

Input:
Feature table

	F1	F2	F3
S1	0	1	5
S2	3	0	2
S3	4	2	6

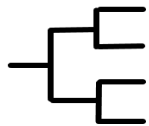
+

Metadata

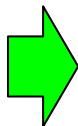
	MD1	MD2
S1	A	X
S2	A	Y
S3	B	Z

+

Phylo Tree*



* optional



Runs:

DEseq2

AIDEx2

EdgeR

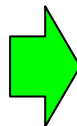
ANCOM-BC

MaAsLin 2

Metagenomeseq

Corncob

Songbird



Output:
**Snakemake report of differential abundance
results and interactive visualization**

