

Magnoliids preliminary results

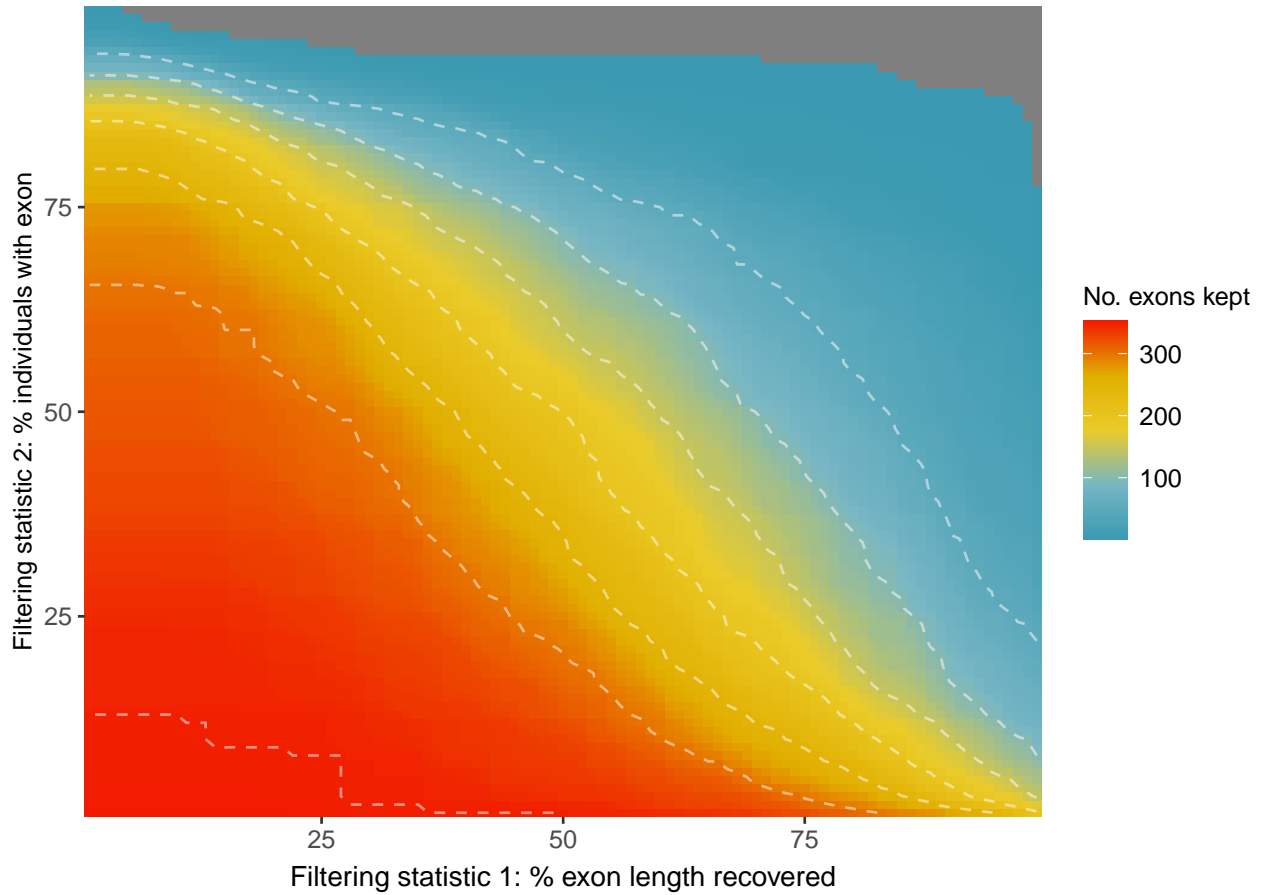


Figure 1: A plot showing the number of exons recovered under a range of filtering thresholds based on two parameters. The x-axis shows first filtering parameter: the percentage length of the exon that was recovered. The second filtering parameter, on the y-axis, is the percentage of the total number of individuals for which an exon was recovered. A given combination of x and y values yields a number of exons kept after filtering at these parameter values. This number is represented by a colour gradient where deep red shades indicate more exons were kept after filtering. Grey cells are used when no exons were kept. White, dashed lines are contours that demonstrate the 3d structure of the data, or the rate of change of the number of exons recovered as filtering parameters are varied.

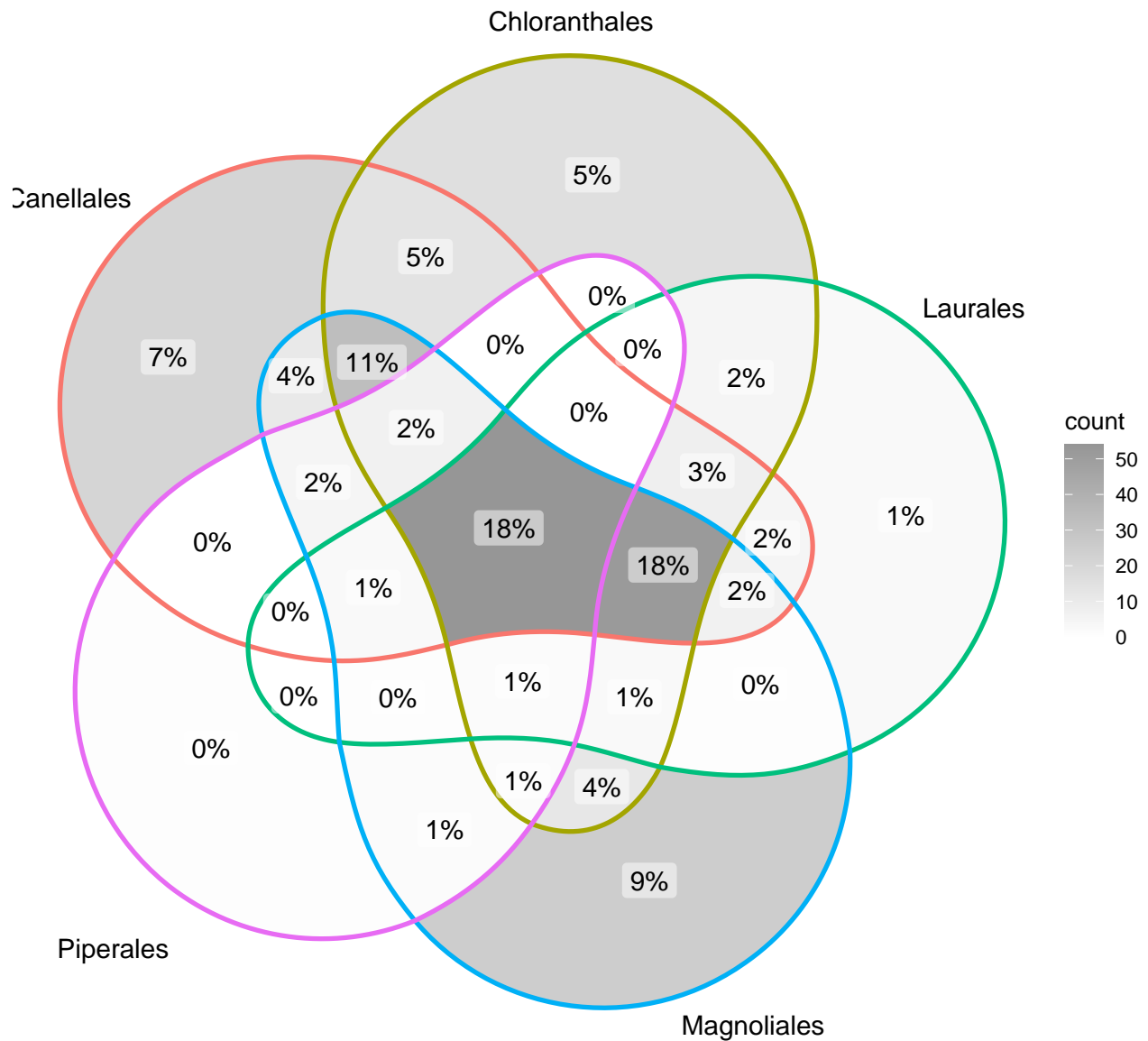


Figure 2: Venn diagram showing overlap of exons in each order. Individuals were split by order into different datasets. Filtering was then done independently on each of the five datasets. Overlap among exons across orders was then calculated. This is shown as proportion of total exon dataset in each segment. Greyscale gradient represents the raw number of exons belonging to each segment.

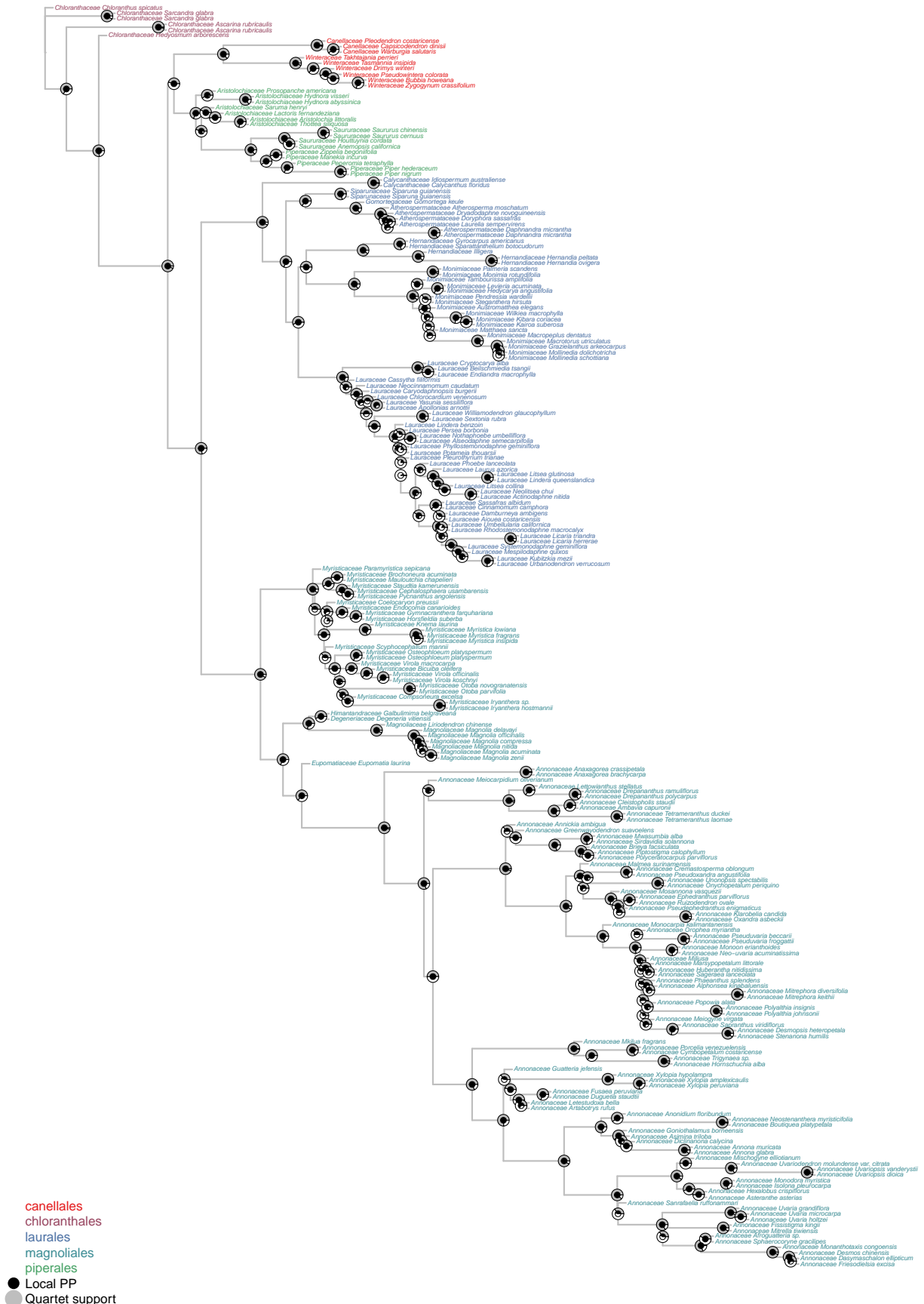


Figure 3: ASTRAL-III tree annotated with local posterior probability (LPP) and Quartet Support (QS). Inner pie charts on nodes show the value of LPP for the preceding branch (0-1) in black and white. Outer pie charts show QS in grey and white. QS is the proportion of the highest-frequency quartet at each branch i.e. if the QS value is 60% then 60% of gene (supercontig) trees contain a quartet that matches the relationship shown in the ASTRAL tree. Filtering was done based on exon recovery statistics per locus (>