

seismic align

Sequencing Reads (FASTQ)

RNA Chemical Probing

DMS-MaPseq

SHAPE-MaP

ETC-MaP

Other Library Types

RNA editing

Bisulfite-seq

SNP quantification

→ Reads

Alignment Map (BAM)

```
AGTCCTTATGGCTTATC
AGTCCTTATGGCTTATC
AGTCCTTATGGCTTATC
TCTTCTGGCTTATCCTGG
TTATGGCTTATCCTGGAC
ATGGAATGTCCTGGAC
GGCTTATCCCTGGAC
AGTCCTTATGGCTTATCCTGGAC
Reference Sequence
```

seismic relate

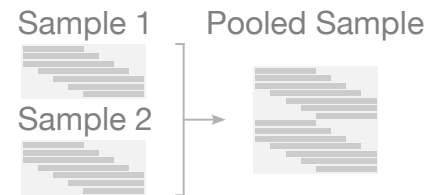
Types of Relationships

- Match
- Deletion
- Ambig.
- Insertion
- Substitution to ...
- A
- C
- G
- T

Matrix of Relationships



seismic pool

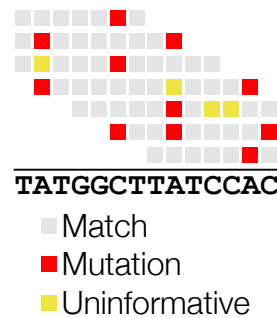


seismic mask

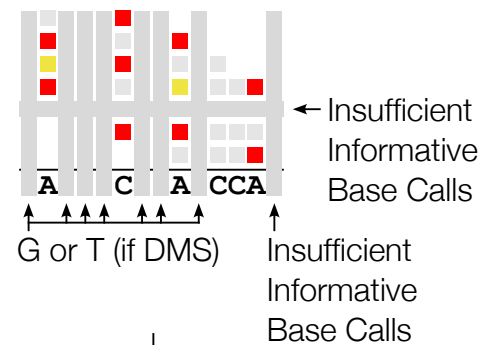
Select Region



Specify Mutation Types



Filter Reads and Positions

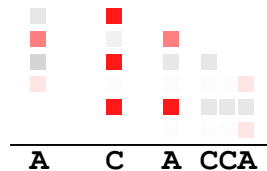


seismic cluster

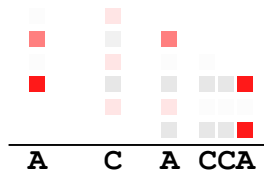
Probability of Cluster Membership

0.0 1.0

Cluster 1 (57%)



Cluster 2 (43%)

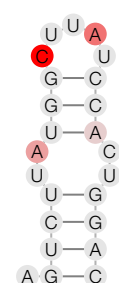


seismic join

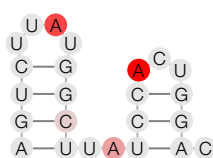


seismic fold

Cluster 1



Cluster 2

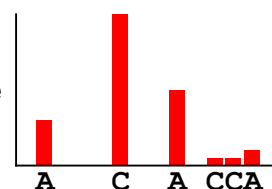


Mutation Rate

0.0 1.0

seismic graph

Cluster 1



Cluster 2

