

# Understanding Outputs

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## Overview

We will analyze example output found in `SLIDE/test/out/0.01_1_out`

This is the general workflow:

1. Evaluate latent factor performance using `ControlPerformancePlot.png`
2. Look at top features in each latent factor using `plotSigGenes_marginals.png` and `plotSigGenes.png`
3. Look at interactions between latent factors with `plotInteractions.png`
4. Look at gene lists in `gene_list_Z.txt` files
5. View SLIDE results and parameters in `SLIDE_LFs.rds`
6. View correlation networks of significant latent factors after running `plotCorrelationNetworks`

## Evaluate latent factor performance using `ControlPerformancePlot.png`

This plot shows how the significant latent factors perform relative to their knockoff counterparts:

- The red line is the true performance of the significant latent factors (either correlation for continuous response/Y or AUC for binary response/Y).
- The blue density shows the performance of the knockoffs for the stand-alone/marginal latent factors
- The green density shows the performance of the true marginal latent factors paired with knockoffs for the interaction latent factors

A good model should have:

- **performance red line should be highest** (better performance) and to the right of both the blue and green densities - this indicates that there signal in the significant latent factors.
- **green density should be slightly higher than blue**, since we are using the true marginal latent factors paired with knockoff interaction latent factors - we are trying to evaluate whether the interaction latent factors are meaningful
- **blue density has the lowest performance**, as knockoffs for our marginal latent factors should not have signal

```
knitr::include_graphics("examples/out/0.01_1_out/ControlPerformancePlot.png")
```

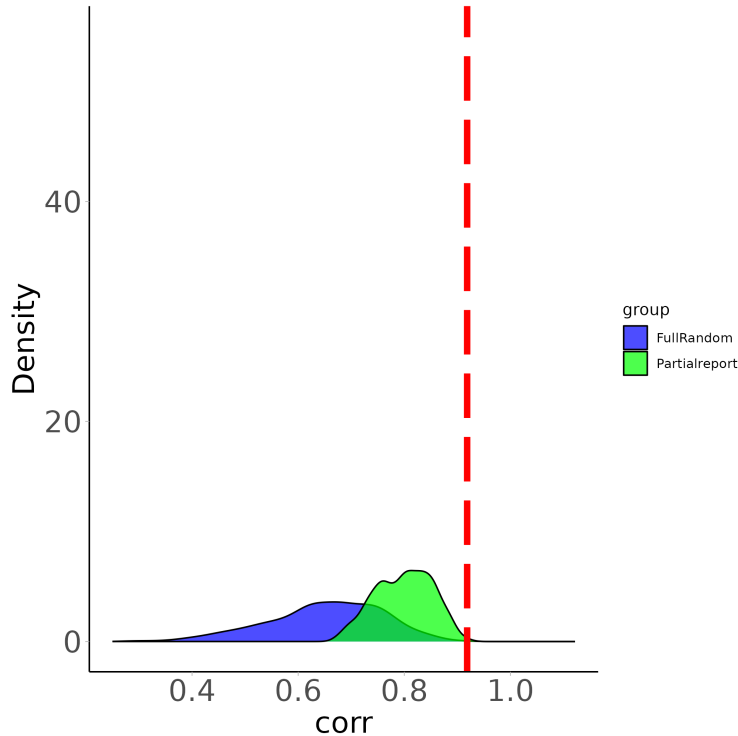


Figure 1: Significant Latent Factor Performance

Above is an example of a model with great performance. In some cases, you may find that the green density overlaps perfectly with the blue - in this case, the interaction latent factors are not meaningful. If you find that all three (blue, green and red) perfectly overlap, then this indicates a lack of signal in the significant latent factors and there are a few options:

1. Increase `spec` parameter (increase FDR control for choosing latent factors)
2. Re-cluster latent factors using different `delta` and `lambda` parameters - it is possible the latent factors are a poor fit to the data (too many latent factors will overfit = increase `delta`; too few latent factors will be over-clustered = decrease `delta`)

The data for this plot is stored in `ControlPerformance.rds`; the `ControlPerformancePlot.rds` has the plot object for the ggplot above.

## Look at top features in each latent factor using `plotSigGenes_marginals.png` and `plotSigGenes.png`

The `plotSigGenes_marginals.png` shows the top features in the stand-alone/marginal significant latent factors. By default, we show the top 10 features by loading (features that contribute most to the latent factor), as well as the top 10 univariate features (features that have high correlation or AUC with response/Y). Each latent factor shows 20 features - the bottom 10 are the highest univariate and the top 10 are highest by latent factor loading.

```
knitr::include_graphics("examples/out/0.01_1_out/plotSigGenes_marginals.png")
```

## SLIDE Marginal Variables

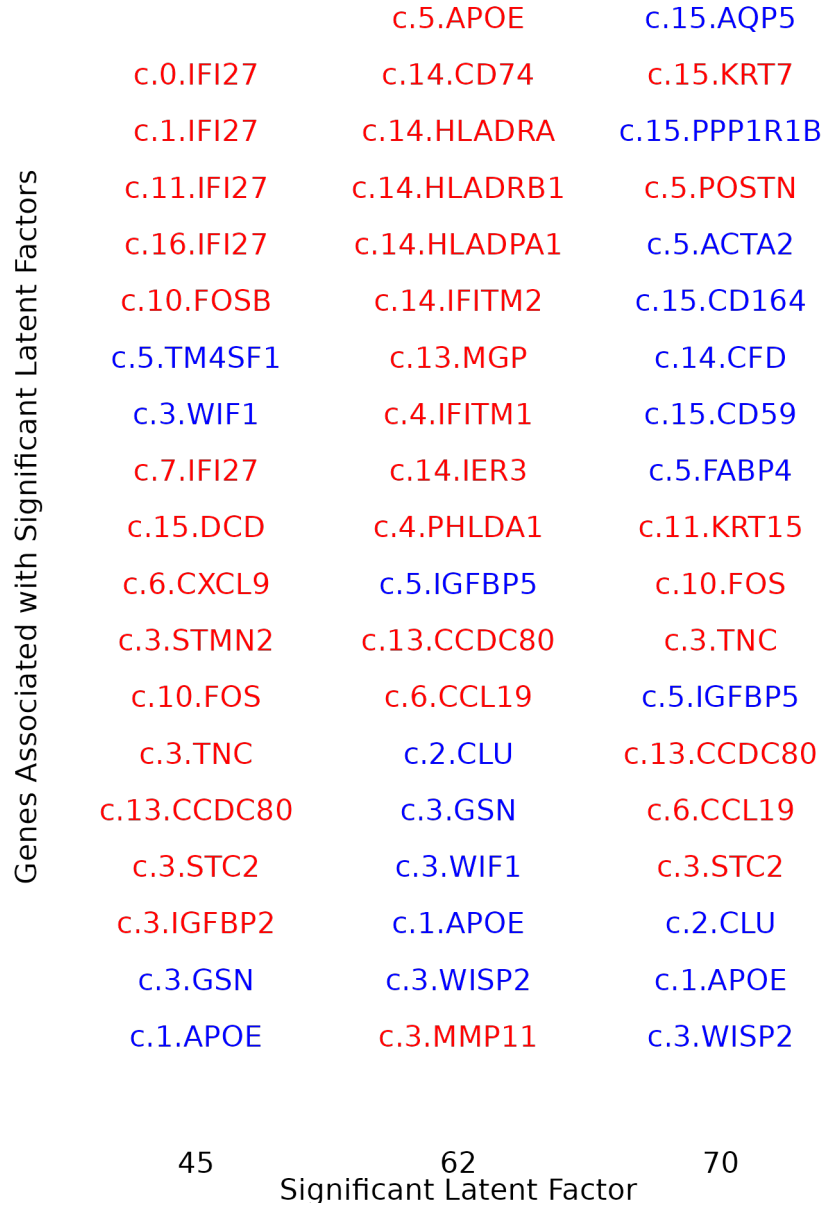


Figure 2: Marginal Significant Latent Factors

We also include plots showing both the marginal and interaction latent factors in this format; here, the bolded/italicized latent factors are the stand-alone/marginal latent factors and the plain text are the interactions.

```
knitr::include_graphics("examples/out/0.01_1_out/plotSigGenes.png")
```

Significant Latent Factors - Marginals (bold/italic) and Interactions

Genes Associated with Significant Latent Factors	c.2.IL6					
	c.2.CSF3				<b>c.5.APOE</b>	<b>c.15.AQP5</b>
	c.11.AREG		<b>c.0.IFI27</b>		<b>c.14.CD74</b>	<b>c.15.KRT7</b>
	c.5.CEBPD		<b>c.1.IFI27</b>	c.13.DUSP1	<b>c.14.HLADRA</b>	<b>c.15.PPP1R1B</b>
	c.9.CCL20		<b>c.11.IFI27</b>	c.13.CYR61	<b>c.14.HLADRB1</b>	<b>c.5.POSTN</b>
	c.16.FABP5		<b>c.16.IFI27</b>	c.17.GZMB	<b>c.14.HLADPA1</b>	<b>c.5.ACTA2</b>
	c.8.COMP	c.3.IGFBP5	<b>c.10.FOSB</b>	c.13.APOE	<b>c.14.IFITM2</b>	<b>c.15.CD164</b>
	c.12.FOS	c.3.TPPP3	<b>c.5.TM4SF1</b>	c.13.ACTC1	<b>c.13.MGP</b>	<b>c.14.CFD</b>
	c.5.CFD	c.3.IGFBP6	<b>c.3.WIF1</b>	c.13.EGR1	<b>c.4.IFITM1</b>	<b>c.15.CD59</b>
	c.10.DUSP1	c.3.CD55	<b>c.7.IFI27</b>	c.4.DCN	<b>c.14.IER3</b>	<b>c.5.FABP4</b>
	c.3.STMN2	c.3.SLPI	<b>c.15.DCD</b>	c.14.PRX	<b>c.4.PHLDA1</b>	<b>c.11.KRT15</b>
	c.10.KLF6	c.3.TNXB	<b>c.6.CXCL9</b>	c.13.ACTA1	<b>c.5.IGFBP5</b>	<b>c.10.FOS</b>
	c.13.CCDC80	c.3.SAA1	<b>c.3.STMN2</b>	c.8.TAGLN	<b>c.13.CCDC80</b>	<b>c.3.TNC</b>
	c.6.CCL19	c.3.MFAP5	<b>c.10.FOS</b>	c.3.STC2	<b>c.6.CCL19</b>	<b>c.5.IGFBP5</b>
	c.3.STC2	c.5.IGFBP5	<b>c.3.TNC</b>	c.1.APOE	<b>c.2.CLU</b>	<b>c.13.CCDC80</b>
	c.3.GSN	c.3.STMN2	<b>c.13.CCDC80</b>	c.13.TIMP3	<b>c.3.GSN</b>	<b>c.6.CCL19</b>
	c.1.APOE	c.10.FOS	<b>c.3.STC2</b>	c.13.HES1	<b>c.3.WIF1</b>	<b>c.3.STC2</b>
	c.10.FOSB	c.10.TXNIP	<b>c.3.IGFBP2</b>	c.17.MTCO1	<b>c.1.APOE</b>	<b>c.2.CLU</b>
	c.0.S100A2	c.10.KLF6	<b>c.3.GSN</b>	c.13.FLNA	<b>c.3.WISP2</b>	<b>c.1.APOE</b>
	c.4.TCIM	c.3.TNC	<b>c.1.APOE</b>	c.13.CCL2	<b>c.3.MMP11</b>	<b>c.3.WISP2</b>
	4	6	45	60	62	70
	Significant Latent Factor					
						82

Figure 3: Marginal (bolded) and Interaction (plain) Significant Latent Factors

## Look at interactions between latent factors with `plotInteractions.png`

This plot shows a graphical representation of how the interacting latent factors are paired with the marginals. Here, connections from the salmon nodes (marginal latent factors) to the gray nodes indicate latent factor interactions.

```
knitr::include_graphics("examples/out/0.01_1_out/plotInteractions.png")
```

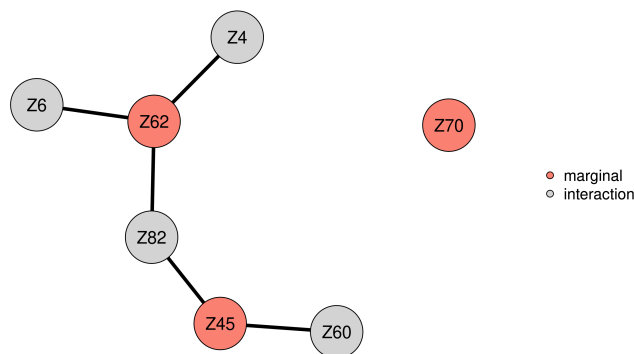


Figure 4: Latent Factor Interactions

## Look at gene lists in gene\_list\_Z.txt files

These outputs provide a table of the top 20 features (same as above in the text plots), and provide the associated latent factor loadings `A_loading` and correlation/AUC `corrs`, as well as the association of each feature with the response `color`. For the color, `Red` is associated with a higher response/Y (or  $Y = 1$  for binary) and `Blue` is associated with a lower response/Y (or  $Y = 0$  for binary).

```
gene_list = read.csv("examples/out/0.01_1_out/gene_list_Z70.txt",
  row.names = 1)
knitr::kable(gene_list)
```

	A_loading	corrs	color
c.15.AQP5	1.0000000	-0.5396689	Blue
c.15.KRT7	1.0000000	0.0387969	Red
c.15.PPP1R1B	1.0000000	-0.5174597	Blue
c.5.POSTN	0.2546804	0.1633278	Red
c.5.ACTA2	0.2097075	-0.0135018	Blue
c.15.CD164	0.2054907	-0.3351158	Blue
c.14.CFD	0.1918422	-0.2628597	Blue
c.15.CD59	0.1816671	-0.1307760	Blue
c.5.FABP4	0.1496629	-0.4573178	Blue
c.11.KRT15	0.1481397	0.1398086	Red
c.10.FOS	0.0146592	0.6363250	Red
c.3.TNC	0.0578869	0.6215166	Red
c.5.IGFBP5	0.0436693	-0.5971263	Blue
c.13.CCDC80	0.1019874	0.5884155	Red
c.6.CCL19	0.0238157	0.5849312	Red
c.3.STC2	0.0469672	0.5823180	Red
c.2.CLU	0.0029181	-0.5696873	Blue
c.1.APOE	0.0111260	-0.5548789	Blue
c.3.WISP2	0.0065220	-0.5531367	Blue

## View SLIDE results and parameters in SLIDE\_LFs.rds

We can see the parameters that were used to run SLIDE in `SLIDE_LFs.rds`

```
SLIDE_LFs = readRDS("examples/out/0.01_1_out/SLIDE_LFs.rds")
names(SLIDE_LFs)
```

```
#> [1] "SLIDE_res"      "SLIDE_param"    "marginal_vals"  "interaction"
#> [5] "feature_res"
```

We can see the parameters:

```
knitr::kable(SLIDE_LFs$SLIDE_param)
```

	x
method	4.0

	x
spec	0.3
fdr	0.1
niter	5.0
f_size	24.0

## View correlation networks of significant latent factors after running `plotCorrelationNetworks`

After running `optimizeSLIDE`, we can run `plotCorrelationNetworks` to generate correlation network plots of the top features in each latent factor.

- **Node color:** Red nodes are associated with higher response/ $Y$  (for continuous  $Y$ ) or  $Y = 1$  (for binary  $Y$ ); blue nodes are associated with lower response/ $Y$  (for continuous  $Y$ ) or  $Y = 0$  (for binary  $Y$ ). This is the same color code as in the `plotSigGenes.png` plots above.
- **Edge color:** Purple edges are positive correlations and green edges are negative correlations between features

Z70

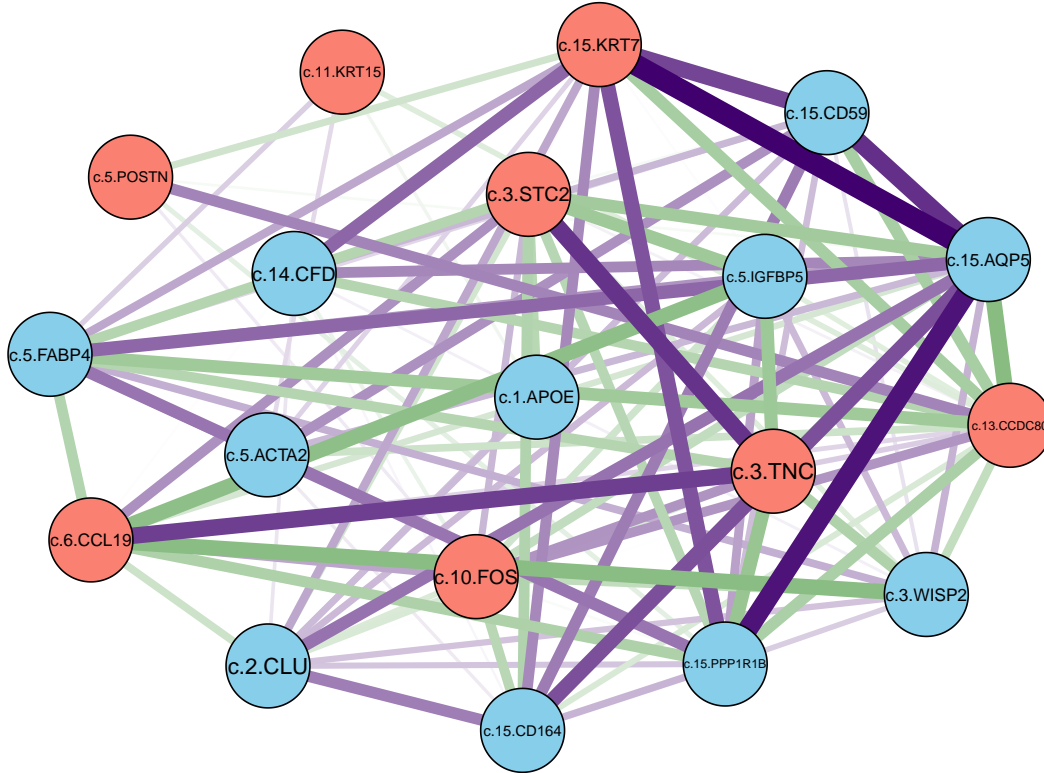


Figure 5: Correlation Network Example