**Chromosomer:** Chromosomer – an open-source cross-platform software that automates the reference-assisted building of genomic chromosomes and is especially effective for large genomes (> 1 giga base pairs). Chromosomer constructs draft chromosomes based only on alignments between fragments (contigs or scaffolds) to be arranged and a reference genome, thereby improving analytical and annotation opportunities for the index species assembly.

To map fragments to a reference genome, Chromosomer uses results of pairwise alignments between the fragments (contigs and scaffolds) and the chromosomes of the reference genome. The alignments are required to have associated score values that reflect the length and identity of the aligned regions. In addition, the start and end positions of aligned regions in both the fragments and the reference chromosomes are required.

**STEPS:**

1. From pairwise alignments, determine fragments that can be anchored to a reference according to the ratio of their first and second greatest alignment scores. If the ratio is greater than the predefined threshold, which is the algorithm parameter, then the fragment is anchored to a position corresponding to its alignment with the greatest score. Otherwise, the fragment is considered unplaced if these two alignments are located on different reference chromosomes or unlocalized if both alignments are located on the same chromosome.
2. Using fragment anchors, map the fragments to the reference chromosomes. Unlocalized and unplaced fragments are excluded from the assembly.
3. Resolve overlaps between mapped fragments by inserting gaps between them.
4. Produce a map describing fragment positions at a reference genome and output assembled chromosome sequences and lists of unlocalized and unplaced fragments.

**Diagram

Description automatically generated**

**ASSEMBLY PARAMETERS:** Chromosomer introduces two parameters that influence the assembly process. The first parameters is the alignment score ratio threshold, which is used to distinguish anchored and unplaced fragments. If the score ratio of the two fragments alignments with the highesh scores exceeds the threshold, then the fragments is considered anchored, otherwise it is considered unplaced and is excluded from further analysis. The alignment score ratio threshold must be a positive number greater than one.

The second parameters is the insertion size- the size of a gap which is inserted between overlapping regions. The insertion size is recommended to be equal to or greater than the sequencing library size.

**INSTALLATION:** conda install -c bioconda chromosome

Or

pip install chromosomer

**pip** will automatically resolve Chromosomer dependencies and install missing packages.

**Assembling chromosomes**

A typical chromosome assembly involves two steps. First, a fragment map is derived from fragment alignments to reference chromosome sequences. Second, FASTA sequences of the assembled chromosomes are obtained from the produced fragment map and the original fragment sequences.

The first step is carried out with fragmentmap in the following way:

chromosomer fragmentmap alignment\_file gap\_size fragment\_lengths output\_map

The second step is implemented in the assemble routine:

chromosomer assemble map fragment\_fasta output\_fasta