

Sputum gene expression deconvolution

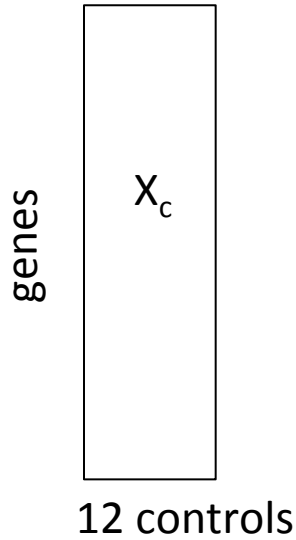
Gerstein Lab

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**Cell type fractions (%)
matrix W**

Gene expression matrix X



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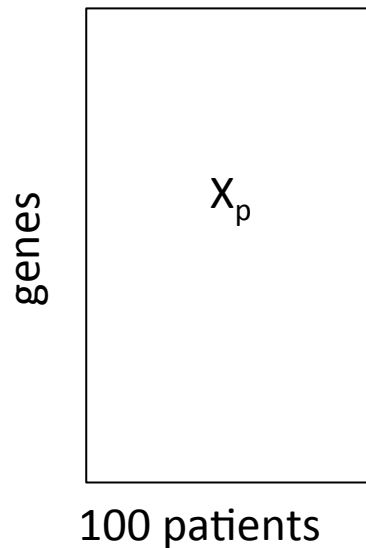
W_c
12 controls 5 cell types (Neutrophils, Eosinophil, Macrophage, Lymphocyte (Low), Bronchial (Low))

**Infer cell type gene
expression signature S
from known X and W**

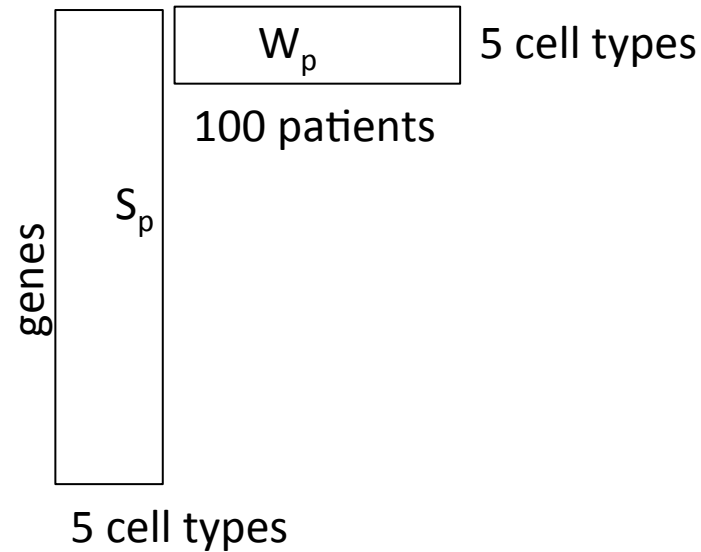
$$X=SW \Rightarrow$$

$$S=XW^* \text{ s.t.}$$

$$WW^*=I$$

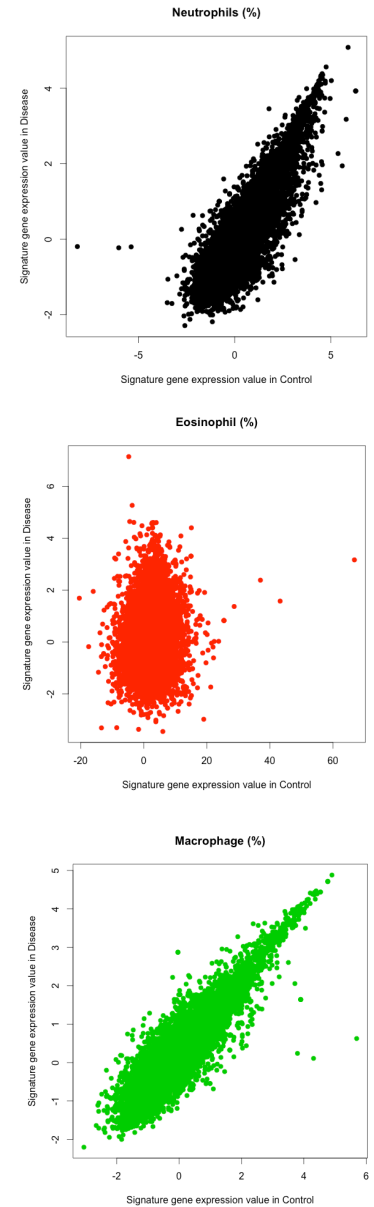
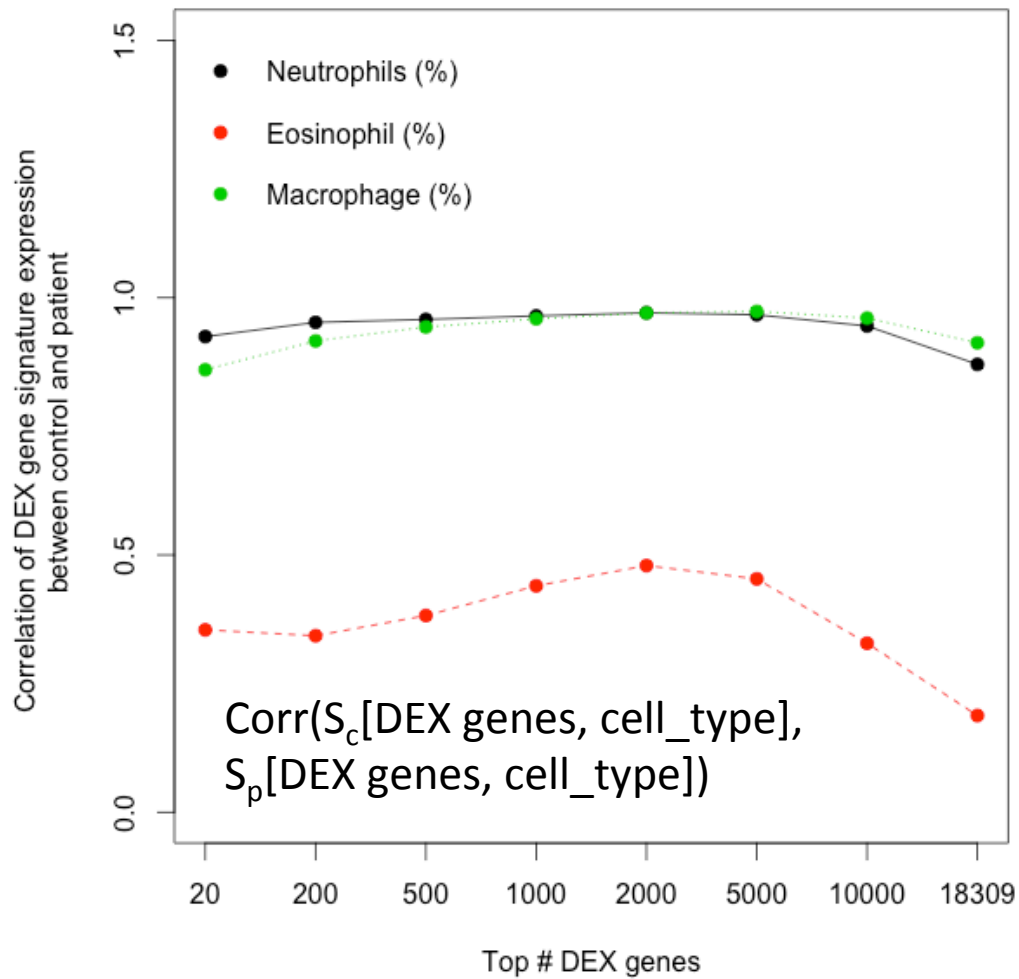


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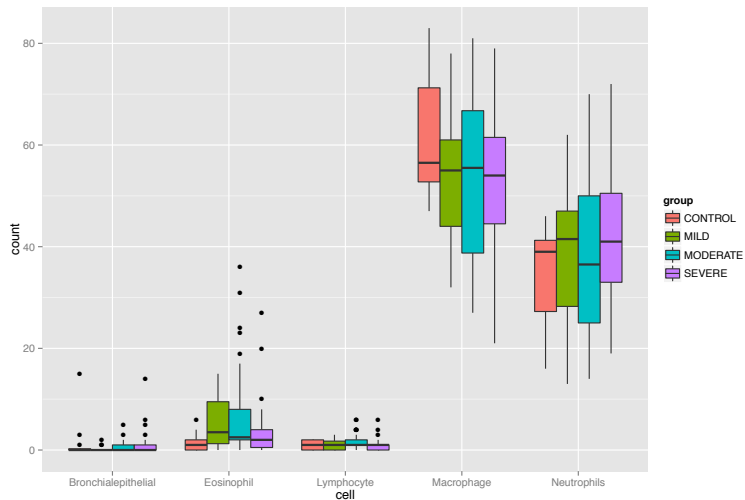


W_p 5 cell types
100 patients

3 cell type signature correlation between control and disease



Cell types across samples

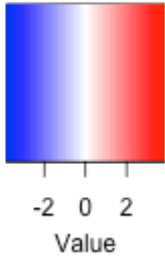


Deconvolution using least-square fit.

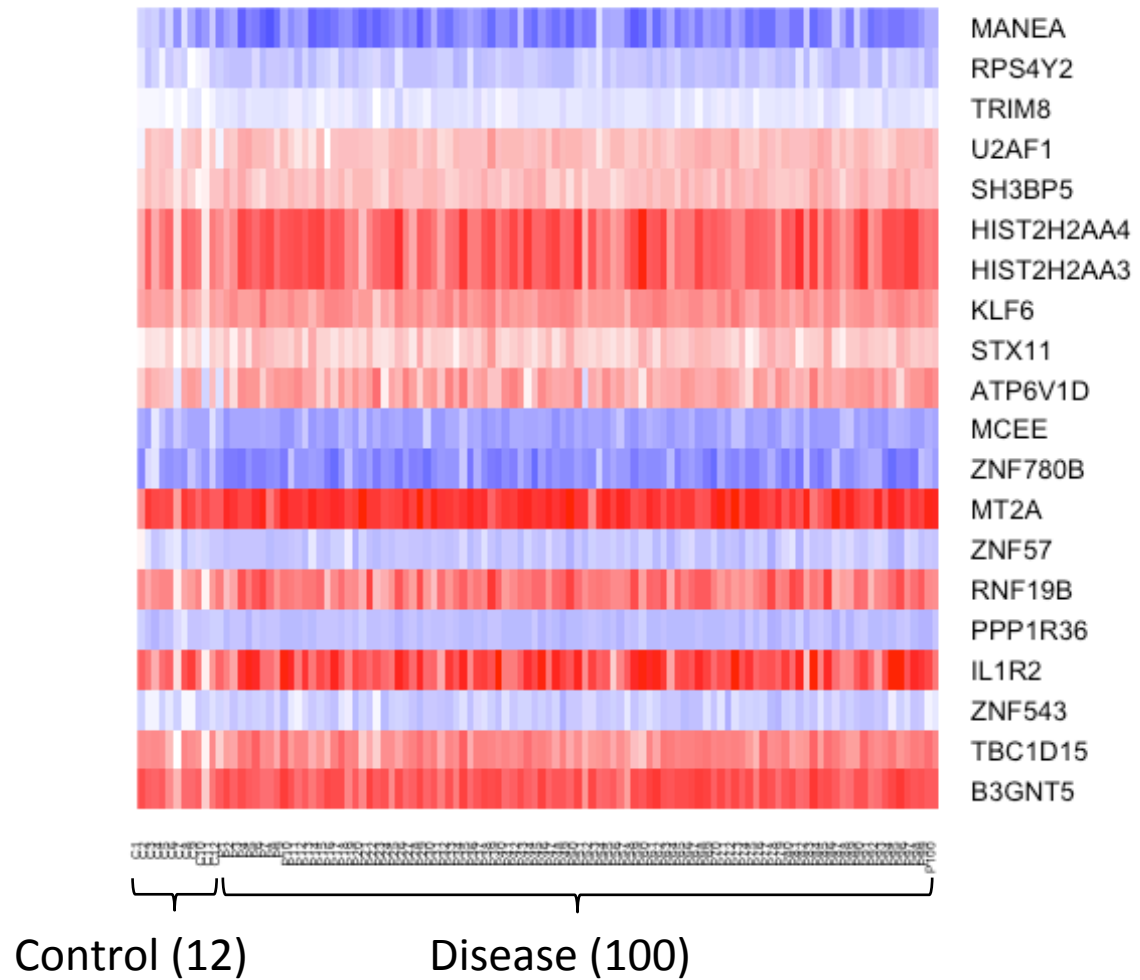
- ① 5 cell types, control vs all-astham
- ② 5 cell types, control vs severe-asthma
- ③ 3 cell types, control vs all-asthma
- ④ 3 cell type, control vs severe-asthma

For $FDR < 0.05$, all above comparisons have no significant genes identified; while $FDR < 0.1$, the last(4th) comparison finds: DEFA3, DEFA1 and RPS4Y1(ribosomal protein) in Microphase cell line.

Color Key

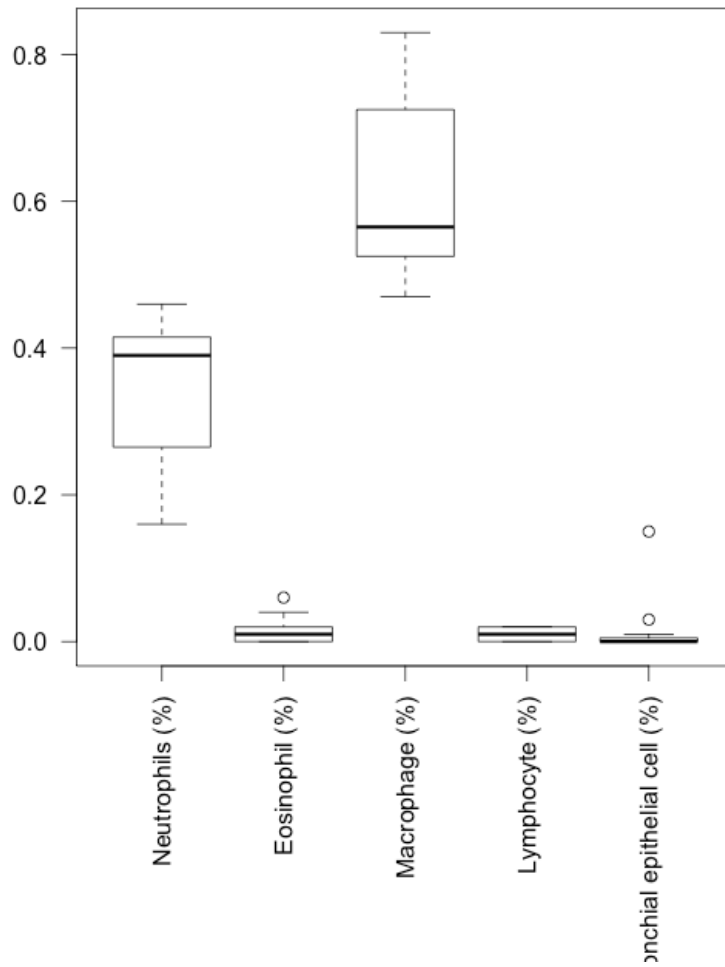


Top 20 differential expressed genes

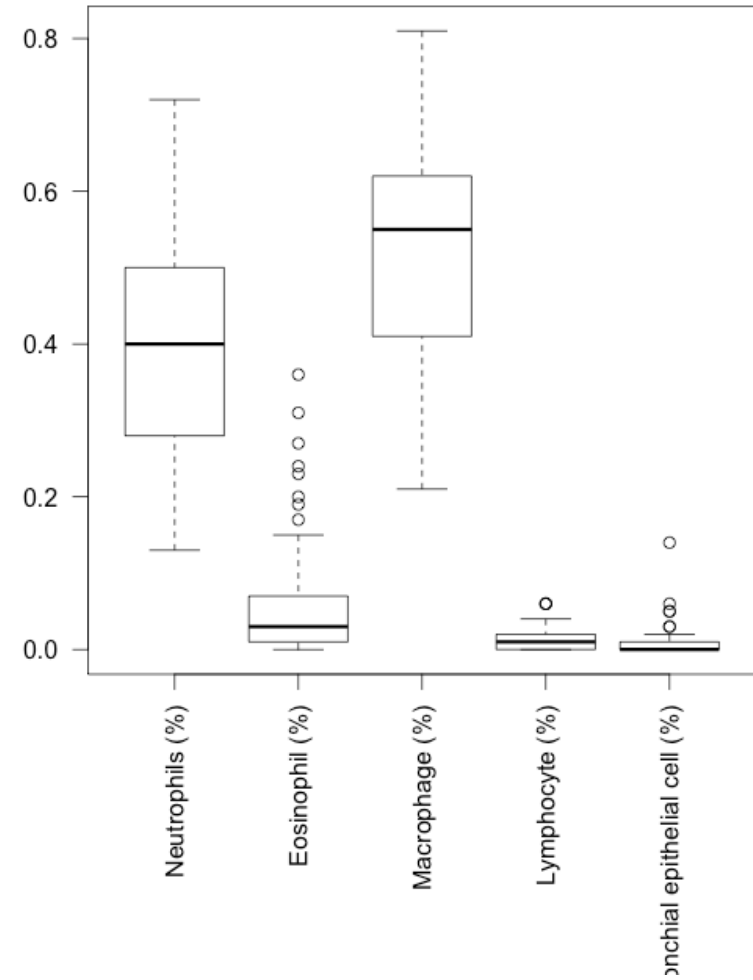


Cell type fraction distributions

Control (12)



Disease (100)



5 cell types

