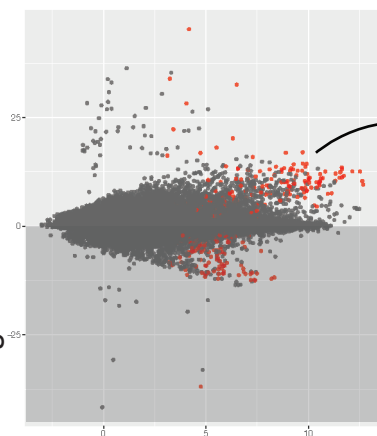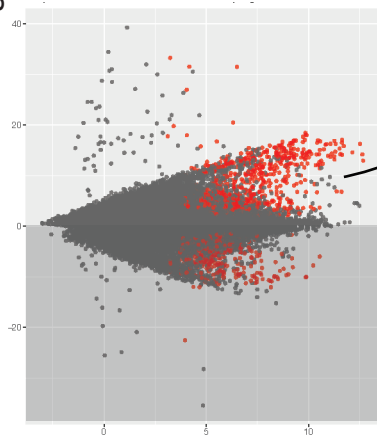**① Identify differential expression in species X**

Tissue A vs B

Log fold change

Significantly upregulated genes in tissue A vs B

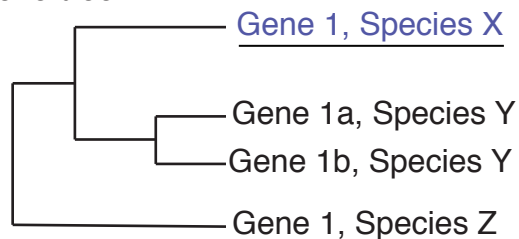**Significantly upregulated genes in tissue A**

Tissue A vs C

Significantly upregulated genes in tissue A vs C
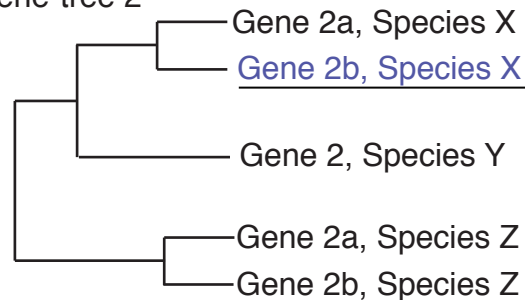
Log normalized mean counts

② Identify gene tree membership

Significantly upregulated gene-trees in tissue A

Gene-tree 1

Gene 1, Species X
Gene 1a, Species Y
Gene 1b, Species Y
Gene 1, Species Z

Gene-tree 2

Gene 2a, Species X
Gene 2b, Species X
Gene 2, Species Y
Gene 2a, Species Z
Gene 2b, Species Z

...

n gene trees

③ Compare gene-tree membership across tissues / species

Tissue A, Species X:
Gene-tree 1
Gene-tree 2
Gene-tree 3

Tissue A, Species Y:
Gene-tree 1
Gene-tree 2
Gene-tree 3

Tissue A, Species Z:
Gene-tree 1
Gene-tree 2
Gene-tree 3

Tissue A, Shared:
Gene-tree 2

Zooid specific gene(-trees): Significantly upregulated gene(-trees) in tissue A − (Significantly upregulated gene(-trees) in tissue B + Significantly upregulated gene(-trees) in tissue C)

Species specific gene-trees: Significantly upregulated gene-trees in tissue A, species X − (Significantly upregulated gene-trees in tissue A, species Y + Significantly upregulated gene-trees in tissue A, species Z)