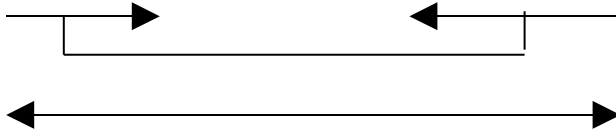


chimer-anno_ca node command

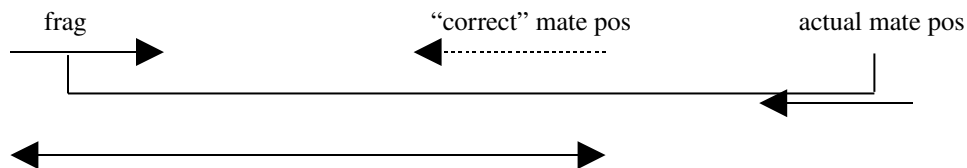
display a coverage plot consisting of 4 lines:

- **good coverage**, that means the fragment and its mate are within a $3 \times \text{stddev}$ interval around the link mean and not misoriented. Then the covered distance is counted as covered.



The above distance is covered, that is the count is increased by one.

- **bad coverage**, that means the fragment and its mate are not within a $3 \times \text{stddev}$ interval around the link mean or the mate is misoriented. Then the distance between the frag and the correct position of the mate is counted as covered.



The above distance is counted as bad coverage.

- **misplaced coverage**, here we count the distance between the frag and the actual position of its mate, i.e. in the above picture from the start of the frag to the end of the mate.
- **misoriented coverage**, here we count the frag to mate range in the case that the mate has the wrong orientation

the following options can be chosen in the popup window:

cutoff: that means for each end of the coverage that many bases are disregarded from the count, such that a region of zero clone coverage is not “spoiled” by some bases sticking into that region.

clones only: that means for coverage only clones are used, not single fragments

use contig iid: if this box is checked, the below number refers to a contig IID. Otherwise to a bactig IID

2k links: use 2k links

10k links: use 10k links

50/60k links: use 50/60k links