

FeatureCounts explore

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Objective of analysis

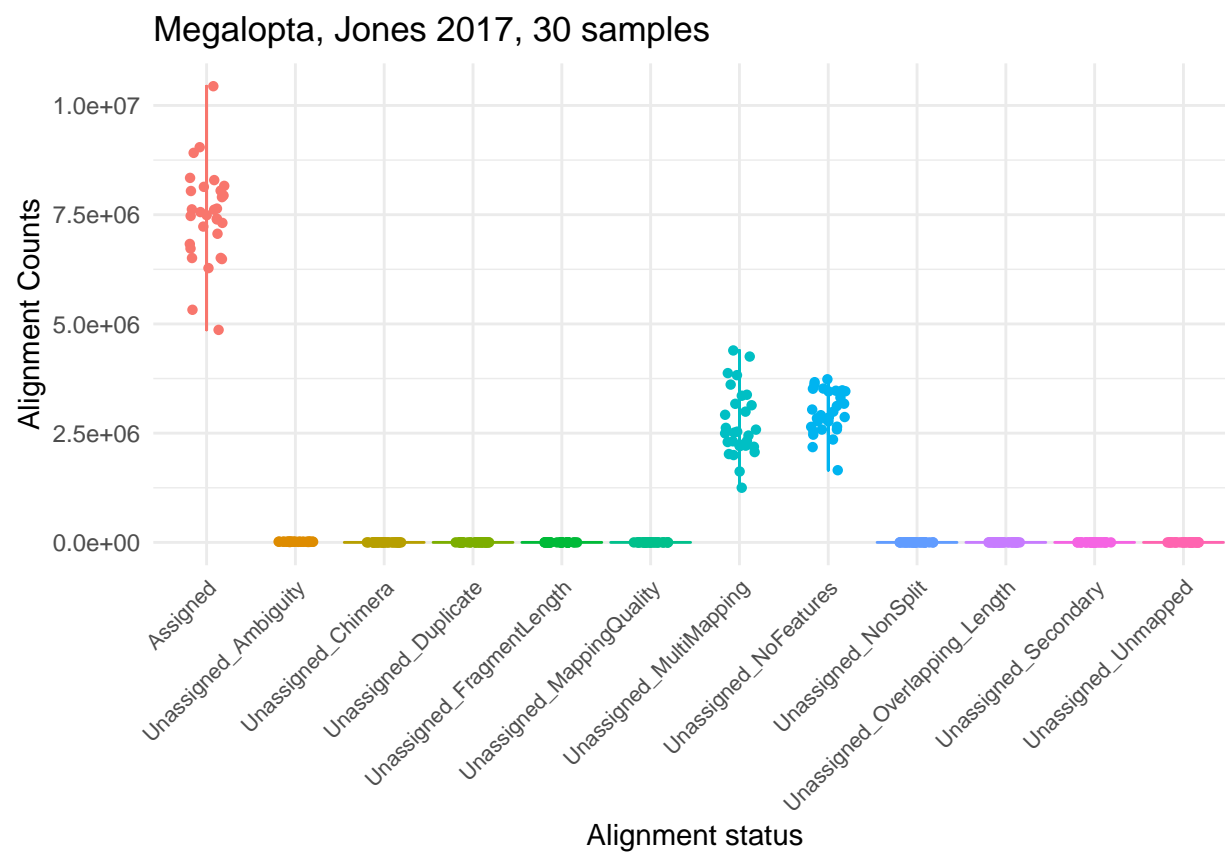
Exploring the results of FeatureCounts per species. We aim to have a high ratio of Assigned:Unassigned alignments.

Analysis steps:

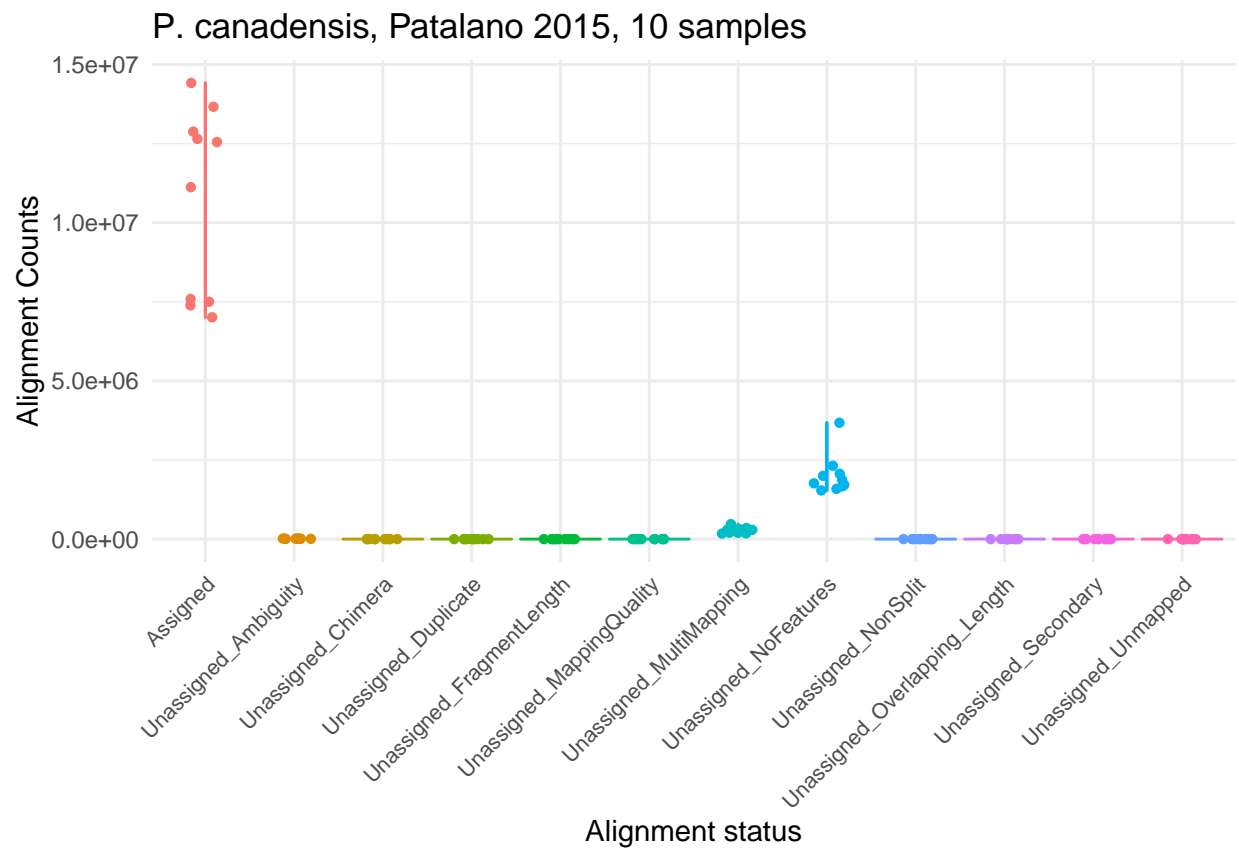
- Obtaining data
- Aim 1: *Megalopta genalis*
- Aim 2: *Polistes canadensis* Patalano
- Aim 3: *Polistes dominula* Taylor
- Aim 4: *Liostenogaster flavolineata* Taylor
- Aim 5: *Ceratina australensis* Rehan 2018

Megalopta genalis

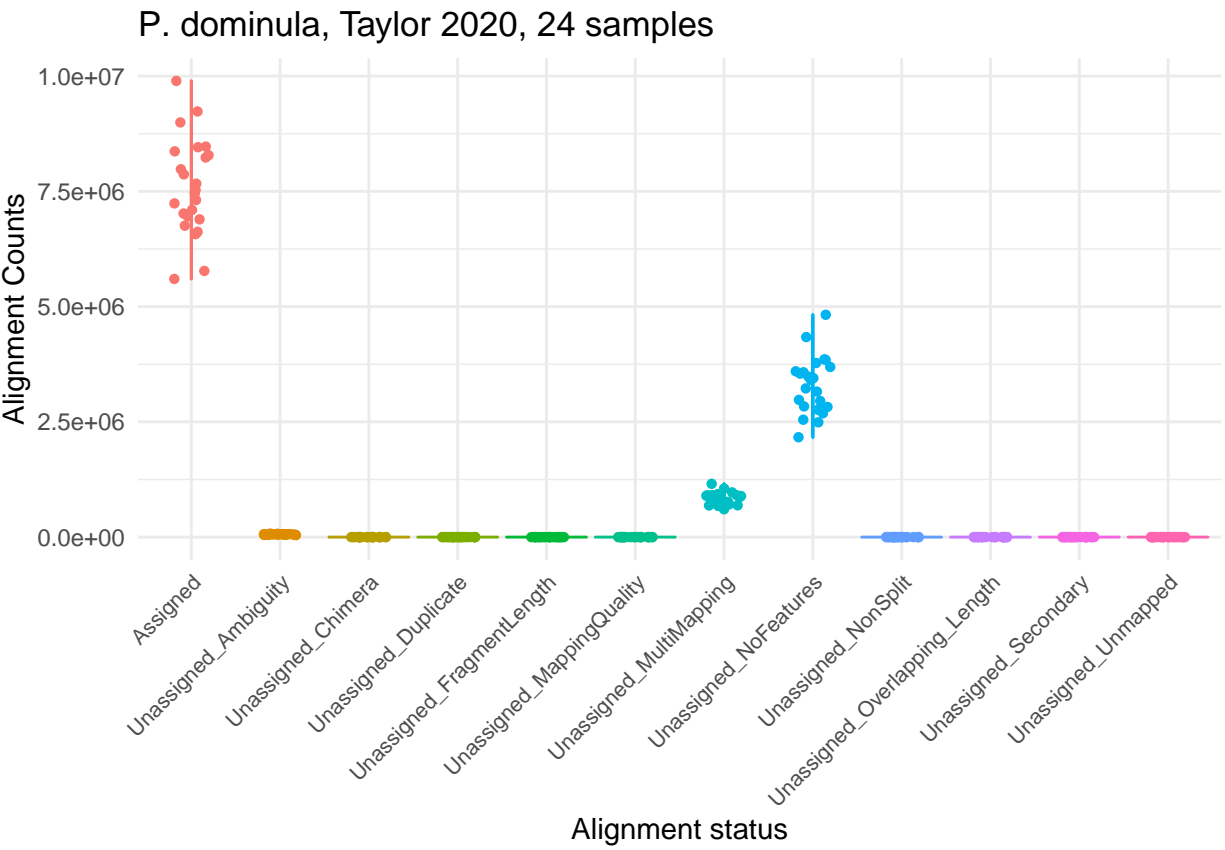
We ran Nextflow pipeline twice, because samples were prepared using a strand aware library, resulting in half the samples presenting a forward strandedness status and the other half a reverse strandedness. The forward-stranded samples were run with Neftlow flag `-forwardstranded`, and the reverse-stranded samples `-reverseStranded`. This produced comparable results from featureCounts.



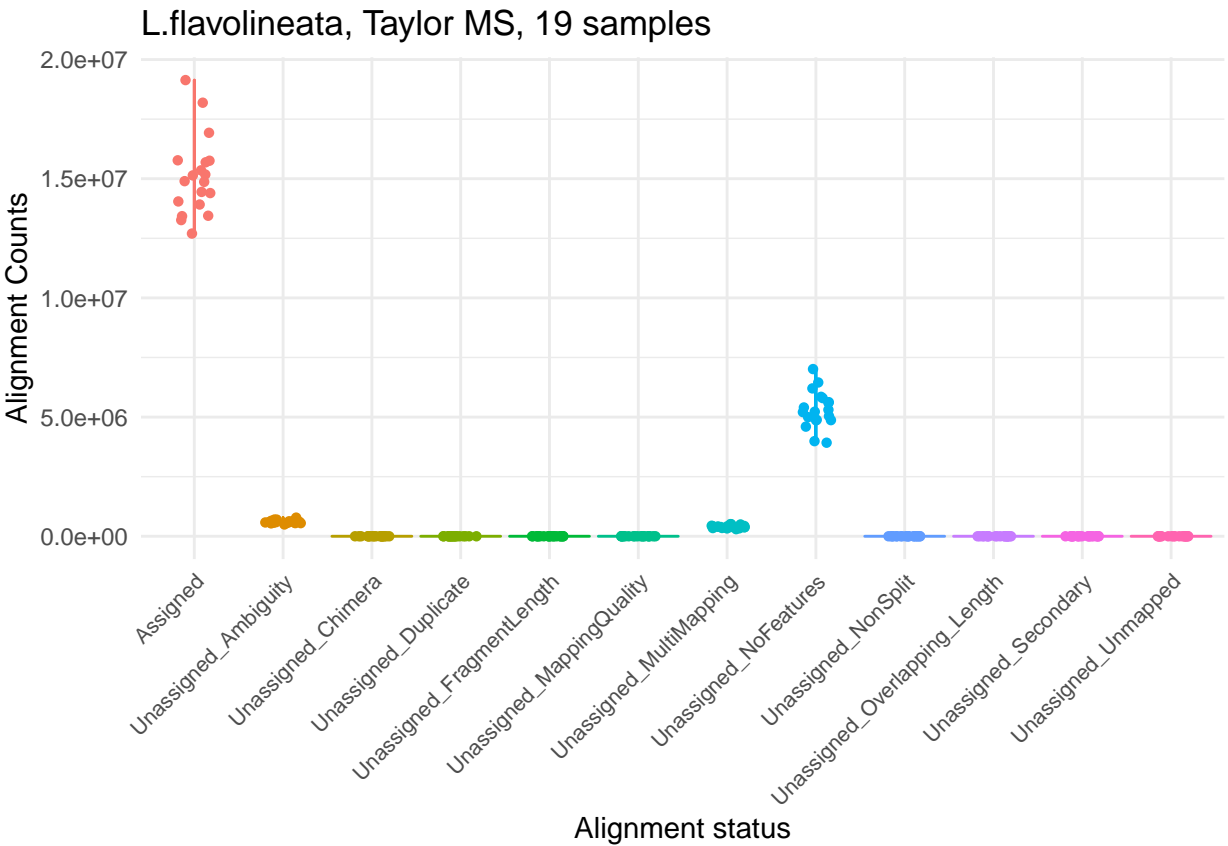
Polistes canadensis



Polistes dominula

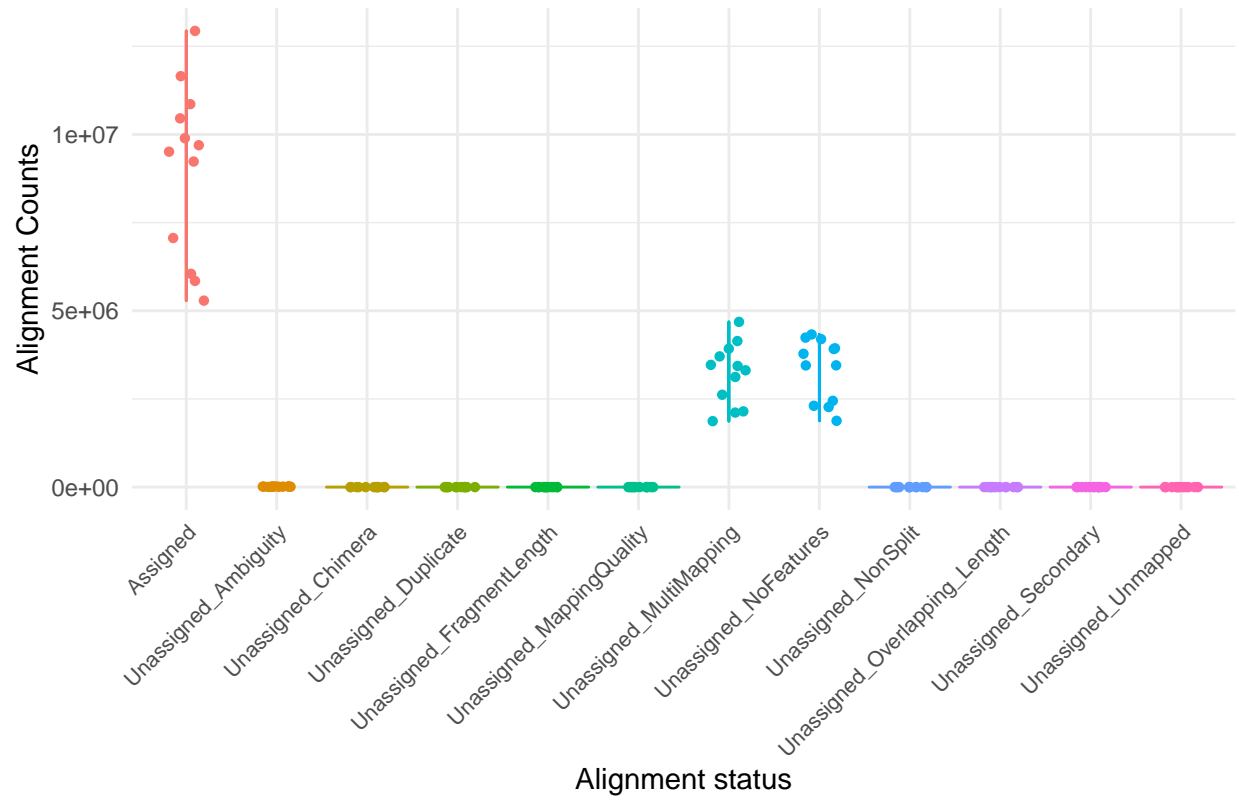


Liostenogaster flavolineata



Ceratina australensis

C.australensis, Rehan 2018, 12 samples



Conclusion

So far, most of the aligned reads are assigned to features (such as exon, gene, CDS).