LaByRInth

An Improved Algorithm for Low-Coverage Biallelic Genetic Imputation

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Outline

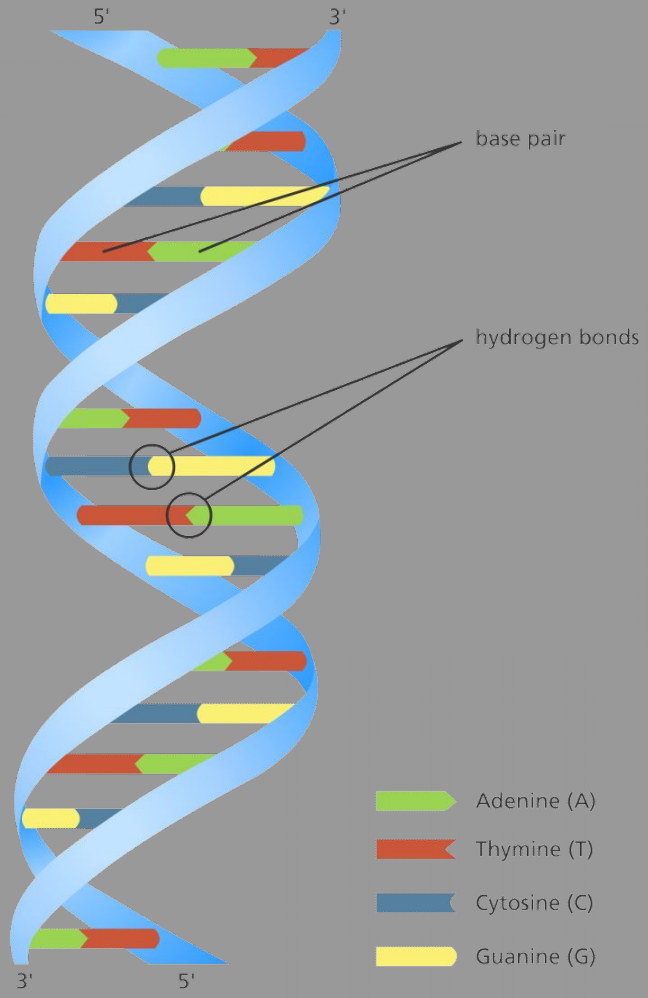
1. Project History
2. Genetics
3. Imputation
    a. LB-Impute
    b. LaByRInth
        i. Modeling
4. Future Work

Kansas State Agronomy

1. Correlate physical features with genetics in wheat and wheatgrass
    a. Plant height
    b. Number of seeds per head
2. Fit equations to data to model distributions
3. LaByRInth imputation

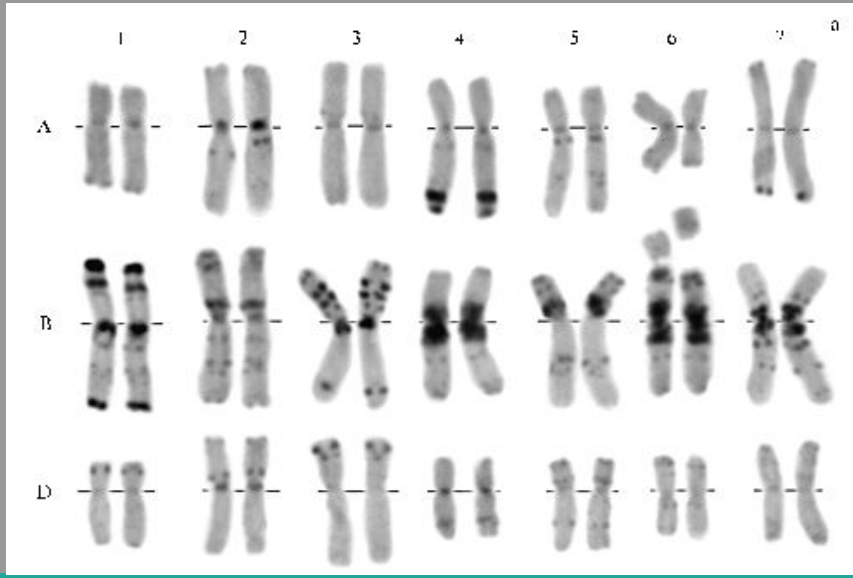
Chromosomes

1. Chromosomes encode genetic information
2. Chromosome is a sequence of bonded bases
    a. A/T and C/G
    b. 5’ and 3’
    c. 5’ATGACACTGTGACA3’ uniquely identifies



Heterozygous and Homozygous

1. Wheat has 42 chromosomes
2. Chromosomes come in pairs (homologs)
    a. Homologs serve same genetic purpose
    b. Base pairs can be completely different
    c. Each parent contributes one chromosome to each homologous pair

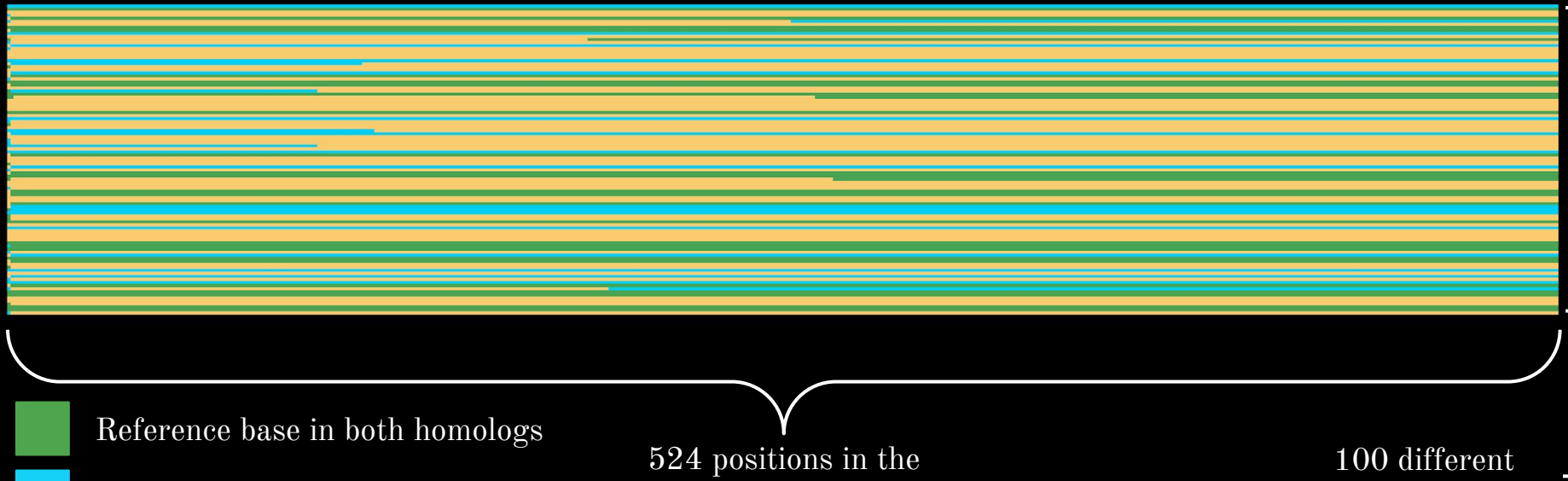


Genetic Imputation

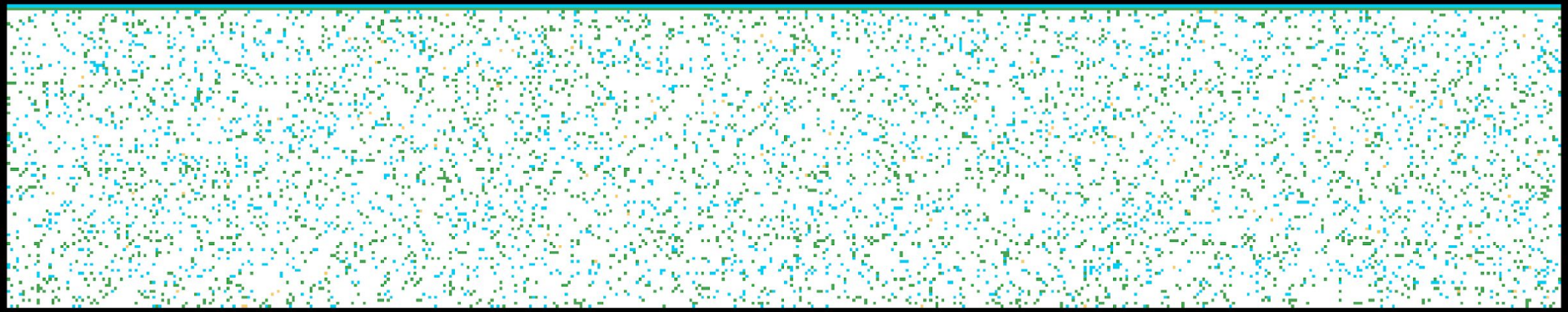
1. Expensive to collect all genetic information
2. Patterns are expected based on known breeding
3. Imputation is used to fill in the gaps
    a. Build a mathematical model of the expected process
    b. Use known genetic sites to infer unknown sites

How well does imputation actually work?

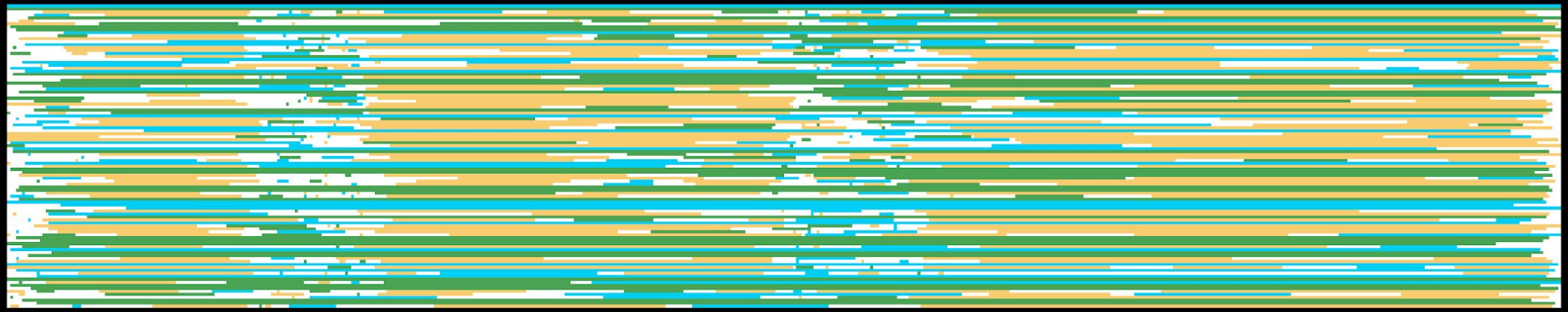
Genetics of a Biallelic Homologous Chromosome Pair



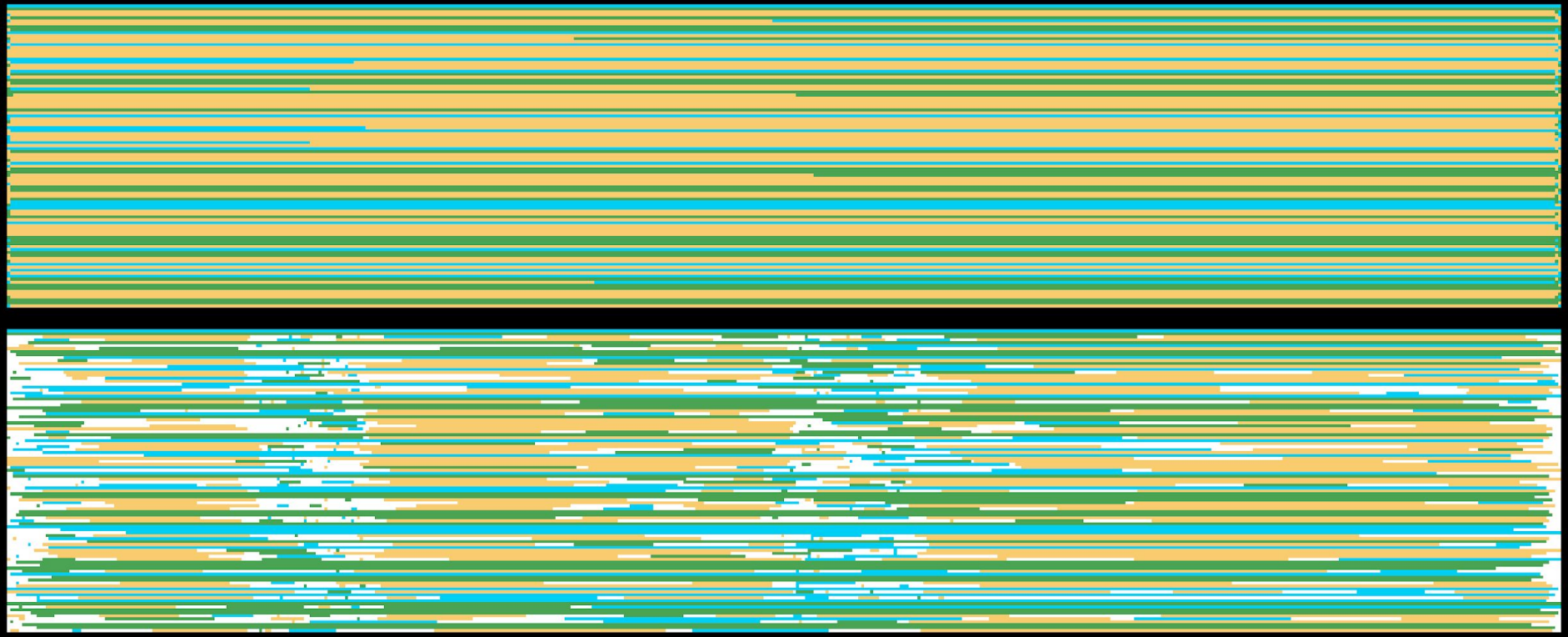
Sampled



LB-Impute

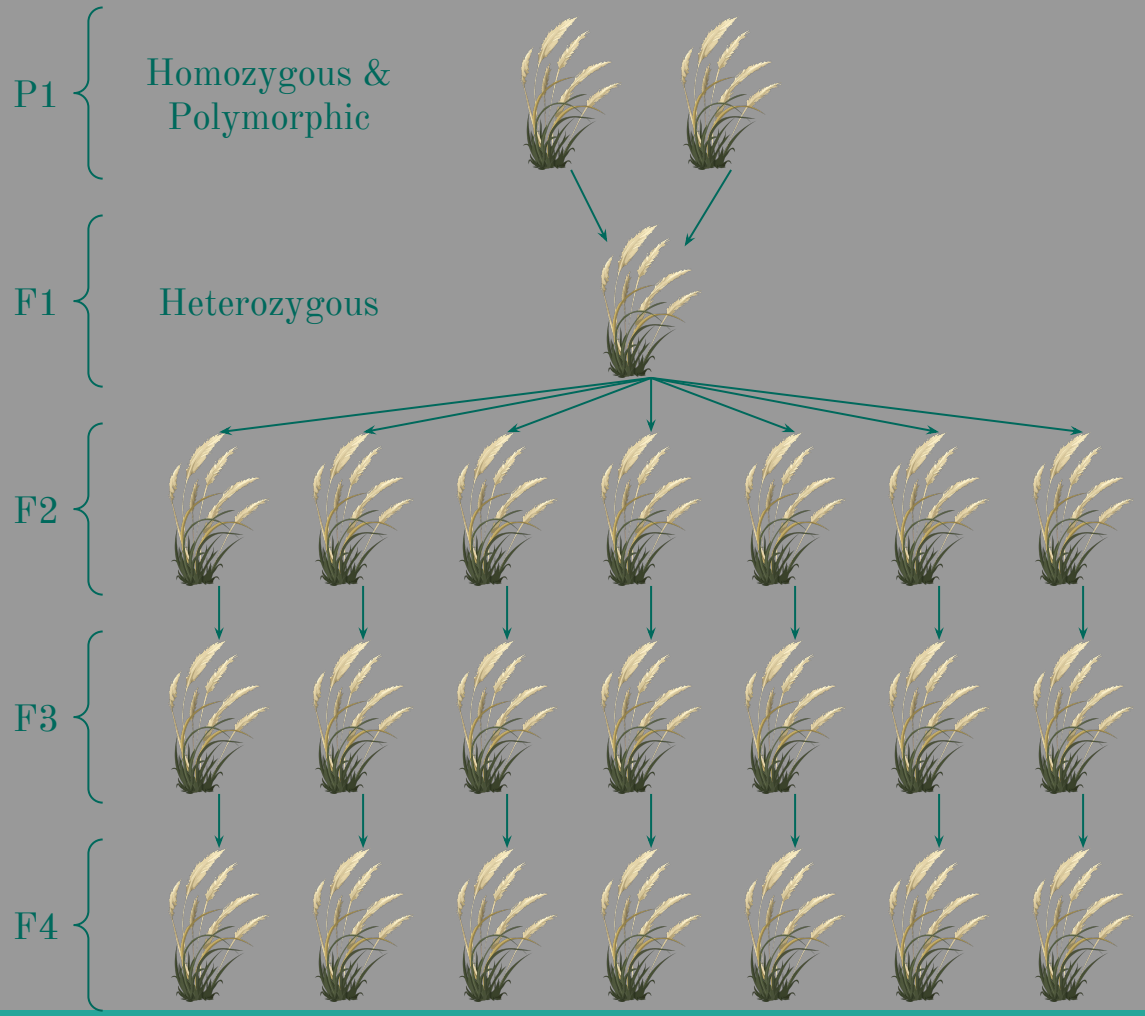


Genetics vs LB-Impute

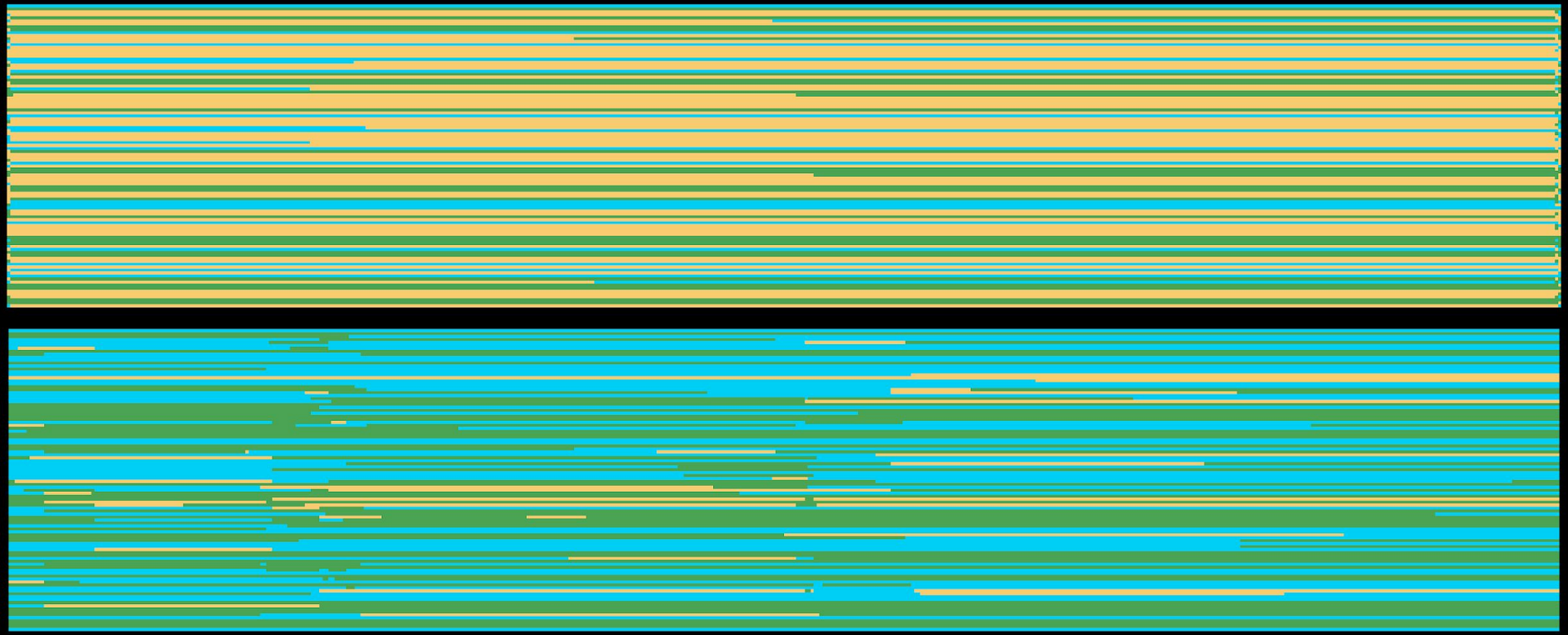


LB-Impute

1. Leaves large sections of the chromosome un-imputed
2. Designed for F2 populations

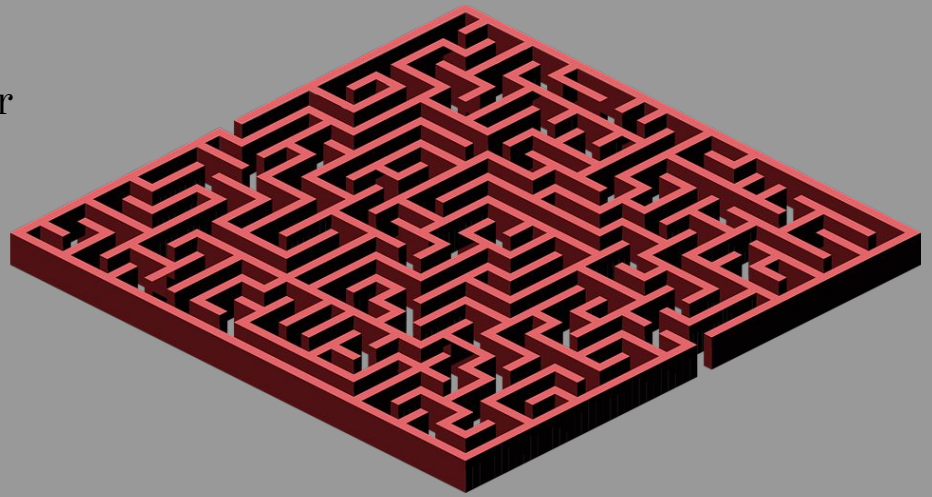


F2 vs F5



LaByRInth

1. **L**ow-coverage **B**iallelic **R**-package **I**mputation
2. Initially supposed to be re-write of LB-Impute (Java to R)
3. Found many areas for improvement
    a. Project took unexpected direction
    b. A few weeks became more than a year
4. Open source



Modeling Strategies

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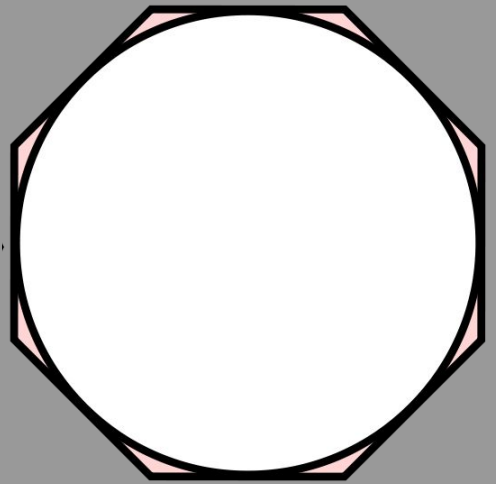
3. An analogy: find the area of a circle
    - Use a polygon to approximate the area
        i. Area of polygon may be able to be exactly computed
    - Use formula πr^2
        i. π cannot be represented exactly

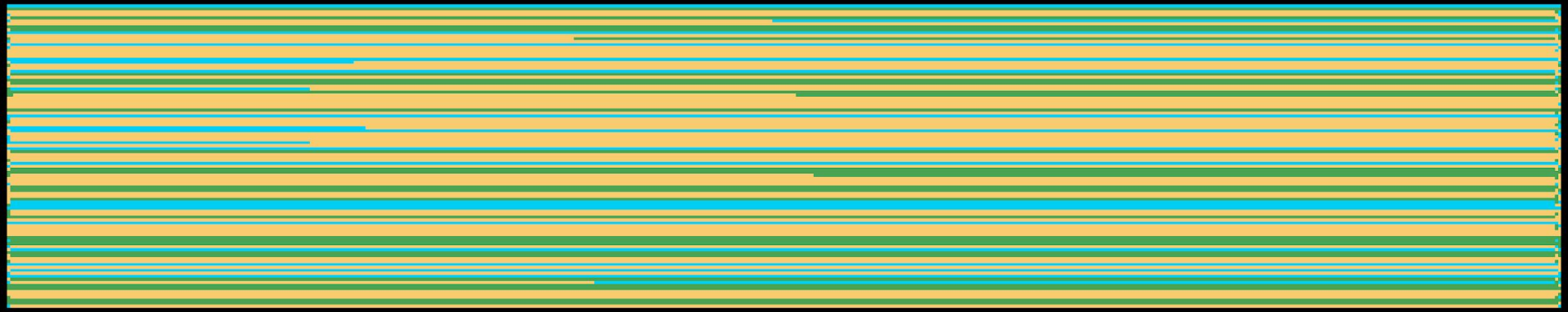


LaByRInth Strategy

1. Have not found a good way to do option 2 (capture biology)
2. Two different ideas for option 1 (exact solution to model)
    a. Extend LB-Impute strategy to other generations
        i. Assumes we can segment the chromosome
    b. New method based on different biological assumptions
        i. Assume limited genetic change during reproduction

How well does LaByRInth work?

Genetics



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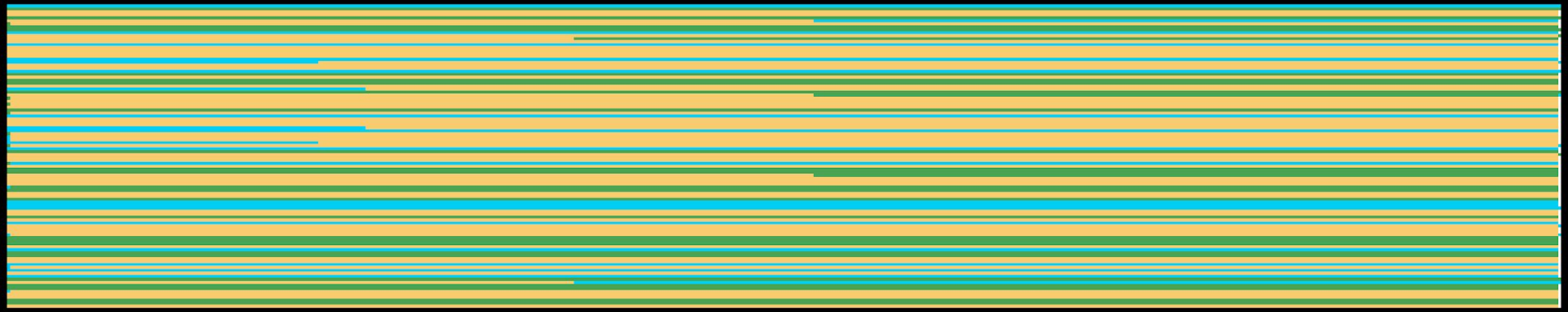
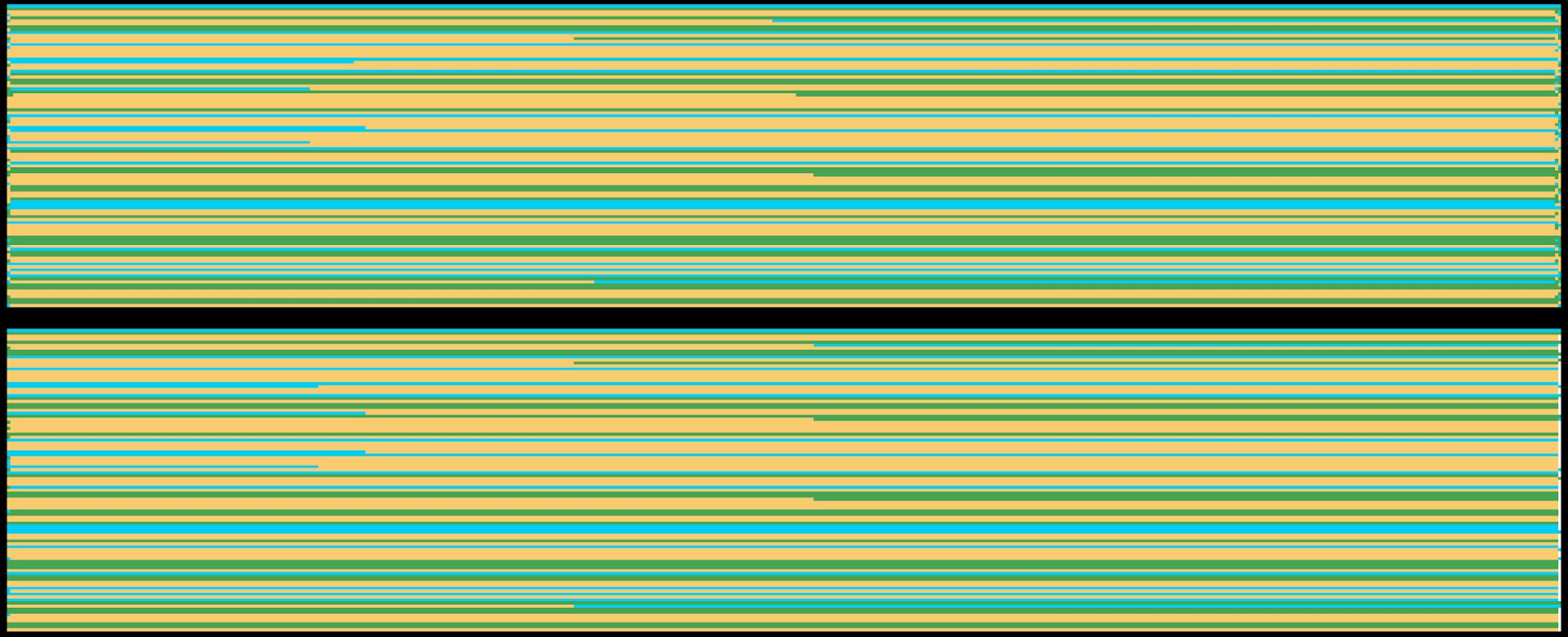


Genetics vs LaByRInth



This Summer

1. Implement and test both concept methods
    a. Real data
    b. Simulated data
2. Write and submit paper
3. Package code and release

Thanks to my advisors,

Dr. Nathan Tintle (Dordt)

Dr. Jesse Poland (Kansas State)

Dr. Mike Janssen (Dordt)

Questions?

Fitting Gaussian Curves