



Lung B cell gene expression signature of emphysema in peripheral blood

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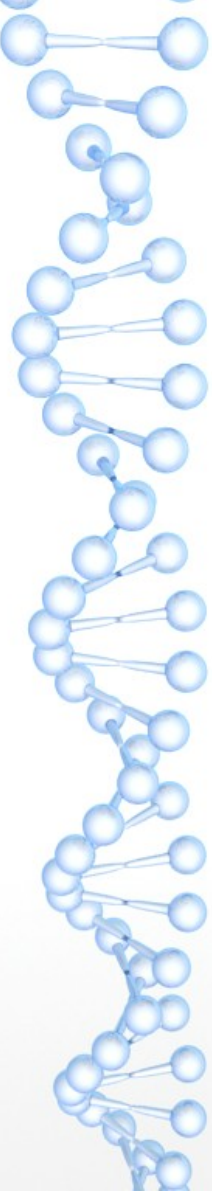
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Significance

- COPD is characterized by progressive airflow obstruction accompanied by chronic inflammation and emphysematous destruction
- Previously identified a COPD-associated network module of co-expressed genes in lung tissue enriched for B cell pathways
- Seek to better understand the transcriptomic B cell signature of emphysema in peripheral blood using this lung module



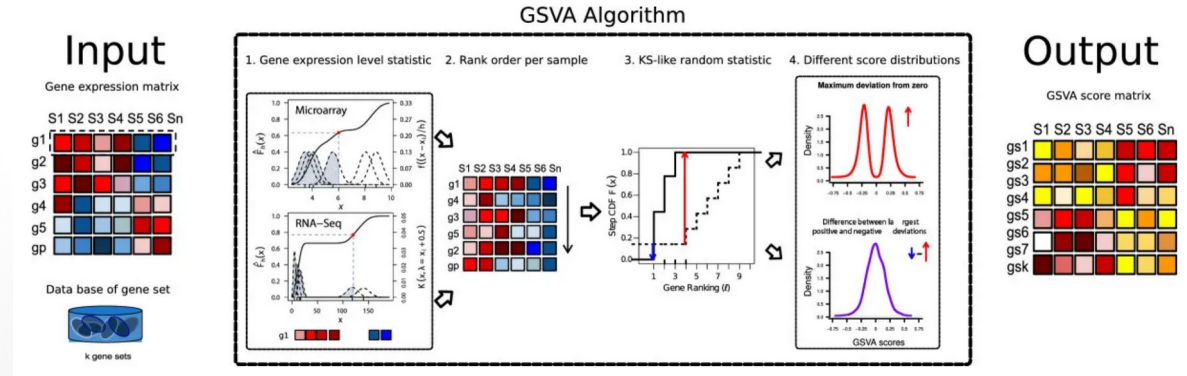
Demographics

(COPDGene RNA-seq data, n = 3,984)

	Cases (n=1601)	Controls (n=1609)	PRISm (n=481)	Never-Smokers (n=206)
Sex (female)	43%	53%	53%	57%
Race (NHW / AA)	79% / 21%	68% / 32%	61% / 39%	86% / 14%
Age (mean - years)	68.3	63.4	62.6	62.3
Current Smoker (Yes)	34%	38%	47%	N/A

B cell module expression score

- GSVA – Gene Set Variation Analysis
 - Estimates variation of pathway (gene set) activity over a sample population
 - Expression matrix --> pathways by subject matrix
- Lung tissue B cell module genes





Methods

- Tested associations between B cell expression score and
 - Percent emphysema
 - COPD status
- Included blood cell proportions in the models
 - Adjusts for variation in B cell abundance
 - Calculated using computational deconvolution
 - Single cell RNA sequencing reference data



Results

- We observed an association between the expression score and
 - Percent emphysema (p-value = 0.002)
 - COPD status (p-value = 0.04)
- Recapitulated the COPD lung tissue finding in peripheral blood
- Score was lower in more severe emphysema and in COPD
- Previous lung tissue study - module expression signature was higher in COPD



Moving forward

- Discordant B cell signatures in lung tissue and blood
 - Previously observed
 - Adjust for B cell proportion in future lung tissue analyses
- Inform personalized treatments and preventative measures
 - Particularly in regards to early detection



Thank You

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