

1 Rhino Study Results

These are the 13 genes that were used in the rhino study.

CXCL10 OAS2 CCL2 CCL8 IL1B IL1RN CASP7 CCR1 TAP1 TAP2
CASP5 TNFAIP6 TNFSF10

1.1 Classifier

For each gene, compute the baseline average (average of t-12 and t0 values for all subjects), baseline standard deviation (using L1 norm for now), and baseline maximum. Set `gene_threshold` to be the `baseline_maximum + 1*baseline_stddev`

Next compute a score for each subject. If a gene ever goes over `gene_threshold` in the given time period (tlower to tupper, default all times), then increment score of subject by 1.

If score is greater than number of genes/3, then subject classified as "SYMP"
If score is less than number of genes/4, then subject classified as "ASYMP"

Here are the results – using ALL time points:

```
Subject 0 = 0, r, classified = g
Subject 1 = 0, g, classified = g
Subject 2 = 9, r, classified = r
Subject 3 = 1, r, classified = g
Subject 4 = 1, g, classified = g
Subject 5 = 1, r, classified = g
Subject 6 = 12, r, classified = r
Subject 7 = 0, g, classified = g
Subject 8 = 0, r, classified = g
Subject 9 = 0, r, classified = g
Subject 10 = 13, r, classified = r
Subject 11 = 1, g, classified = g
Subject 12 = 0, g, classified = g
Subject 13 = 1, g, classified = g
Subject 14 = 9, r, classified = r
Subject 15 = 5, r, classified = r
Subject 16 = 0, g, classified = g
Subject 17 = 0, g, classified = g
Subject 18 = 9, r, classified = r
Subject 19 = 8, r, classified = r
```

There are 5 errors: subject 0, 3, 5, 8, 9. NOTE that Subject numbers are 1 less than those used in data set.

- 0 and 8 : were mild, but shed+sero - scored 0
- 3 and 5 : were ramp and shed, but no sero - scored 1
- 9 : mild and neither shed nor sero - scored 0

Color coding is as follows in these plots:

- (1) Green: Asymp.
- (4) Red: Symp













