' not found
```

Figure 1: Mean squared errors (MSE) for SUCCOTASH (SUCC), LEAPP, CATE, RUV, SVA, and OLS

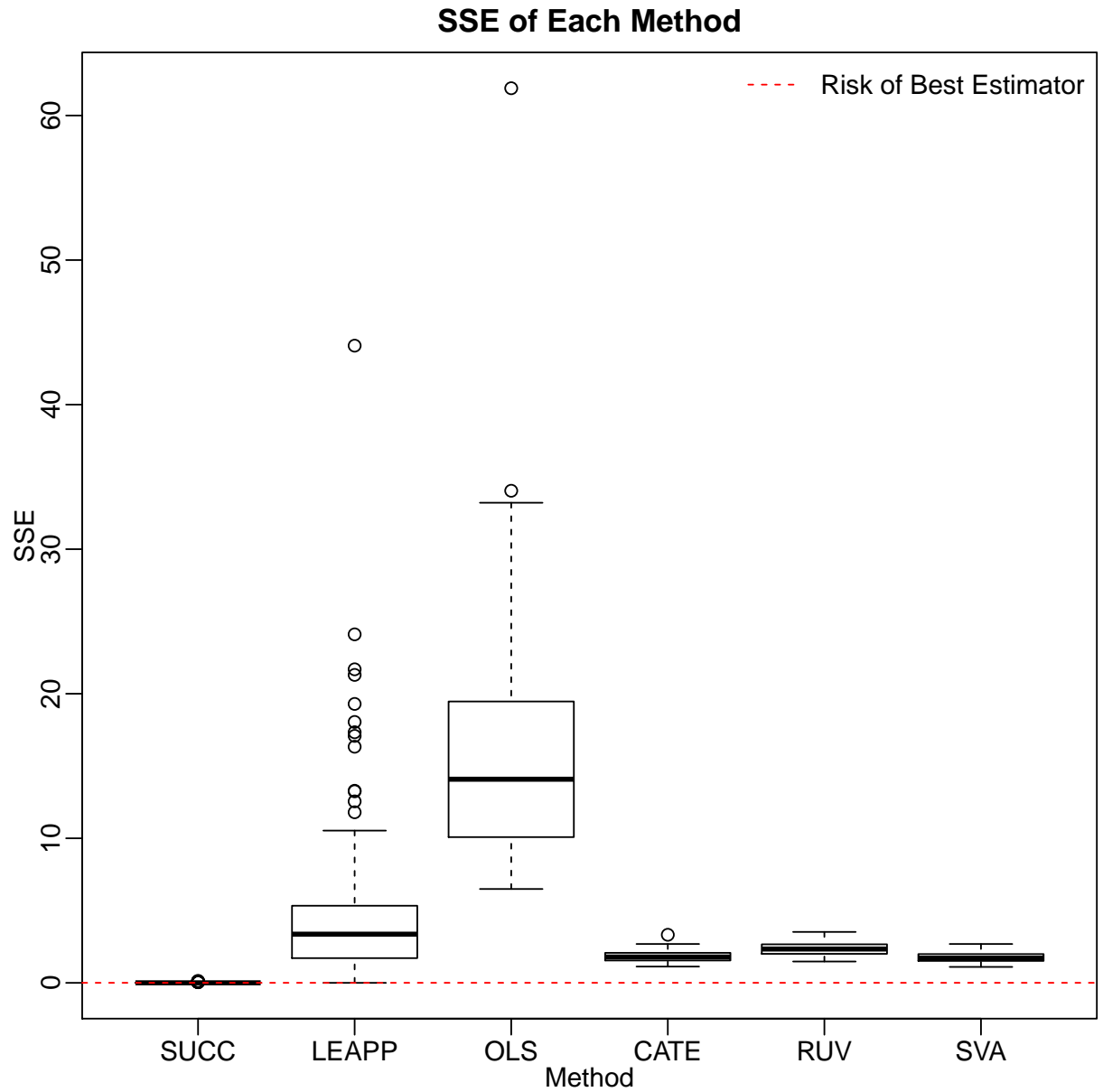
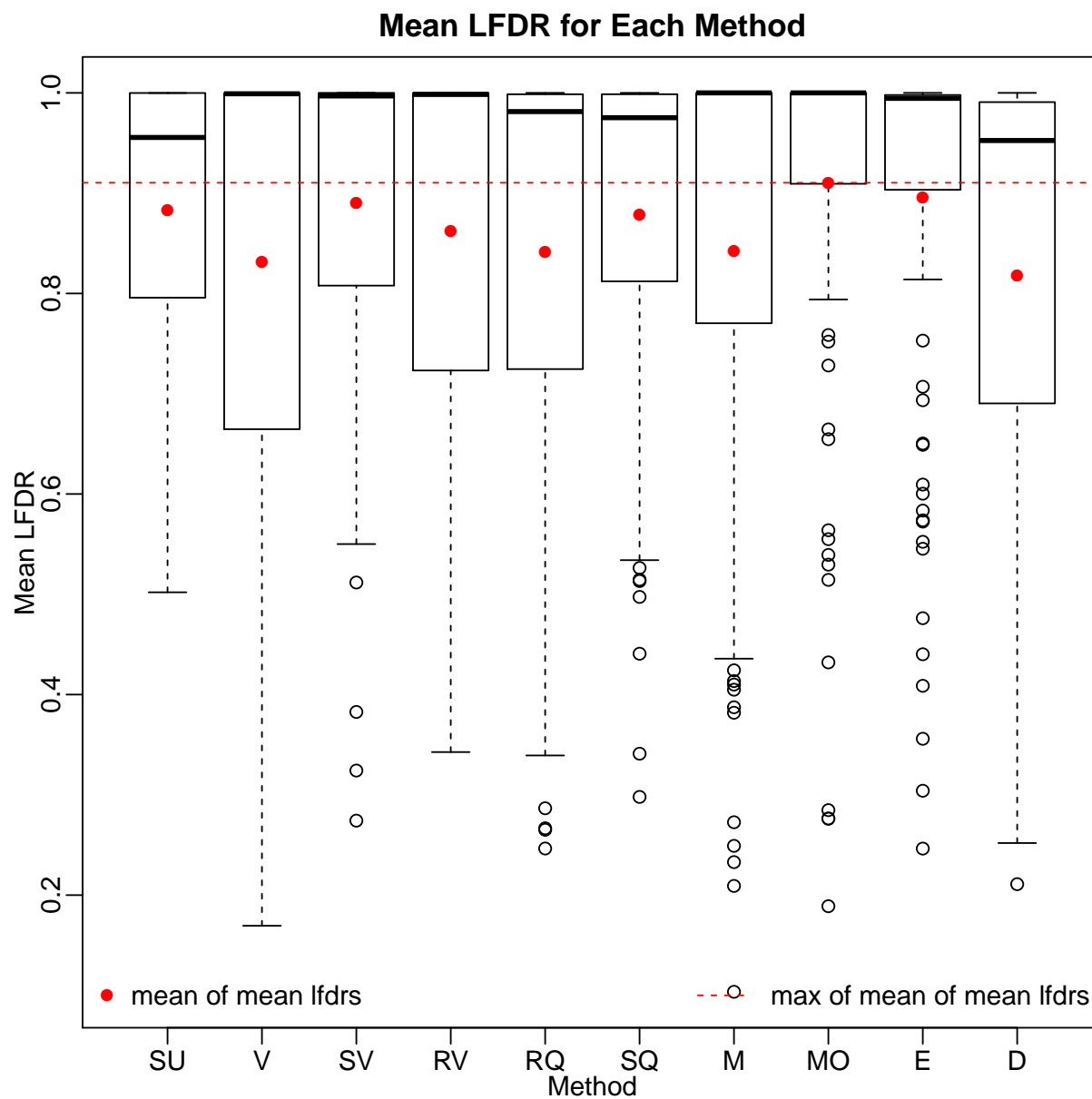


Figure 2: Mean lfdr for SUCCOTASH (SU), VOOM (V), SVA and VOOM (SV), RUV and VOOM (RV), RUV and quasi-binomial glm (RQ), SVA and quasi-binomial glm (SQ), Myrna (M), Myrna offset (MO), EDGER (E), DESEQ2 (D).



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