#MassiveSeq Flow Diagram for Iron Hack

Prepare input

Get meta-data

Take text file and put into format that BCBio can parse out

1. Get control samples
2. Get affected samples (cases)

BCBIO

Differential Expression (DE)

RNA

Transcript (Count info)

Variants

Megablast

Docker

Analyses of differences between cases and controls:

PCA

TSNE