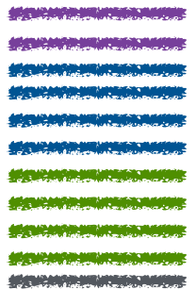
Step 1



miRNA and isomiR counts matrix

import to DESeq2 object

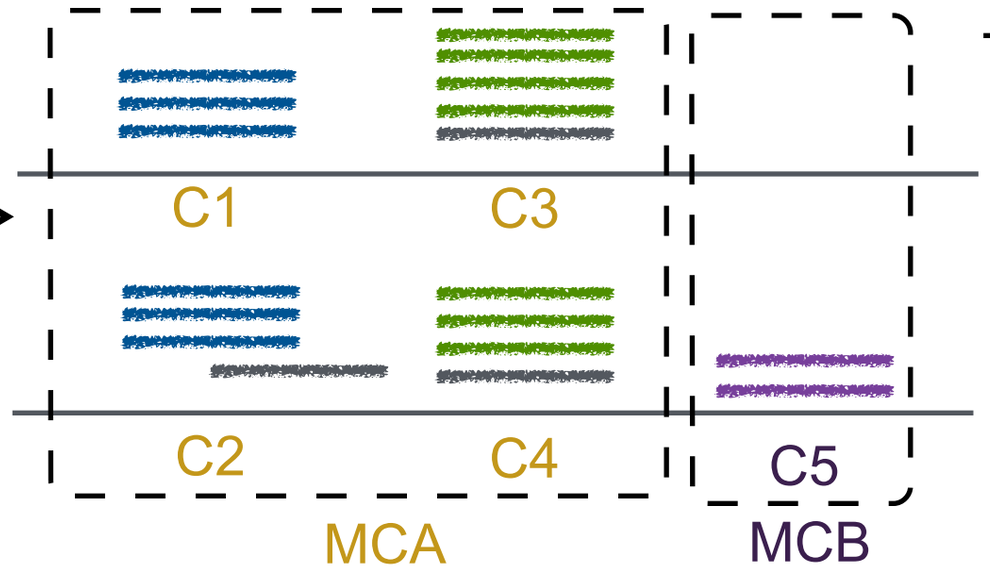
DESeq2 normalization

PLS-DA

Differential expression

Step 5

Clustering and Differential Expression

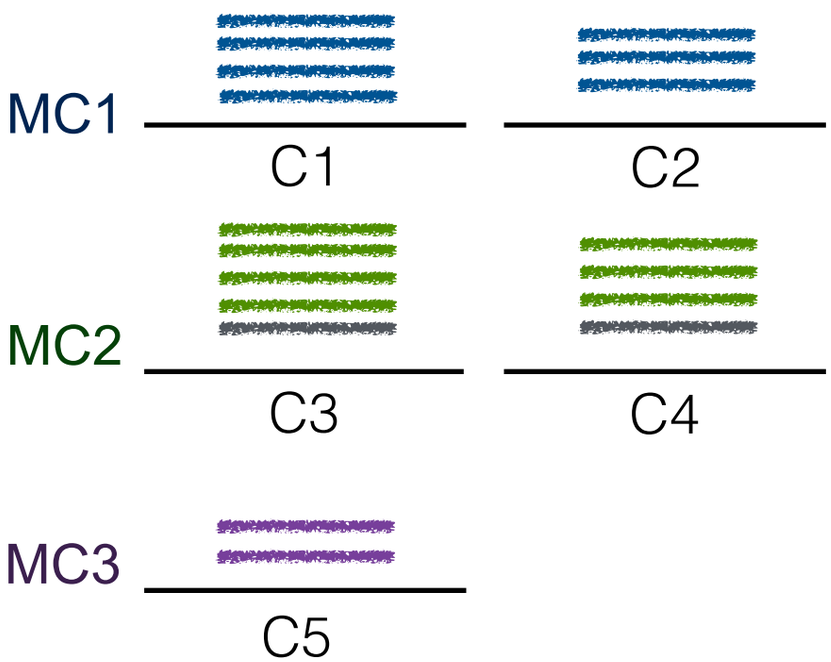


detecting **clusters** on the genome

Step 2

Step 4

Output: generation of sRNA clusters with counts matrix and annotation



Initialize new meta-cluster with 0 clusters (ex:MC1)

calculate similarity matrix among all pairs of clusters.
Iterate though pairs of clusters from most similar to less similar.

Check if pair is >= 60% similar
C1 and C2 in this case

Yes

No

Add both cluster to MC1 if they weren't.
ex C'12 and C'34

mark as conflict.
ex: C'34 with C'12

Remove pair from MCA

Are there more clusters in the primary meta cluster?

Yes

No

sequences to the most populated C.
ex: grey goes with C'34

Yes

any conflict?
ex: C'34 with C'12

No

create second cluster.
ex MCB with C'34

Define clusters
ex. MC1 and MC2

Step 3

Reduction + Correction