/config (Glen)

CloneFinderParams

dataformat (snv, ccf, etc...)

options

binoNum

binoCut

errorRate

/alignment (Glen)

MegaAlignment

encapsulates a MEGA formatted sequence alignment

add seqs

Combine similar sequences

FreqToMegaSeq

From observed frequency to MEGA alignment

Add sequences

Remove redundant sequences

Separate sequences (make alignment for each tumor)

/parsimony (Glen)

MegaMP

Do MEGA-CC

Generate ancestral sequences

TreeAnalyzer

Identify backward/parallel mutations

/binomial (Sayaka)

BinomialReqlicates

Make binomial replicates

SignificanceTester

Test significance of clone

/regression (Sayaka)

CloneFrequencyComputer

Compute F (Single M for all tumors or Each M for each tumor)

/decomposition (Sayaka)

SNPClusterGenerator

Generate sequences of SNV group

SNPGroupCombiner

Make clones by combining SNV groups

SNPGroupMapper

Make clones by mapping SNV groups along MP tree

/parsers (Glen)

CCFParser

TSPParser

For observed SNV frequencies (input)

Make :ref and :alt count for each tumor

CloneFrequencyParser

For clone frequencies

Remove sequences with F=0

AncestralSeqsParser

parses MEGA ancestral sequences file

/tsp\_profiles (Glen)

TumorSampleProfileList

TumorSampleProfile

ReadCounts

def adjust\_snv\_freqs

/clone\_adjustment (Sayaka)

CloneAdjuster

Fix backward/parallel mutations on decomposed clones

Make MP tree and fix backward/parallel mutations if possible

MutationFilter

Remove mutations when tumor does not have mutations

Mask SNVs with parallel/backward mutations

Add unassigned mutations into sequences if possible

\*\*\* decide where to put this \*\*\* Add ancestral sequences at the middle of branches

/output (Sayaka)

CloneRenamer

Rename clones

CloneFrequencyWriter

TreeWriter