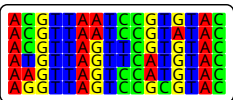
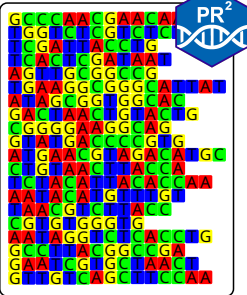


The group you want to find candidate regions

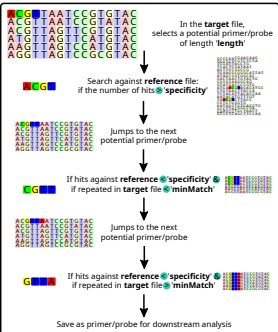


Excluding the group of interest



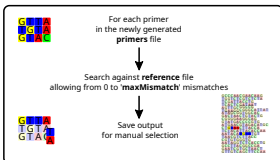
Searches candidate primers/probes by sliding window

```
findPrimer.py -t target -r reference -l length -s specificity -m minMatch
```



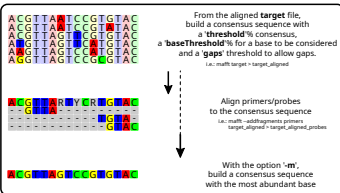
Test primers/probes by allowing mismatches

```
testPrimer.py -f primers -r reference -m maxMismatch
```



Build a consensus of the targeted group

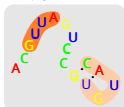
```
alignmentConsensus.py -f target -t threshold -b baseThreshold -g gaps -m
```



ACGTTAGTCCGTGTAC

Use the consensus sequence
with the most common bases
to reconstruct an hypothesized 2D structure

Le.: <https://github.com/mcentral/R2DT>



Check for accessible region
according to established models

Based on the specificity of the probes
(allowing mismatches)

the accessibility of the 2D
(or 3D) structure

Select the best candidate region
and experimentally test the primer/probe



2.

