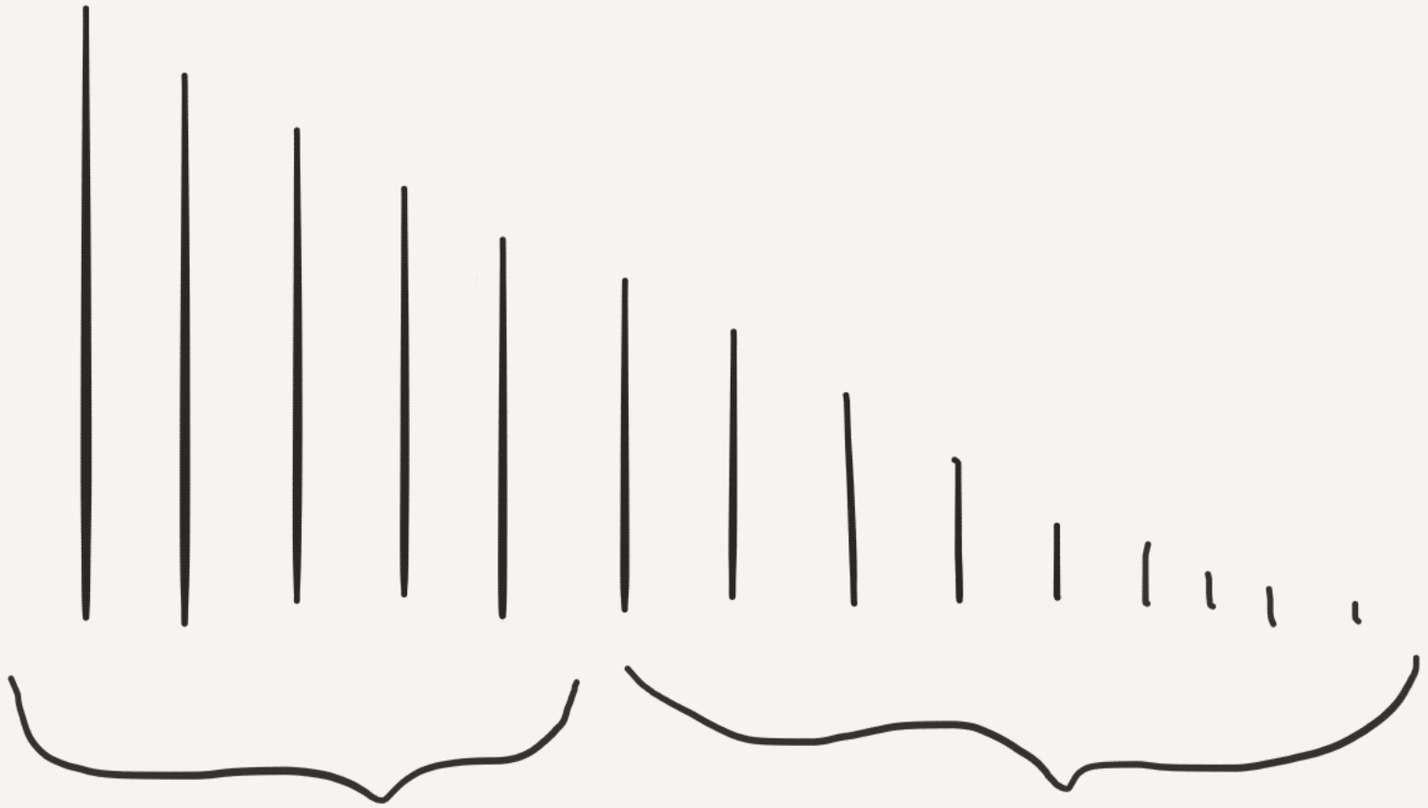
ASSESSING ASSEMBLY QUALITY

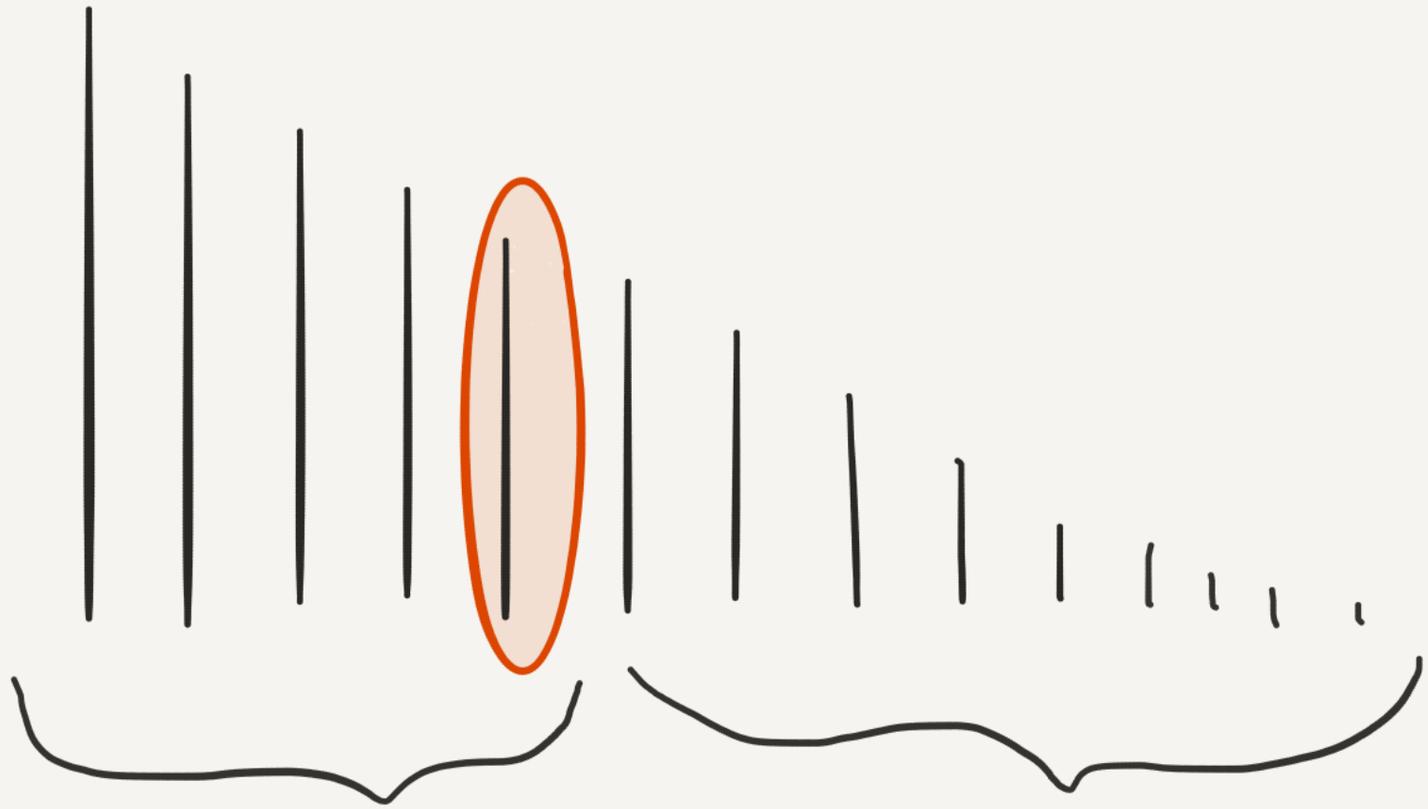
MEASURES OF ASSEMBLY QUALITY

- Contig N50*
- Mapping of "proper" pairs
- # of full length proteins
- Contig ExN50 (to be covered after transcript quantification)

CONTIG N50

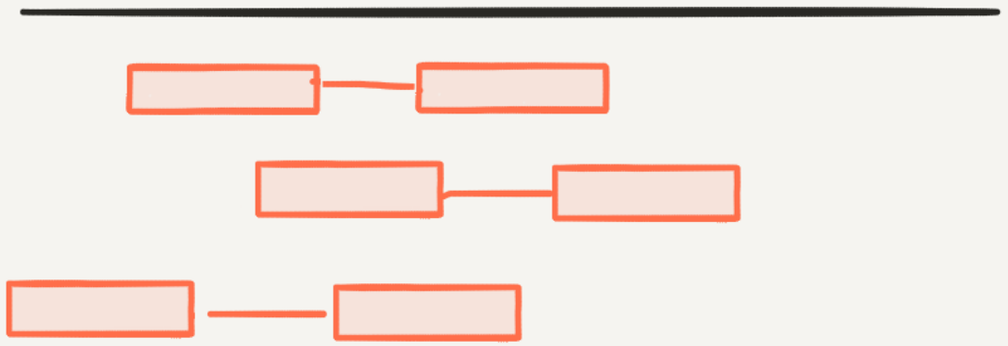
- Like a "weighted median"
- The length of the contig for which half of the total number of base pairs are in contigs of greater or equal length

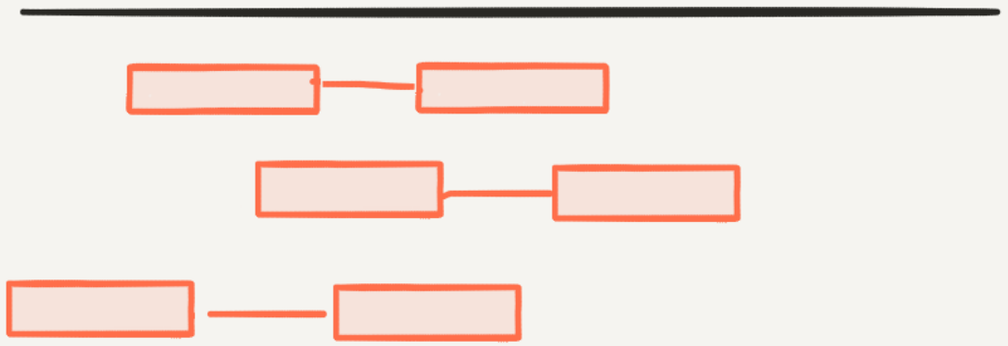


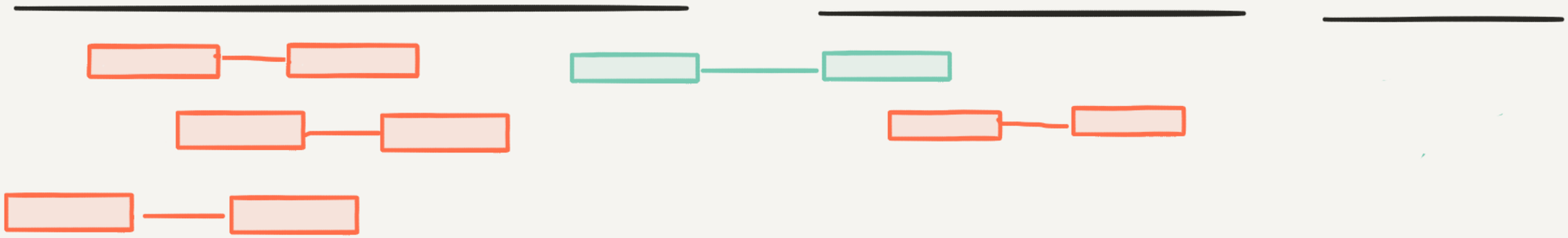


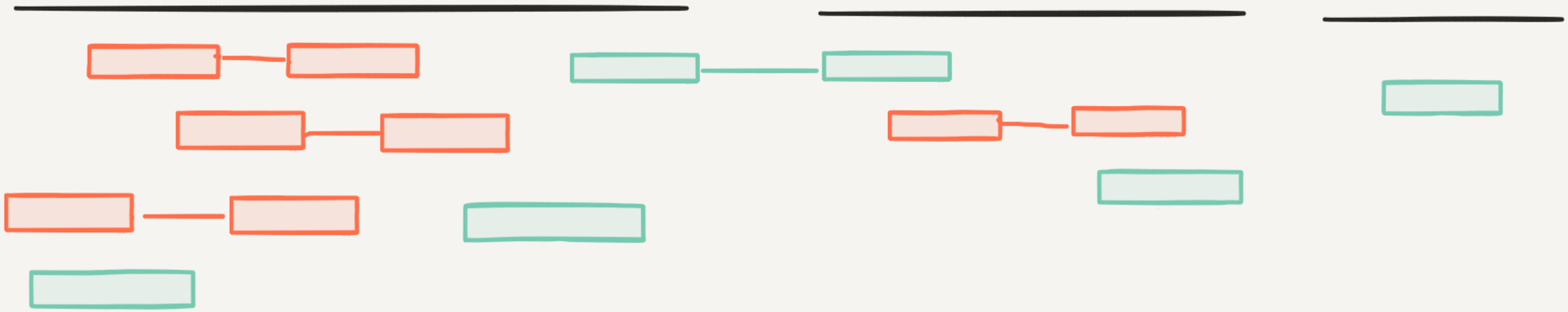
MAPPING OF "PROPER" PAIRS

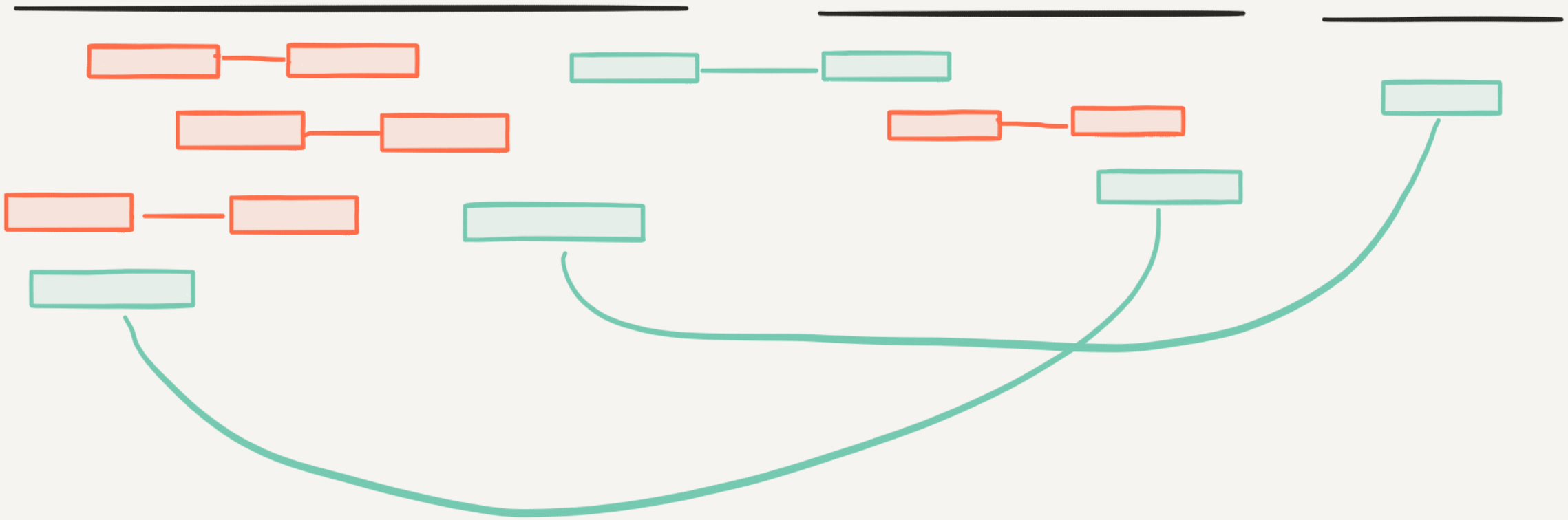
- Map paired end reads back to transcript contigs
- A "proper" map is when both pairs map to the same contig
- An "improper" map is when the pairs map to different contigs











MAPPING OF "PROPER" PAIRS

- Map paired end reads back to transcript contigs
- A "proper" map is when both pairs map to the same contig
- An "improper" map is when the pairs map to different contigs
- The number of reads that properly map is a good measure of contiguity
- The value for a good Trinity assembly is often >70%

NUMBER OF FULL LENGTH PROTEINS

- Use BLASTX to compare to a well-curated database of proteins (like Swiss Prot)
- Number of full length proteins can give you information on how well the transcripts are reconstructed

HANDS-ON

- Go back to https://github.com/SmithsonianWorkshops/SMSC_Conservation_Genomics/tree/master/Day%2007 and follow the “4a_Assessing Trinity assembly quality.md" tutorial