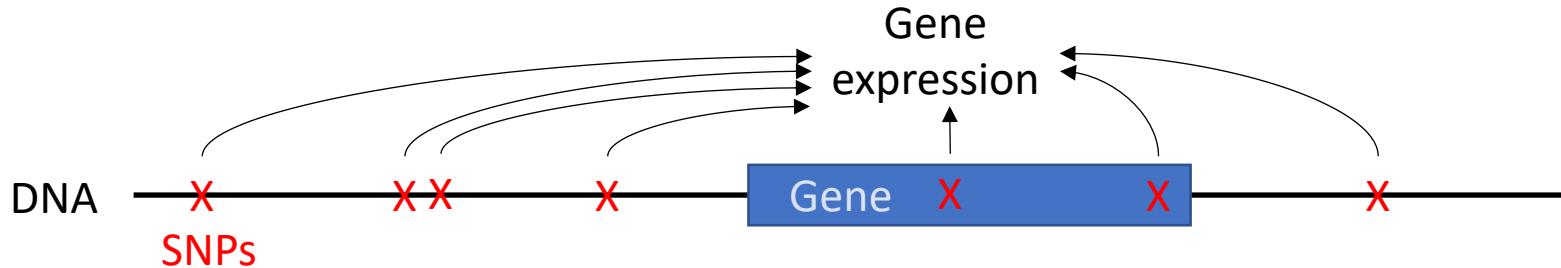


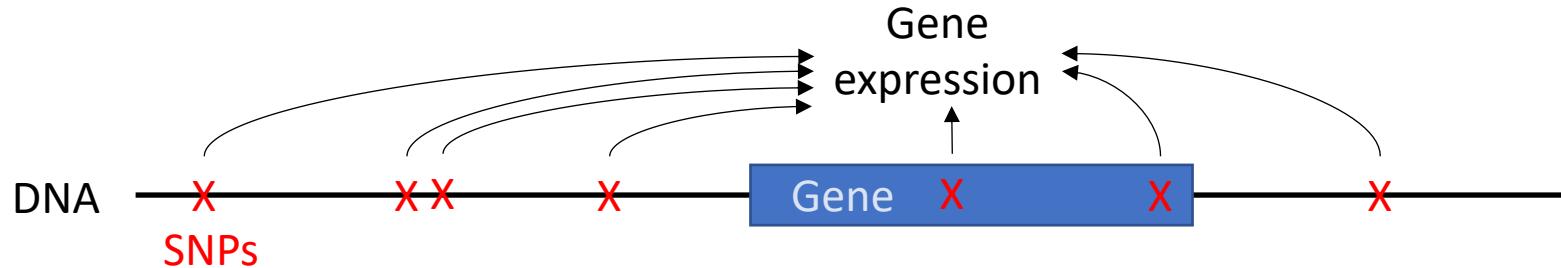
Genetic modulation of gene regulatory processes

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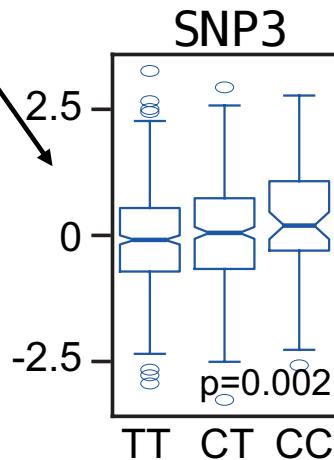
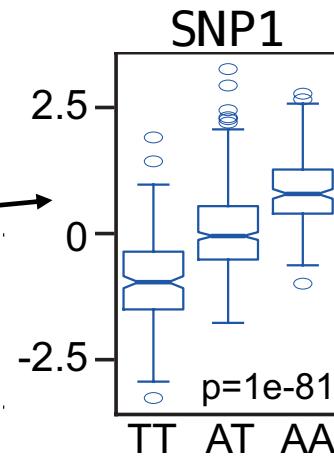
Quantitative trait loci (QTLs)



Quantitative trait loci (QTLs)

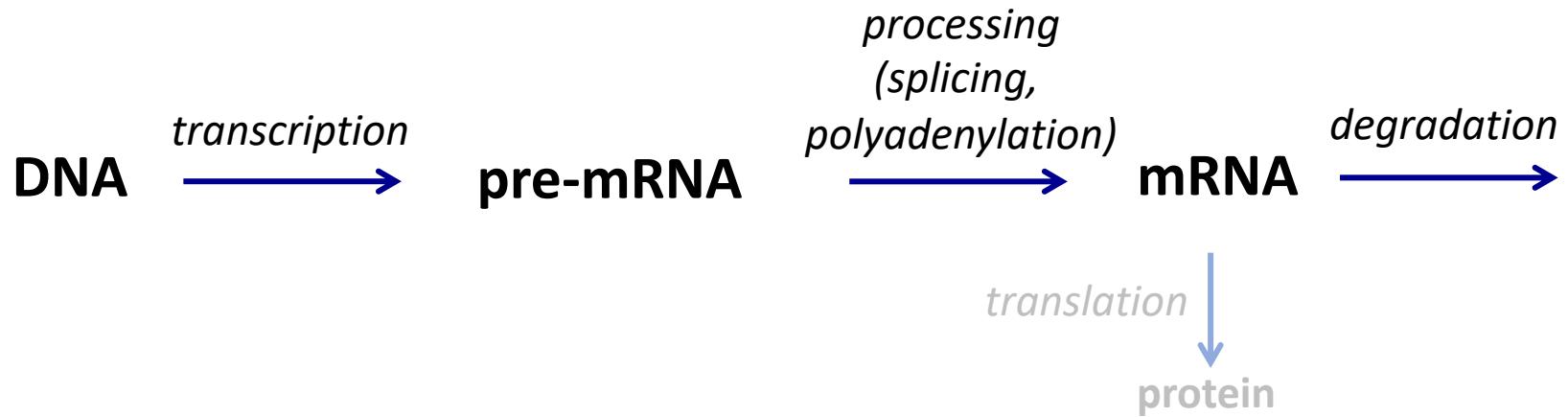


	indiv_1	indiv_2	indiv_3	indiv_4	...
SNP1	0	0	1	2	...
SNP2	1	2	1	0	...
SNP3	0	2	1	0	...
SNP4	1	1	0	2	...
...

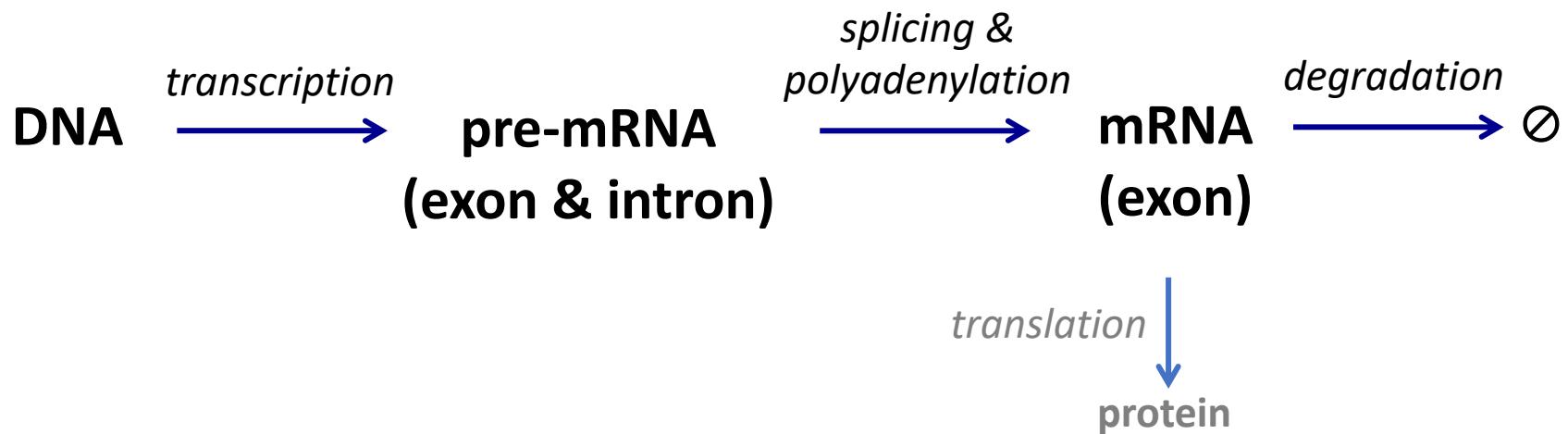


gene1	17	13.5	12	14	...
gene2	1.3	2.8	1.7	0.9	...
...

Regulation of gene expression

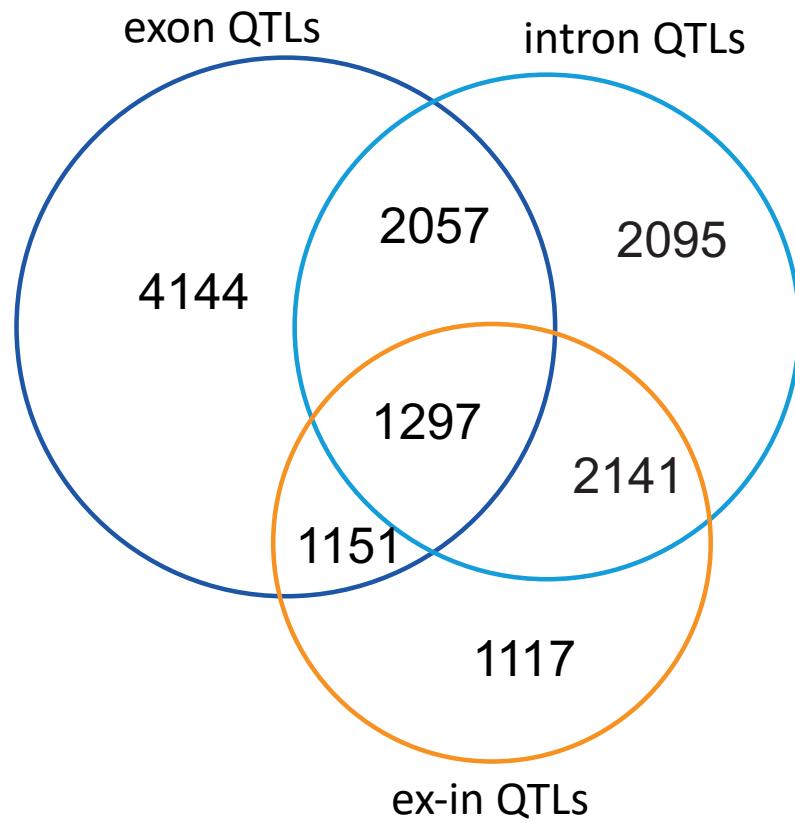
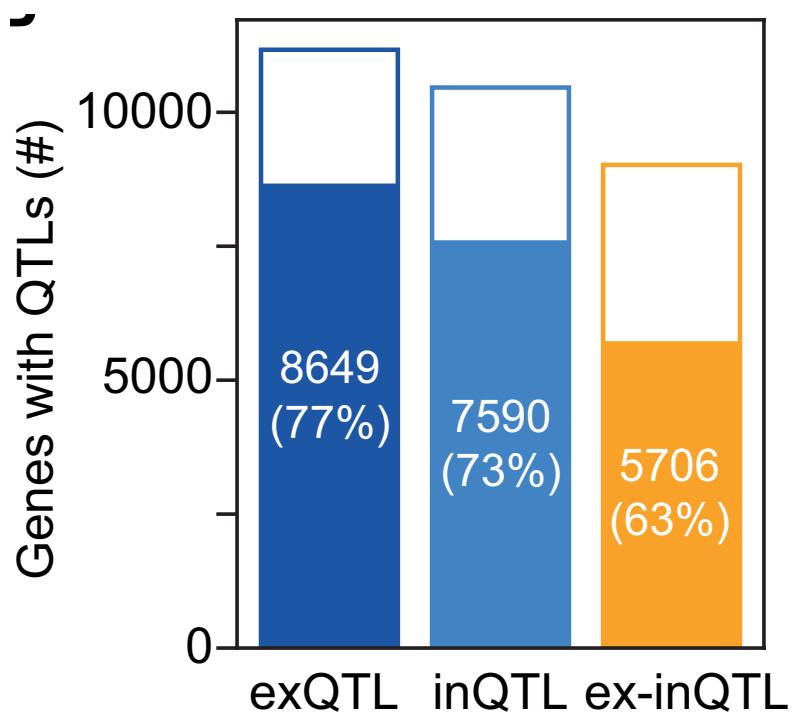


Regulation of gene expression

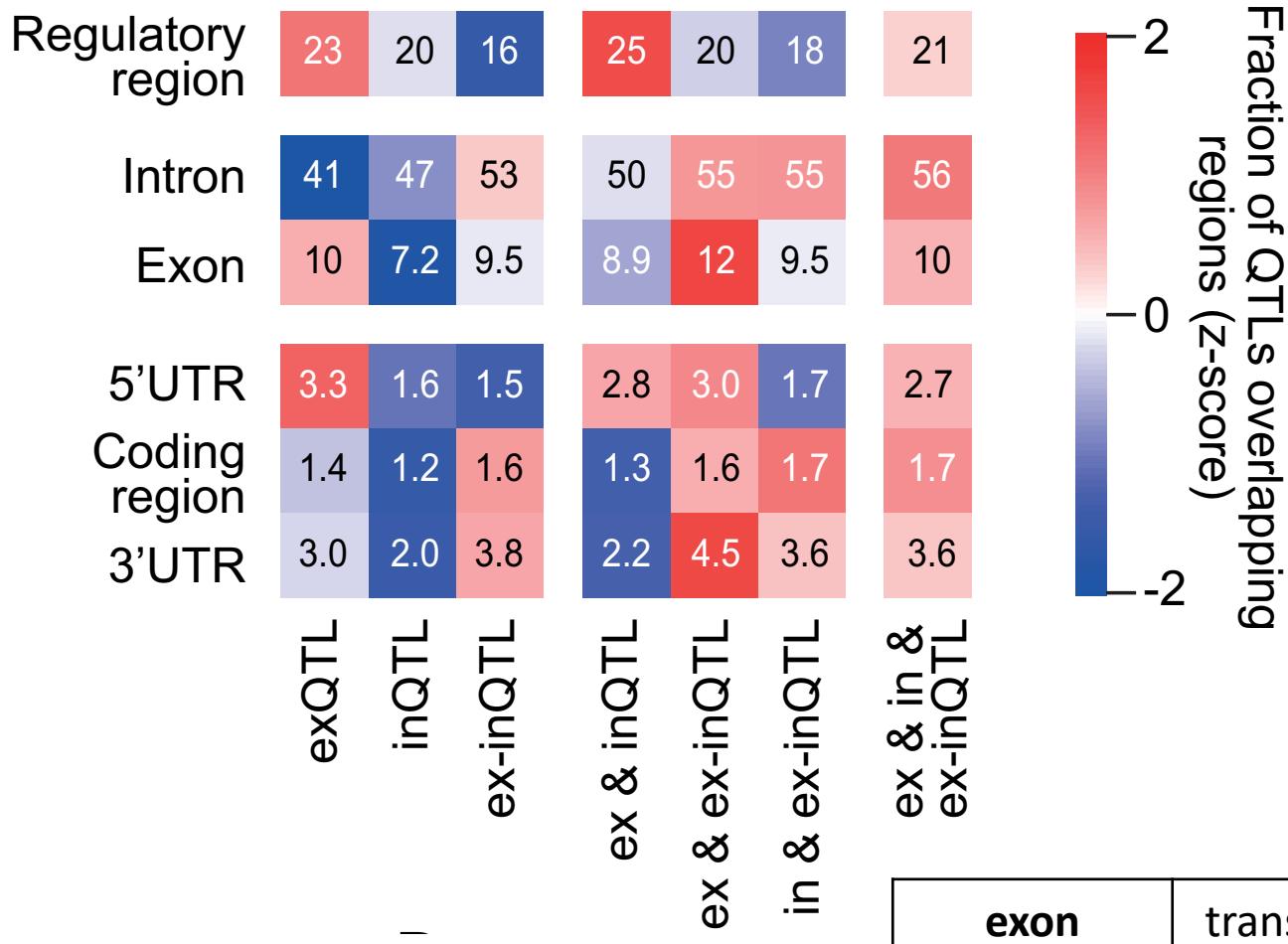


	Biological process
exon	transcription & mRNA stability
intron	transcription & splicing
exon/intron	splicing & mRNA stability

QTLs of exon and intron levels and their ratio

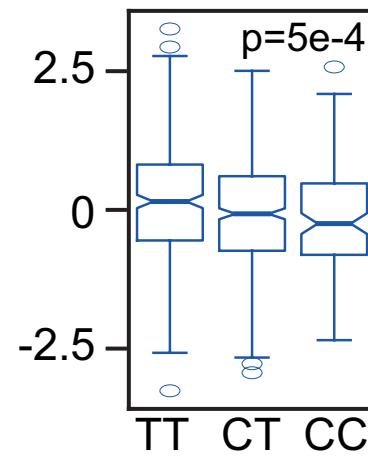
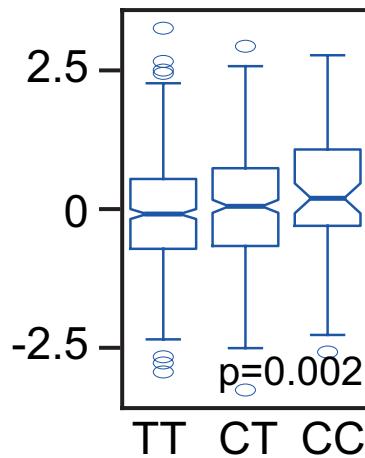
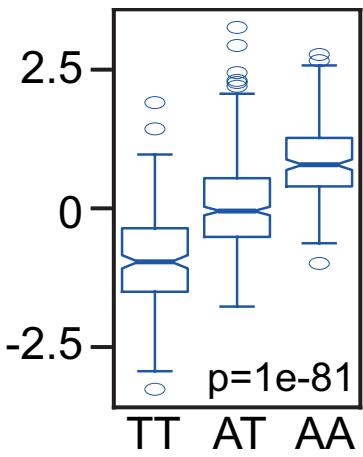


Regions of QTLs and shared QTLs



exon	transcription & mRNA stability
intron	transcription & splicing
exon/intron	splicing & mRNA stability

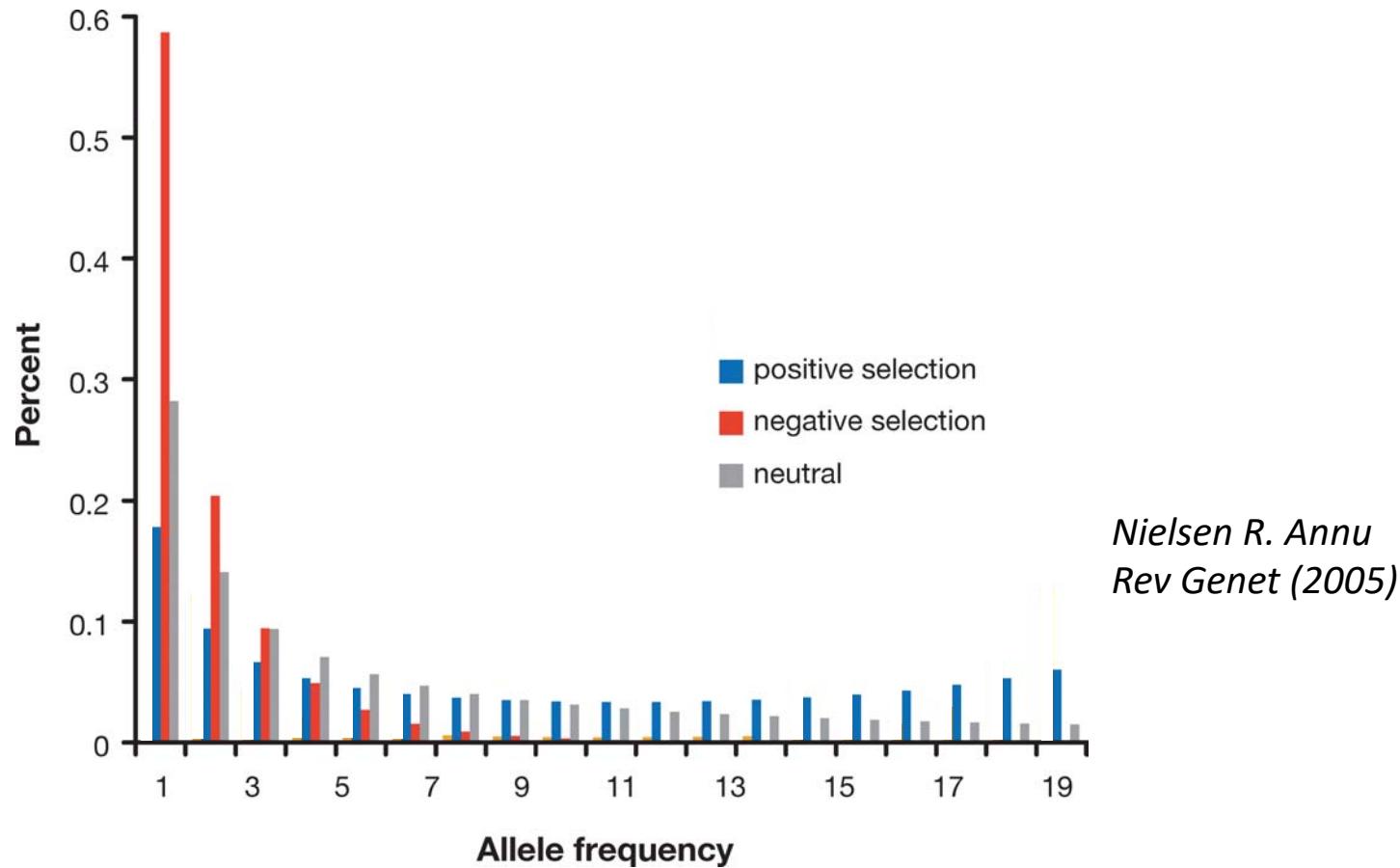
Effect sizes (regression slope)



- Are effect sizes different for transcriptional, RNA processing and post-transcriptional processes?
- Do effect sizes decrease with distance from a gene?

QTL effect sizes and allele frequencies

- Are effect sizes correlated with the allele frequencies in a population?
(stronger molecular effect -> stronger fitness difference?)



- Is this similar for e.g. secondary QTLs?
- What about QTLs overlapping GWAS loci?

What you will learn

- Data Analysis with Python
- Plotting with Python
- Integration of QTL data with allele frequency data

Questions: anneke.brummer@unil.ch