

Lab Meeting 7/16/19

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Sorghum QTL Mapping - Background

1. Calculate phenotypic parameters from hyperspectral and RGB images
2. Match phenotypic variations with presence/absence of markers in DNA (SNPs)

Result: Identification of areas of sorghum genome which control for economically valuable traits



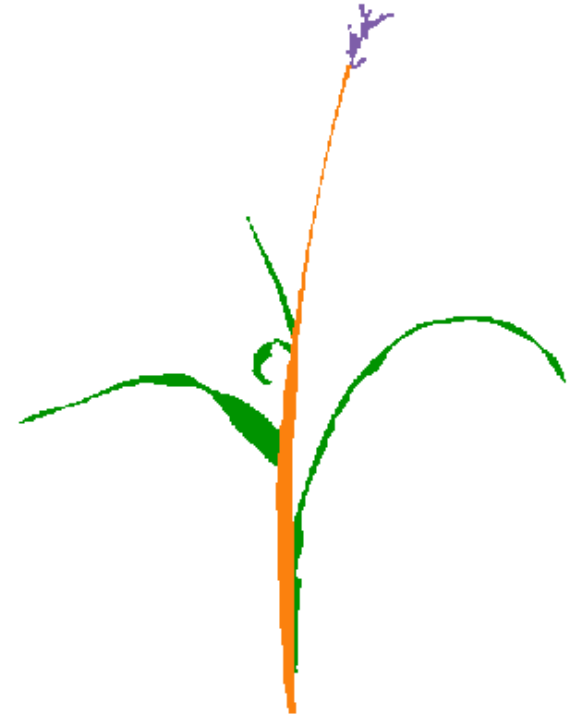
Traits to Identify

General plant shape:

- Stalk height – distance from bottom of stalk to flag leaf node
- # of leaves
- Leaf angle

Panicle characteristics:

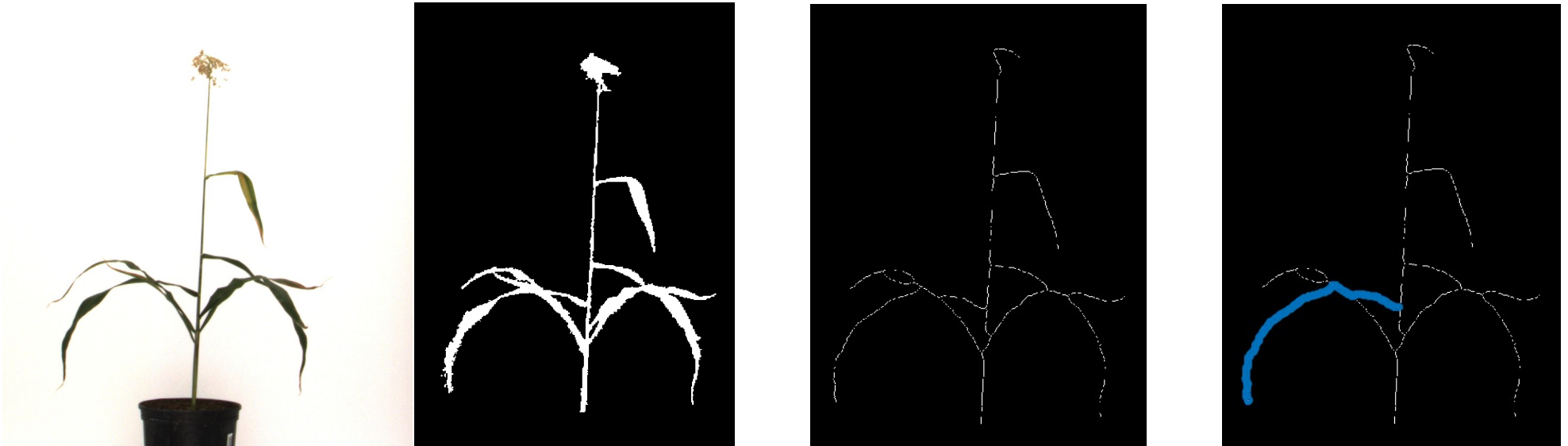
- Panicle size – area of convex hull surrounding panicle
- Panicle openness – empty area in convex hull / total area
- Panicle exsertion – distance from flag leaf node to base of panicle



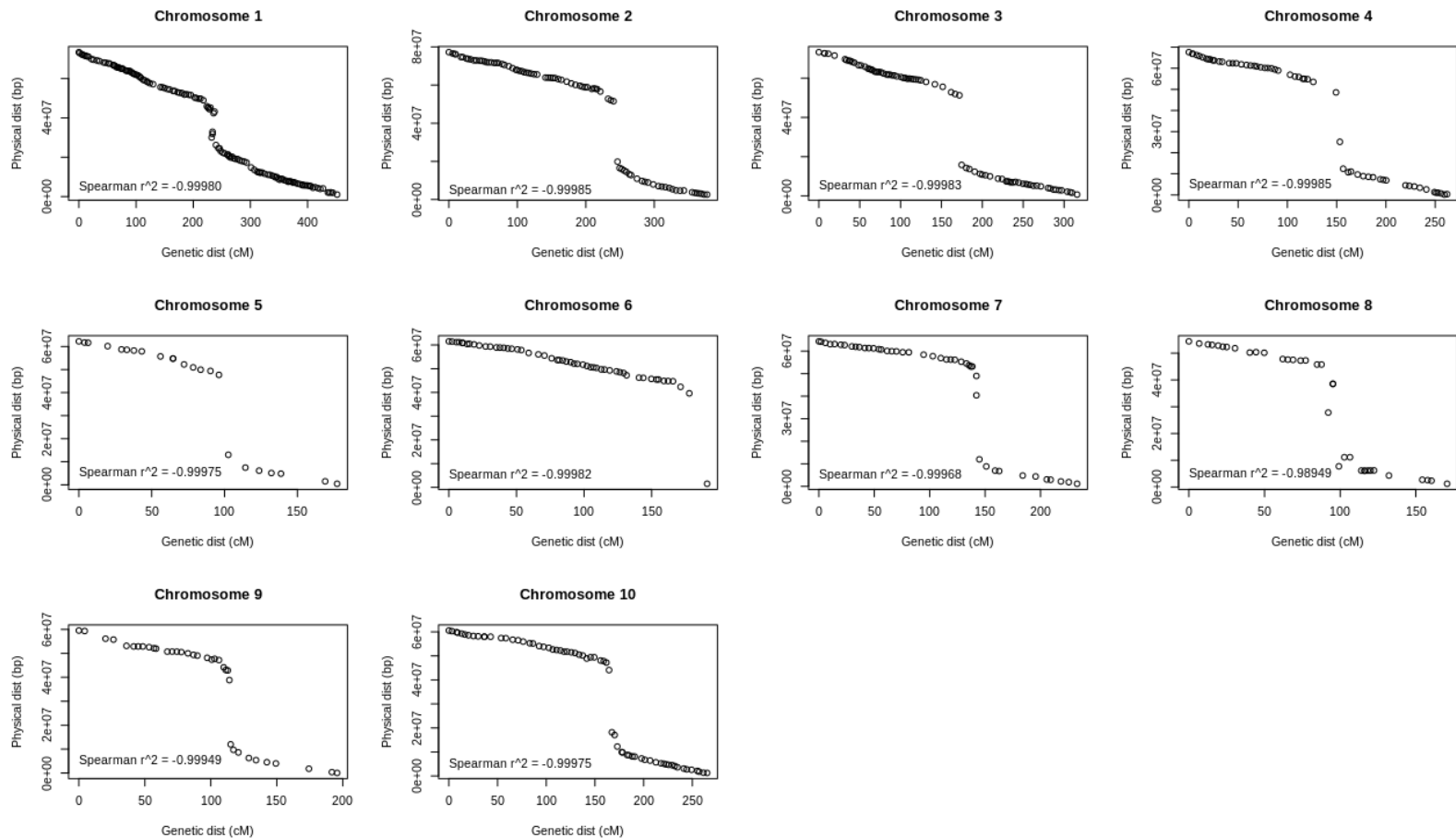
RGB Image Processing – Leaf Angle

Method to separate overlapping leaves:

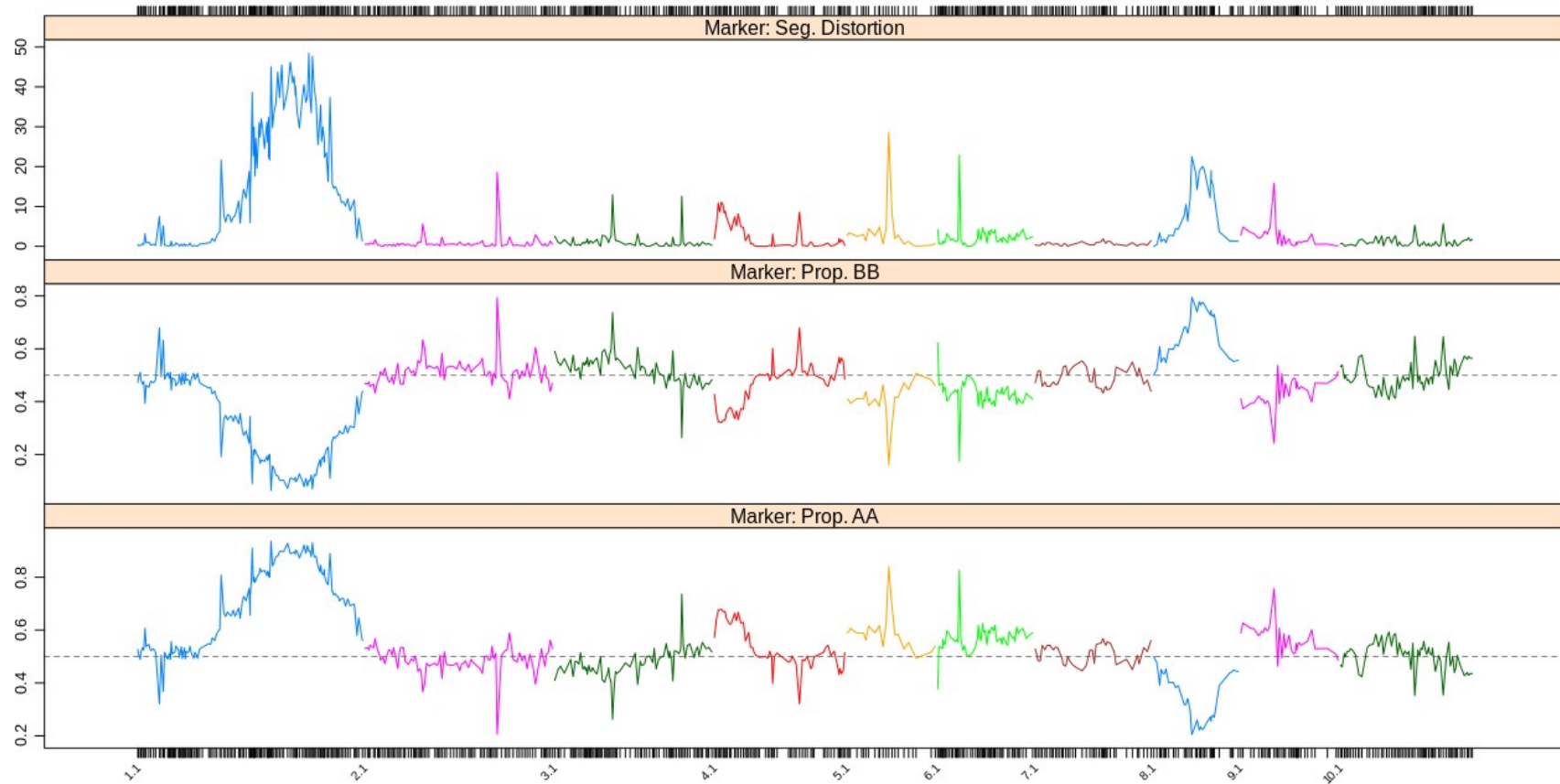
- 1) Skeletonize image
- 2) Identify leaf tips
- 3) Trace all possible paths back to stalk
- 4) Choose smoothest path



QTL Mapping – Genetic Map



QTL Mapping – Segregation Distortion



QTL Mapping – Model Selection

Multiple QTL approach:

- Identify additive QTL, and any interactions between QTL for each phenotypic trait

Procedure:

- Calculate penalties for LOD scores
 - Additional QTL will always increase LOD score of model
 - To minimize false positive selection of QTL, apply penalty
- Stepwise model search
 - Forward selection – add QTL/interactions to model
 - Backward elimination – remove QTL/interactions from model
 - Calculate penalized LOD score after each change
- Estimate effect of each QTL/interaction on phenotype

Stepwise Example

From Broman et al (2009):

- Circles represent possible QTL
 - Numbers = chromosome #
- Lines represent interactions between QTL

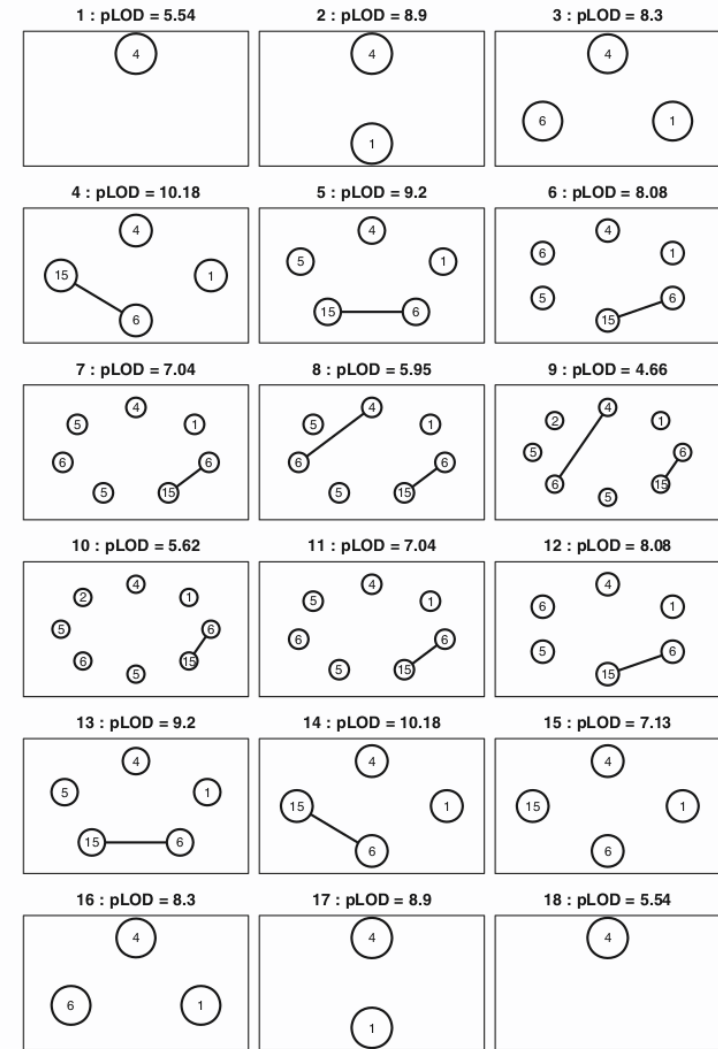


Figure 9.10. The sequence of models visited by the forward/backward search of stepwiseqtl, with the hyper data.