

GWAS in Raspberries: Developmental and fruit traits

Philip Greenspoon

Biomathematics and Statistics Scotland (BioSS)

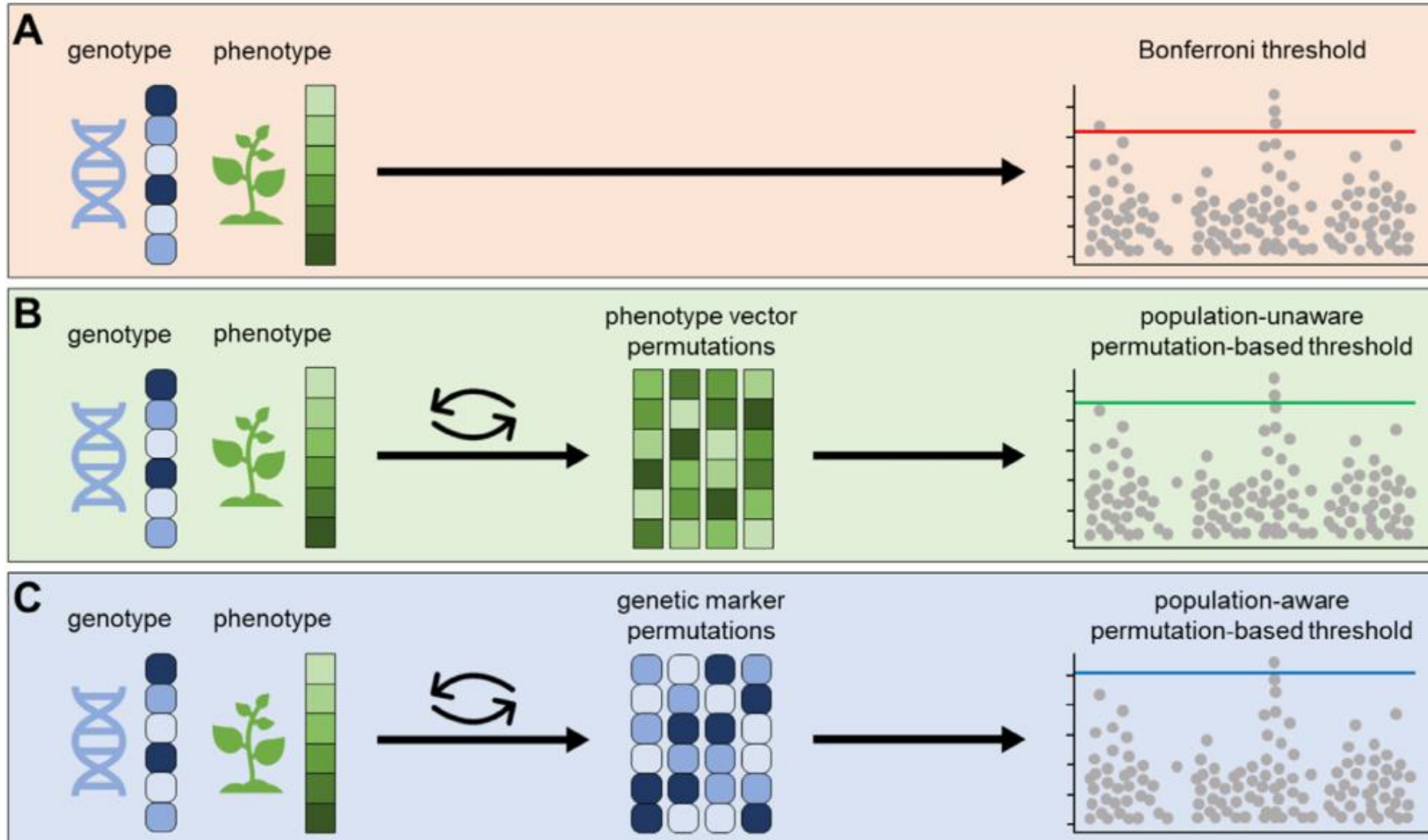
Key question - What parts of the raspberry genome are involved in developmental traits and fruit traits?

- Genomic data: 1080 genotypes and 8239 SNPs
- Phenotypic data:
 - 3 locations: Hutton (264), Italy (46 Spring sel. & variety), England (182 unselected FC)
 - 2 - 3 years of collection
 - 1 – 2 reps
- Development time traits
 - Bud burst
 - Leaf out
 - Flower bud swell
 - Flower open
 - Green set
 - First pink
 - Few red
 - First pick
- Fruit traits
 - Colour
 - Appearance
 - Flavour
 - Texture
 - Brix

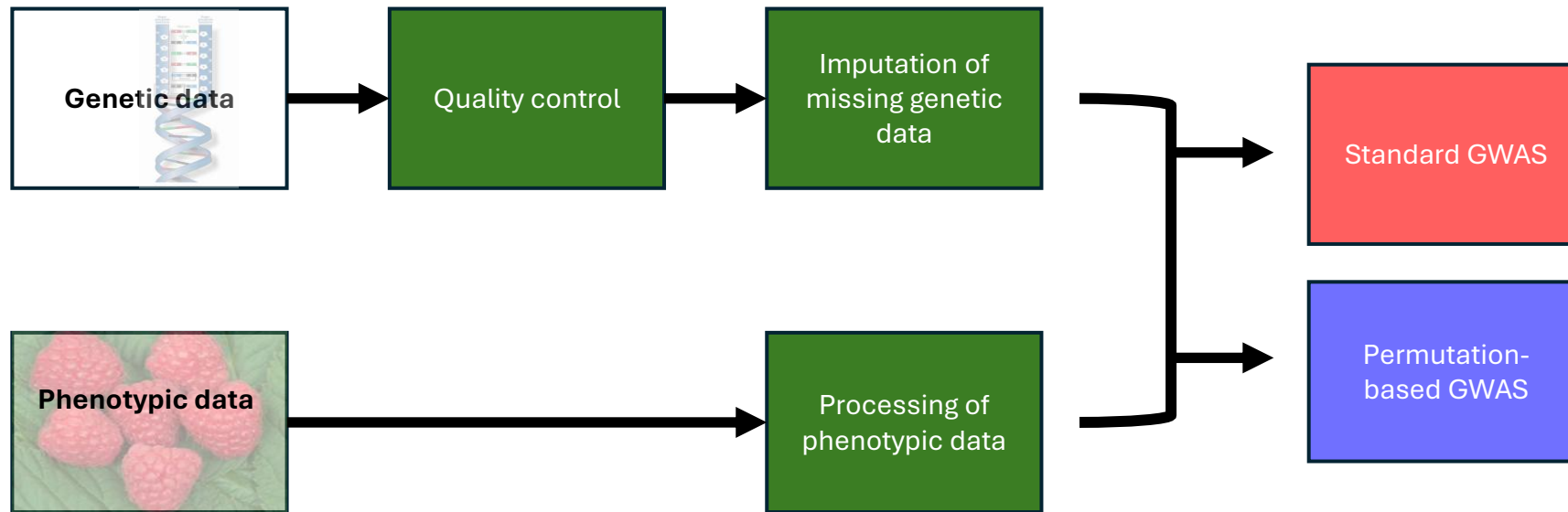
Issue with typical parametric approach to GWAS

- Parametric approaches usually assume independence among sites,
 - Not valid due to linkage disequilibrium among sites
 - Breaching this assumption can lead to **elevated false negatives**
- Assumes normality of residuals.
 - We are dealing with calendar date data that are not normally distributed.
 - Breaching this assumption can lead to **elevated false positives**

Alternative – Permutation approach



Workflow summary



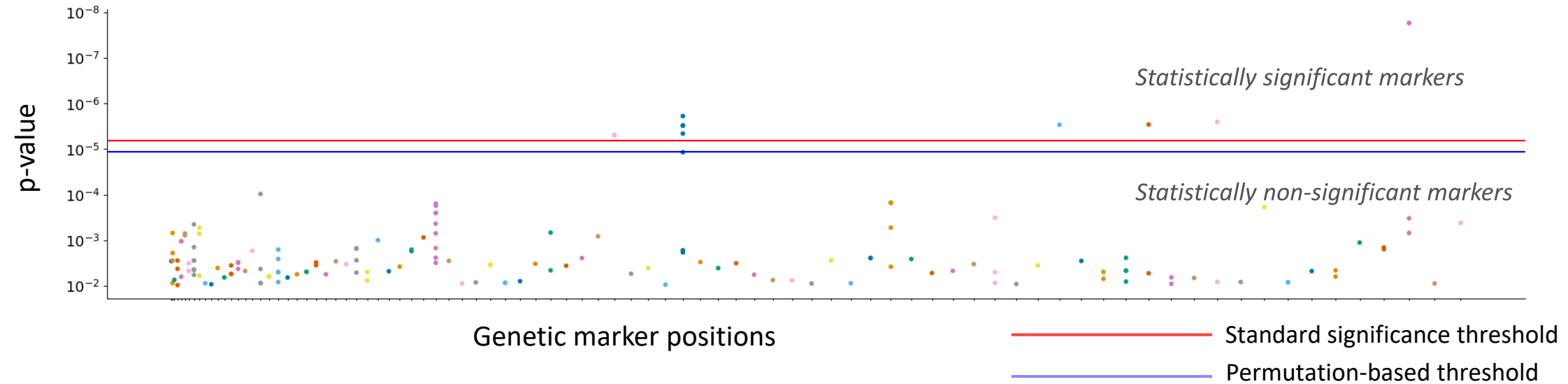
Adjusted phenotypes

- In Hutton data we have two rows per genotype and two years of data
- I add row as random effect and year as fixed effect into a linear mixed model to extract the genetic value of an individual
- Linear mixed model approach to obtain genotypic values

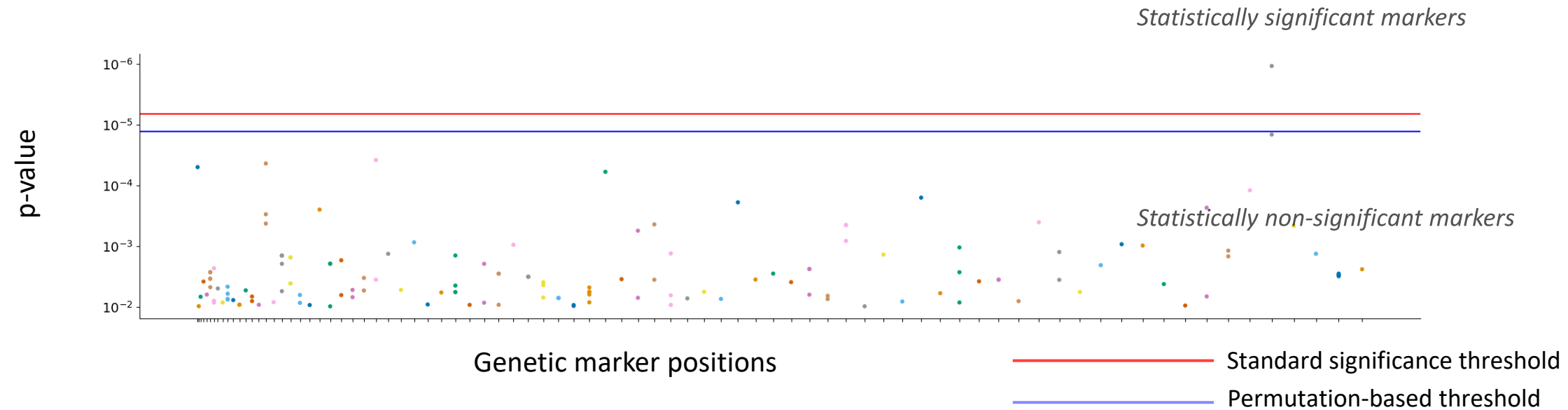
$$y = \mu + g + r + y + e$$

- Take this random effect g as the genetic value instead of the raw phenotypic values

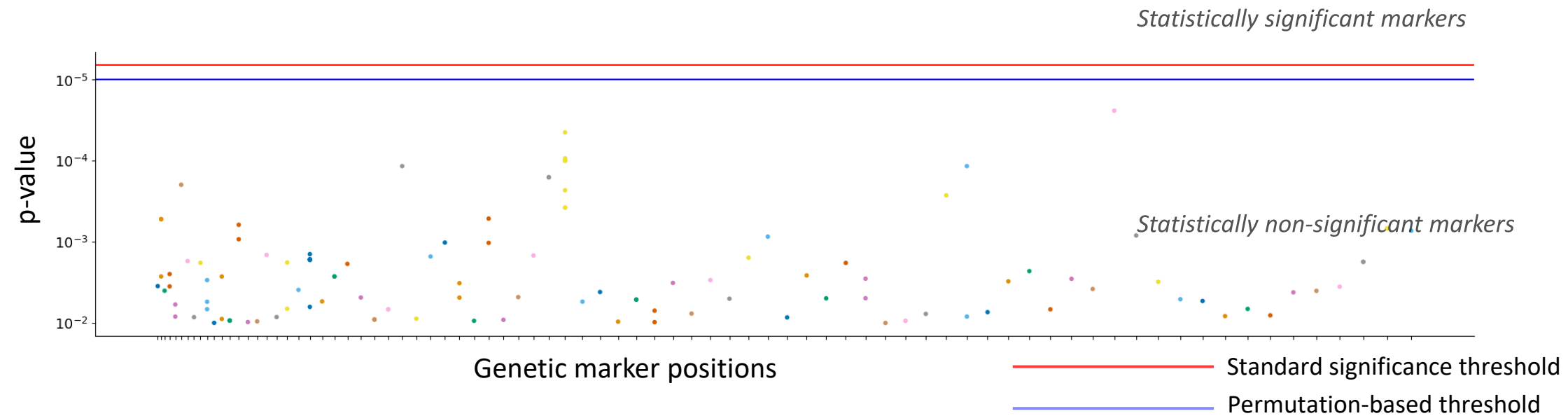
Hutton: Timing of leaf emergence



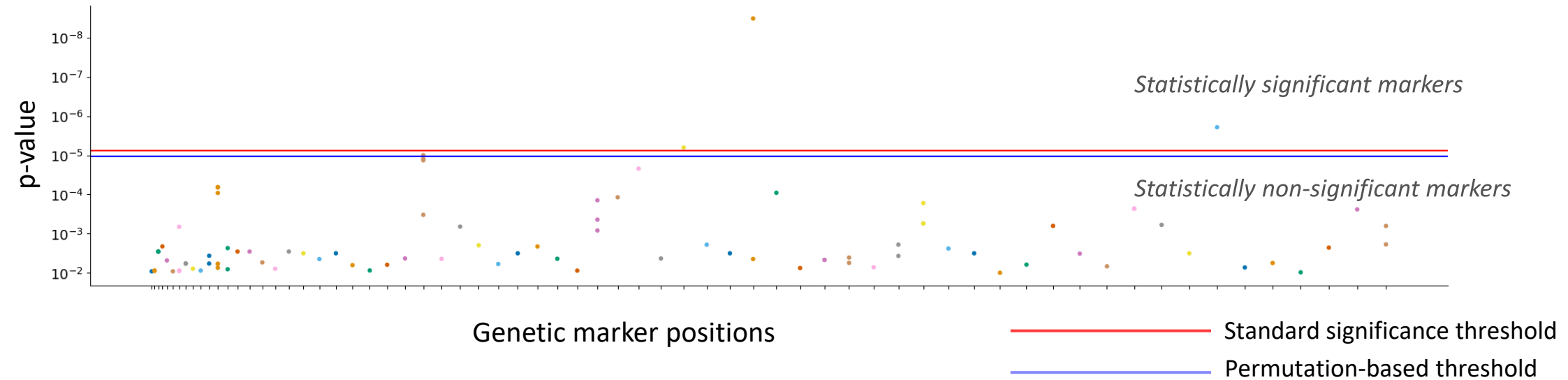
Hutton: PCA1 of developmental traits



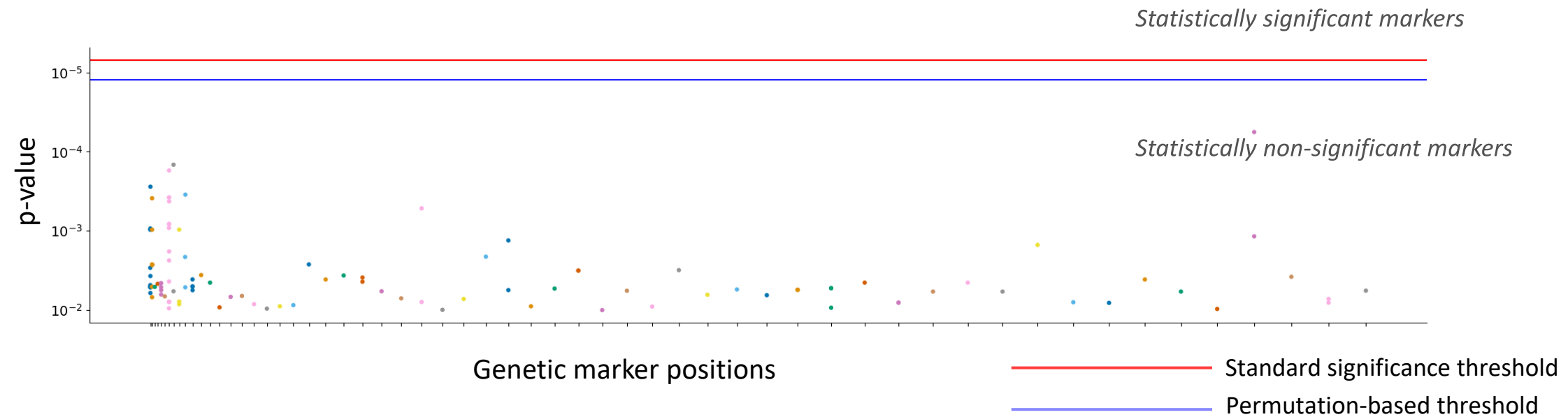
Hutton: Interval between bud burst and flower open



Angus: Fruit colour



G-Berries: Flowers open



Prospects for GWAS in raspberry

- We find a few significant SNPs, but our GWAS would benefit from greater sample sizes to find more and with greater confidence
 - Collect more data, but also extract the most out of the data we have (e.g., spring & autumn, primocane & floricanes)
- Future work should focus on collecting data in a standardized approach emphasizing collection of more individual phenotypes
- Incorporating environmental covariates is an exciting avenue for future work
- Ultimately the SNPs we find can be used for marker assisted selection to improve raspberries more efficiently, by helping us decide which plant material is promising for advancement