

Epistatic effects among lung adenocarcinoma somatic mutations across oncogenesis

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Motivation

- *KRAS* and *TP53* are considered early drivers of LUAD but which is first?
- Smoking causes LUAD but is it just because of more mutations?
- Why is *EGFR* in so many non-smoker LUAD cases?

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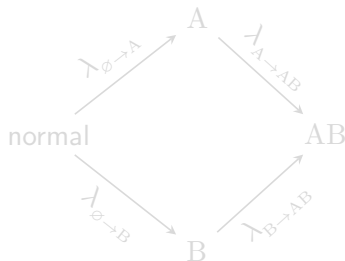
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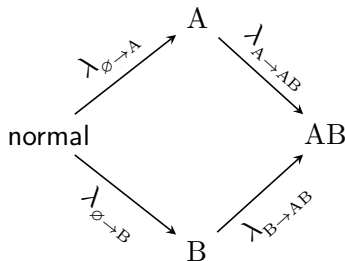
- There is a constant rate at which mutations occur and are selected to high frequency (flux)
- The flux depends on the gene that will mutate as well as the current somatic genotype (previous mutations)



- Epistasis occurs when $\lambda_{\emptyset \rightarrow A} \neq \lambda_{B \rightarrow AB}$
- Given the number of tumors in each genotype we can estimate the fluxes

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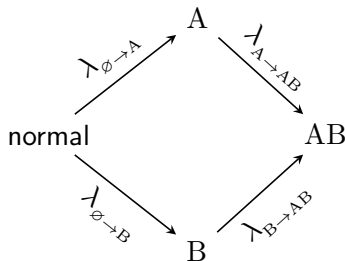
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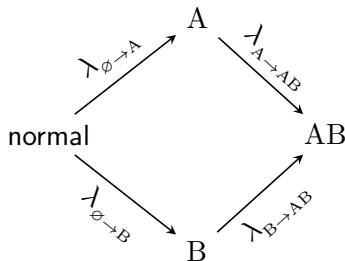
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Deconvolution of mutation and selection

- The flux is deconvolved into the mutation rate of the gene and the strength of selection on mutations of gene
- Mutation rate are obtained for each possible variant of each gene considering:
 - Molecular signatures
 - Gene expression
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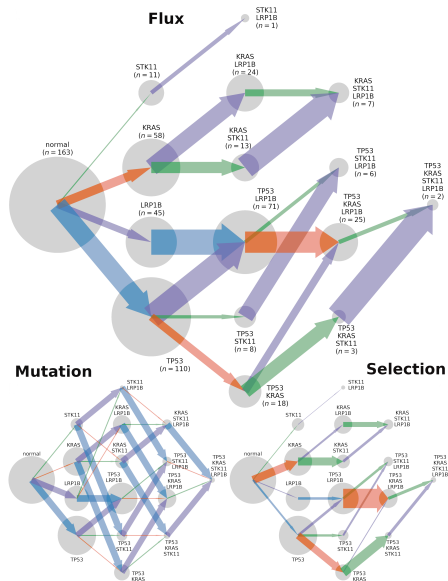
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Epistasis in most commonly mutated genes in TCGA



Larger data set

- How about other genes? What is the effect of smoking?
- Aggregate multiple data
 - 1 The Cancer Genome Atlas (TCGA)
 - 2 AACR Project GENIE
 - 3 Kenfield et al. Tob Control, 2008
 - 4 Chen et al. Nat Genet, 2020
 - 5 Rizvi et al. Science, 2015
 - 6 Hellmann et al. Cancer Cell, 2018
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- Total: 8,487 non-metastatic LUAD samples
- Classified 1,073 smokers and 447 non-smokers with clinical data and COSMIC SBS4

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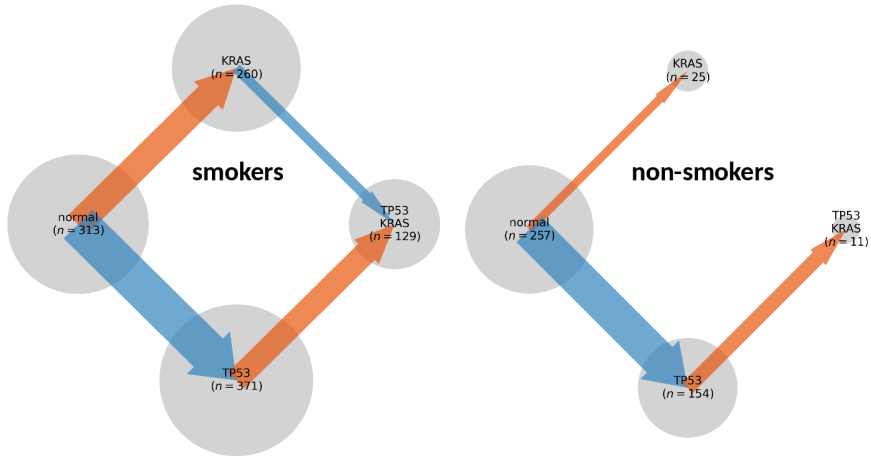
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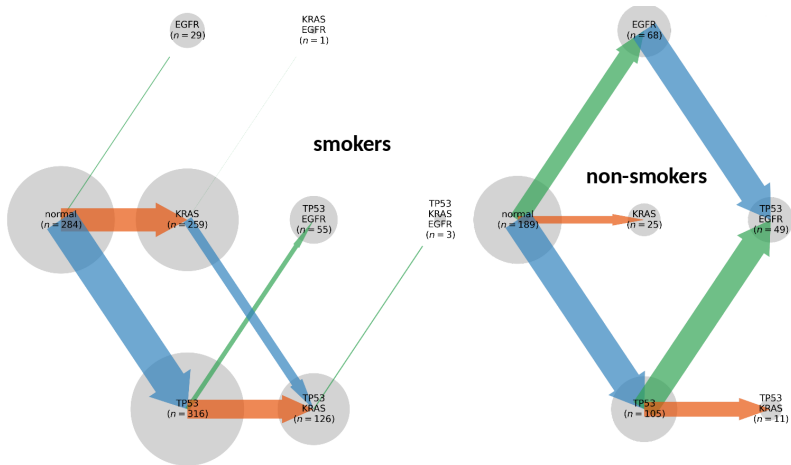
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Epistasis of *TP53* and *KRAS*

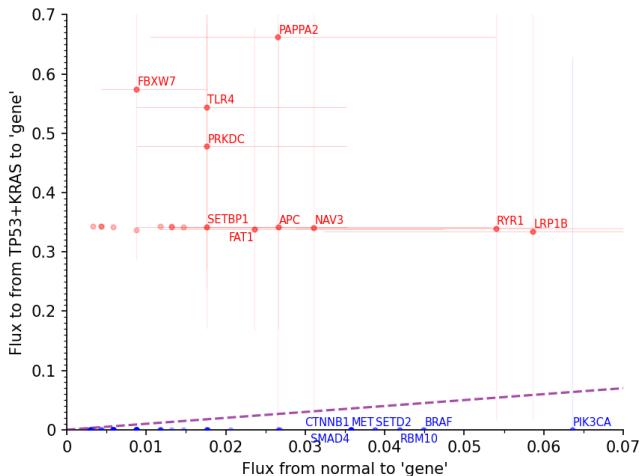


Epistasis of *TP53*, *KRAS* and *EGFR*



Epistasis other genes with *TP53*+*KRAS*

non-smokers



Epistasis other genes with $TP53+KRAS$

smokers

