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Exploring the design of RNA-seq analysis pipeline

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Transcriptome analysis through RNA-Seq data is well-established in model organisms, but the data analysis on other species can be less straightforward. Compared to other kingdoms, genome sequencing projects are far lower in plants, resulting in an increased challenge to the study of crop species. For example, in working with blueberries, we have more than one species of interest, fewer genomic resources than many model plant systems and various levels of polyploidy. When developing a workflow of software tools to analyze this data, a researcher faces decisions among numerous algorithms at each step. We have explored some of the current options available to analyze RNA-Seq data in two situations: first, when the closest reference genome is from a different species and second, when a polyploid species is being sequenced but the closest reference genome is a diploid progenitor species. Results are compared between the usages of a related species reference genome against the utilization of *de novo* transcriptome assemblies. Further, comparisons are made amongst read correcting, quality trimming, and read mapping software choices. We conclude that different software packages and approaches influence RNA-Seq analysis and recommend the election of parameters that maximize desired metrics when using polyploid species and/or a distant reference genome.

Biography

Miriam Payá Milans is a Young Researcher with an international background. On her PhD studies, in Seville Spain, she worked on the molecular and biochemical analysis of genes in the lipid biosynthesis pathway. Part of that research was carried out in collaboration with laboratories at the Universities of Missouri and Guelph. After PhD, she decided to expand into the field of bioinformatics, with her first work done on SNP analysis in octoploid strawberry, in Barcelona. She is currently working as Postdoctoral Fellow at University of Tennessee, focusing on the analysis of RNA-Seq data in several plant species. There, she helps teaching at RNA-Seq analysis workshops and offers bioinformatics support to colleagues.

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