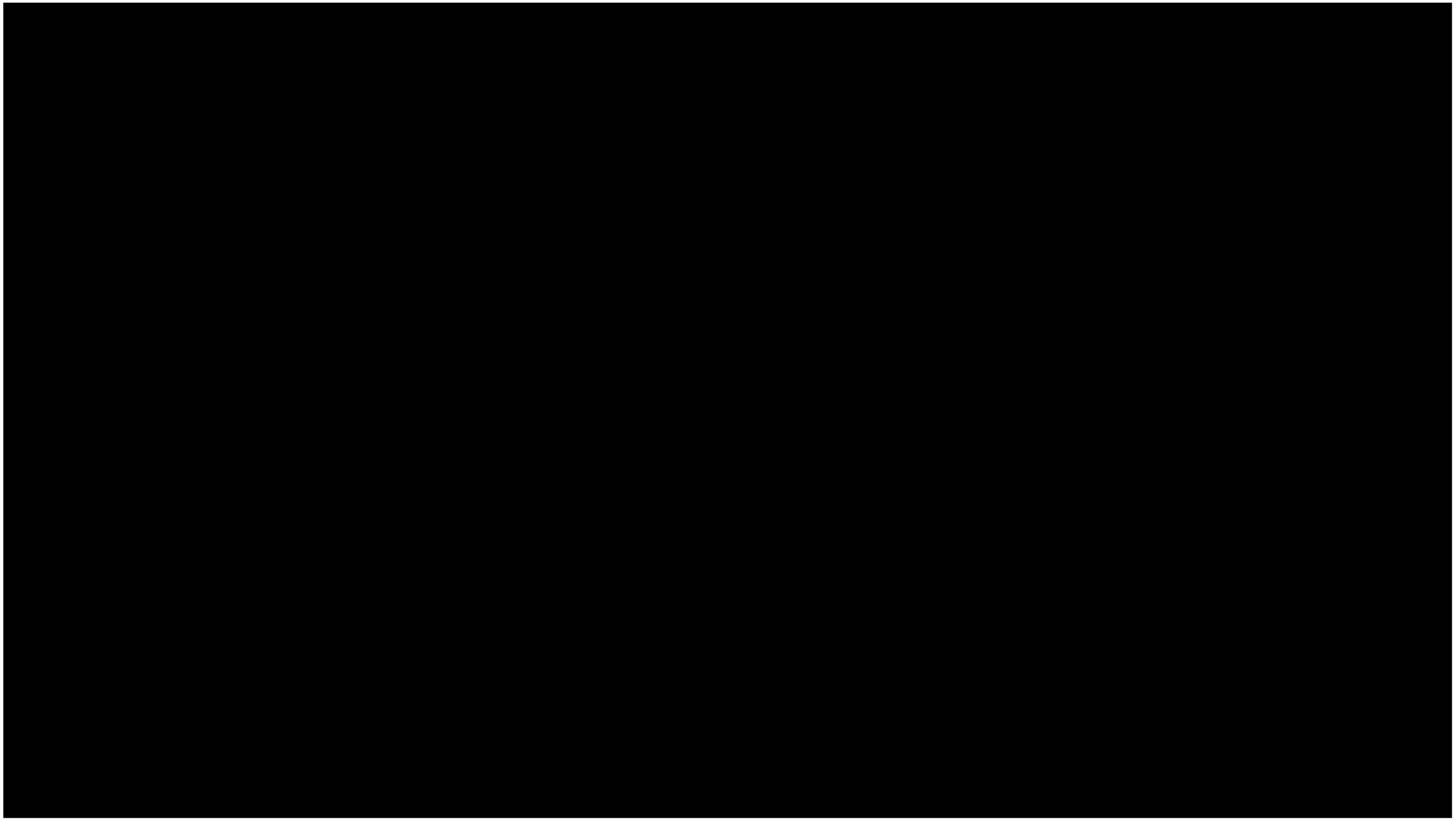

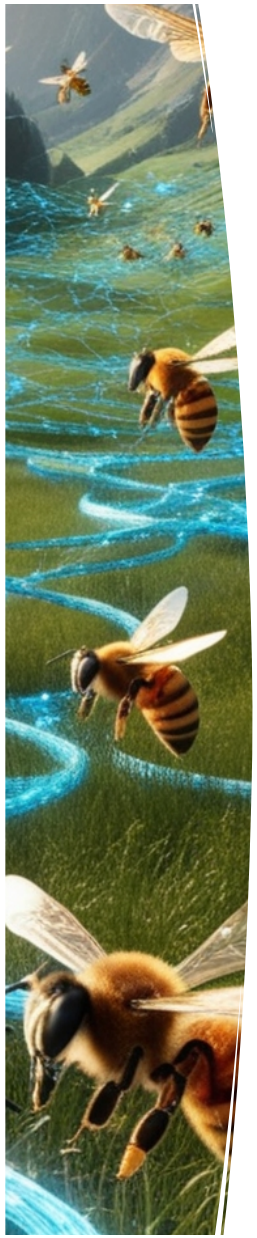

How do we try to track inheritance in honeybees?

High performing queen

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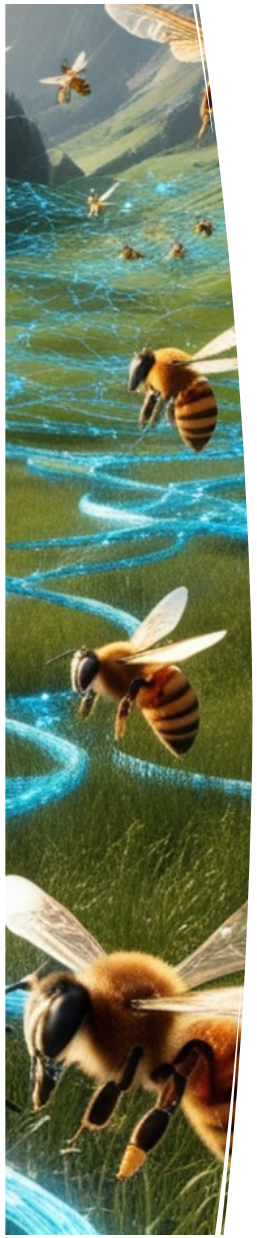

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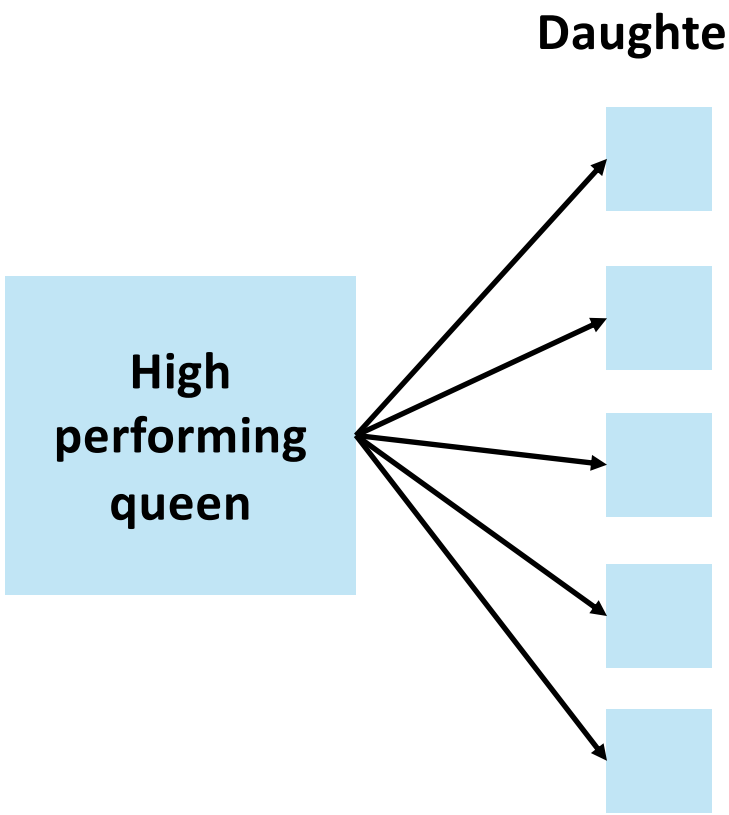

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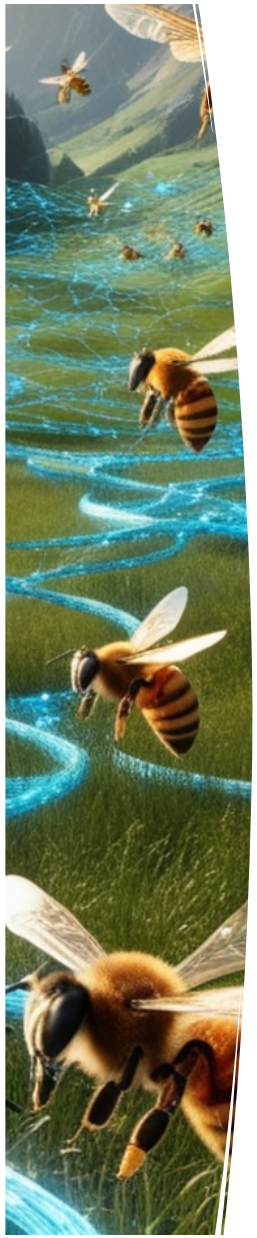

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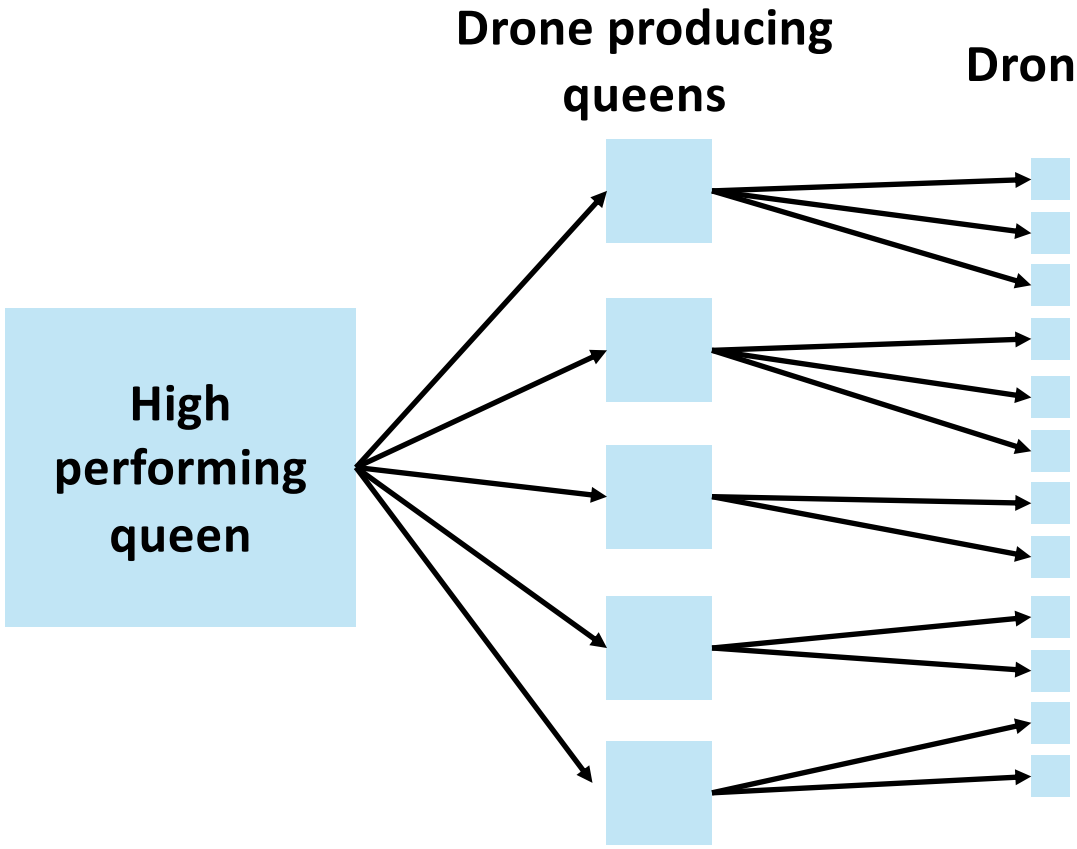

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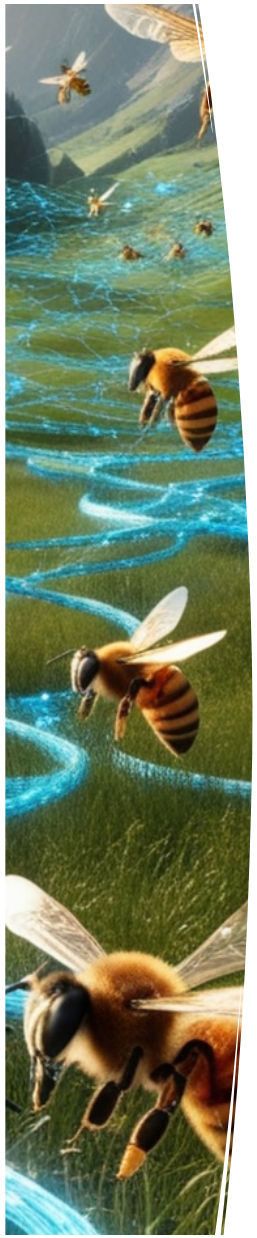

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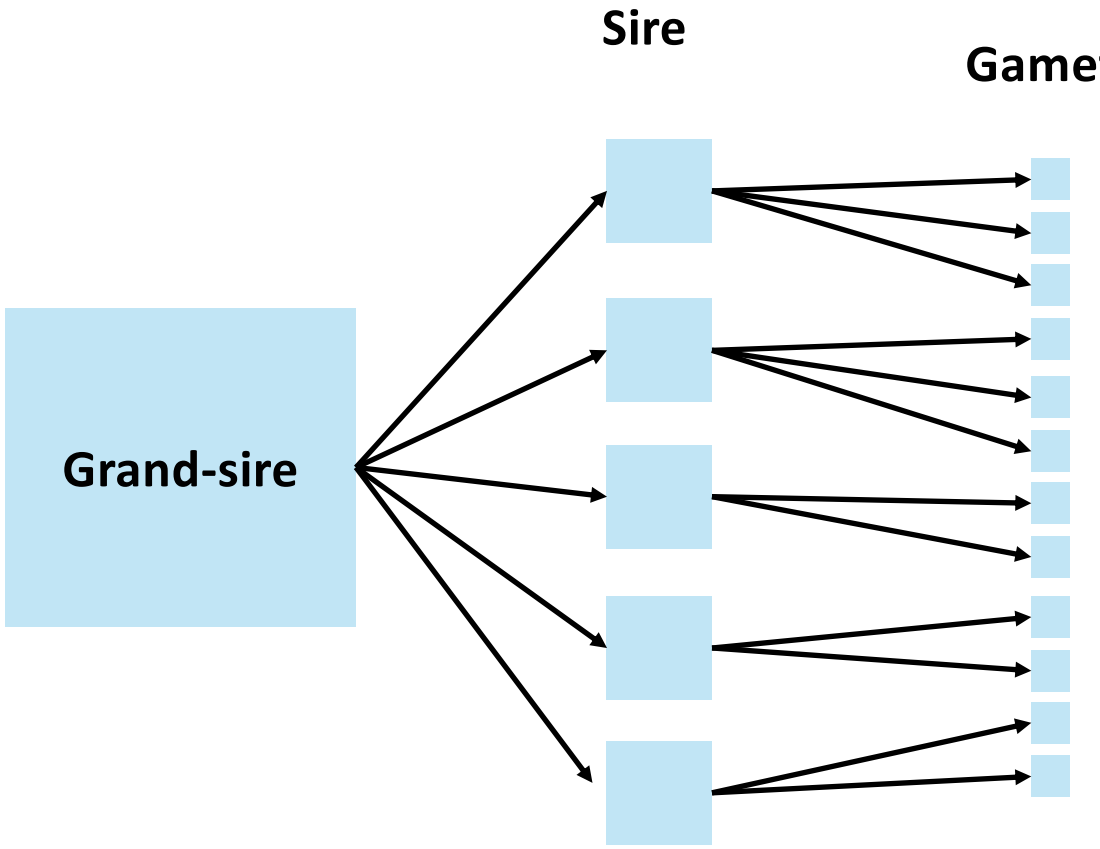

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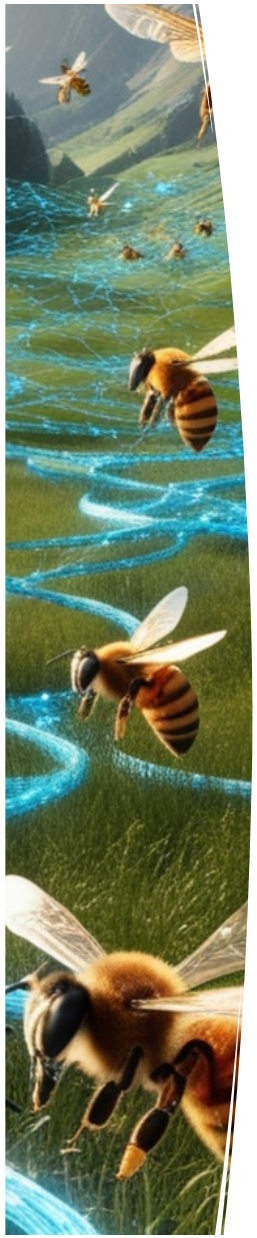

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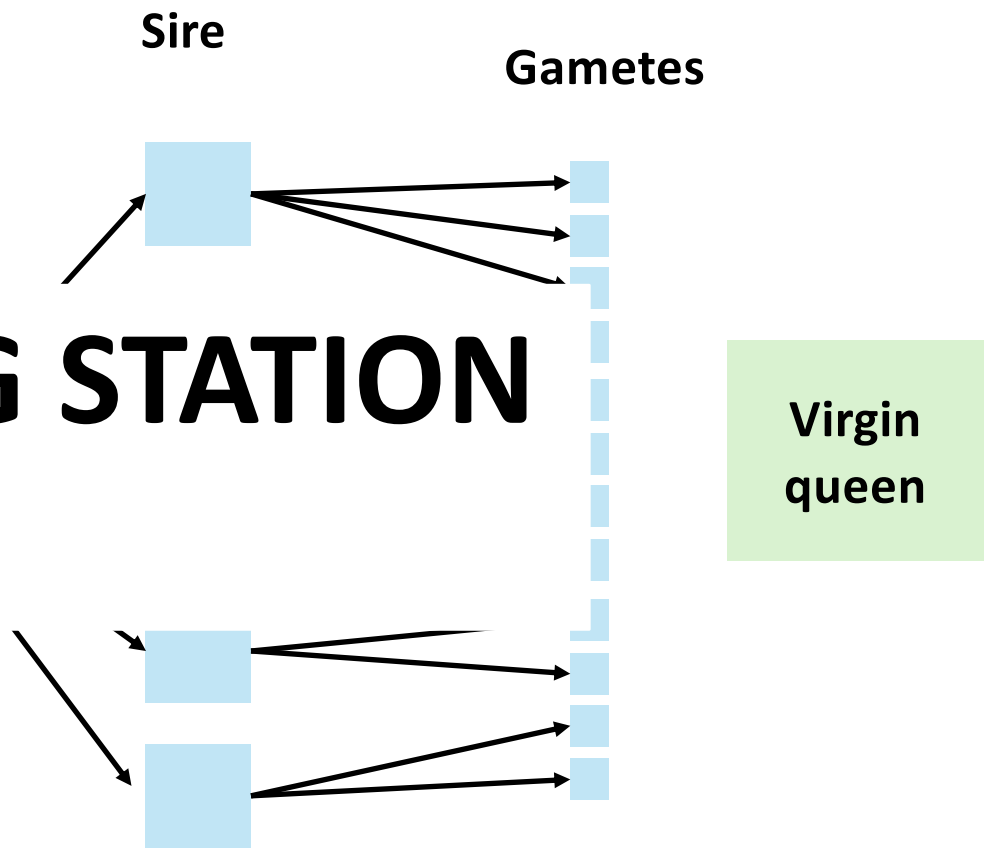

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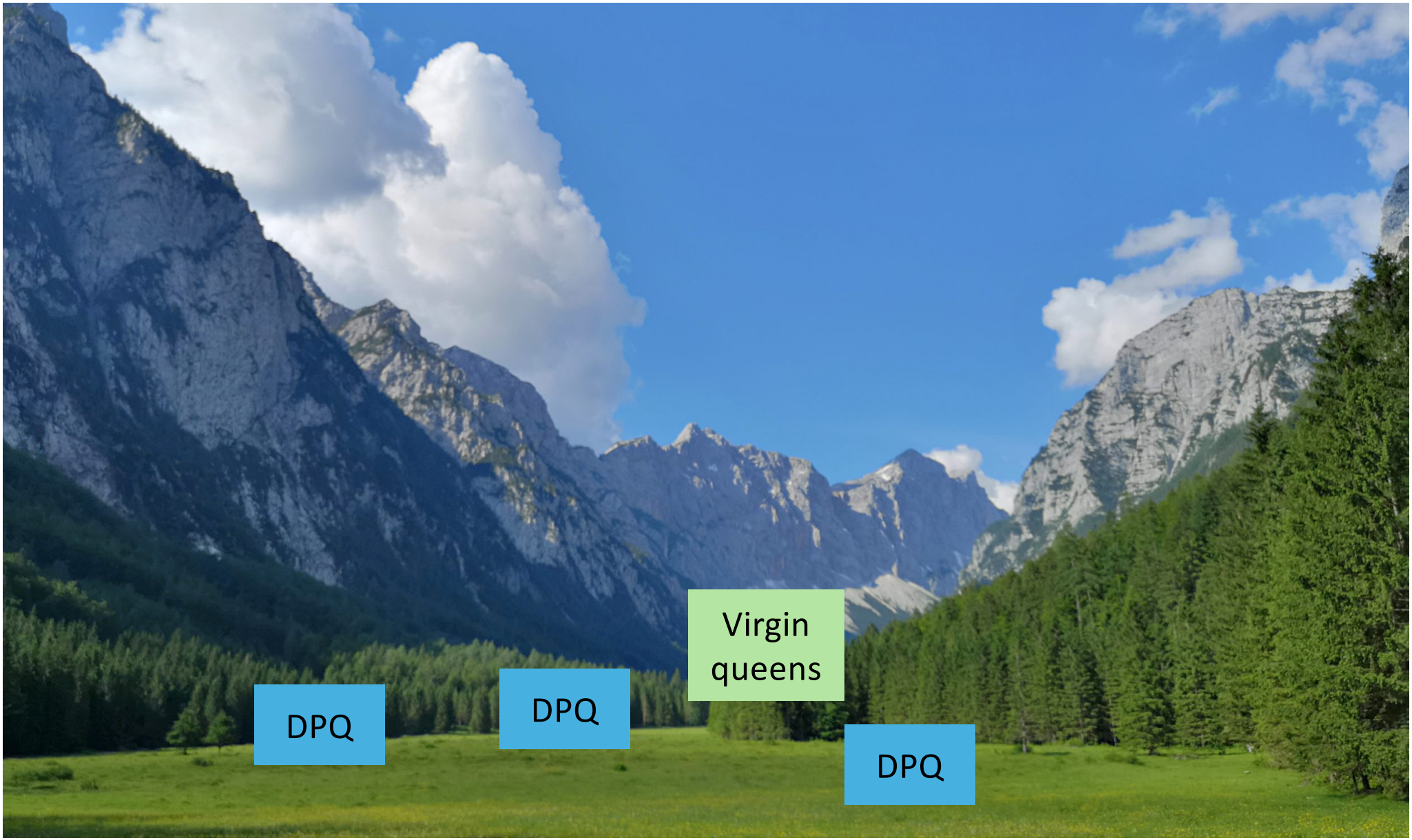
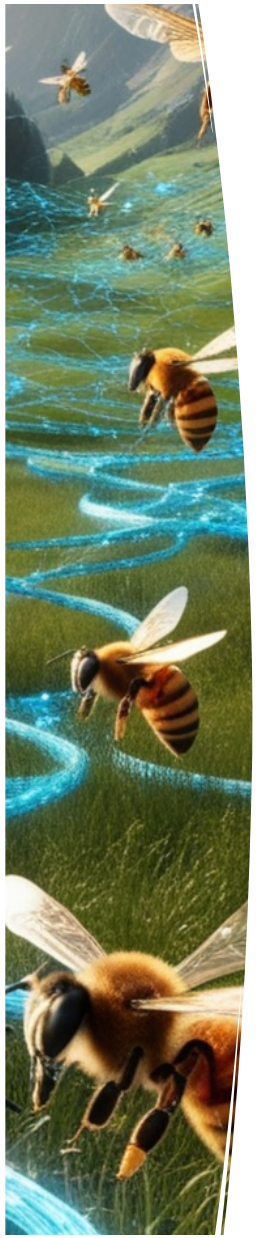

DPQ
DPQ
Virgin queens
DPQ



Evaluate success of mating control

Determine the number of patrilines

EAAP Insect-IMP | Jan 2025 | Athens | jana.obsteter@kis.si

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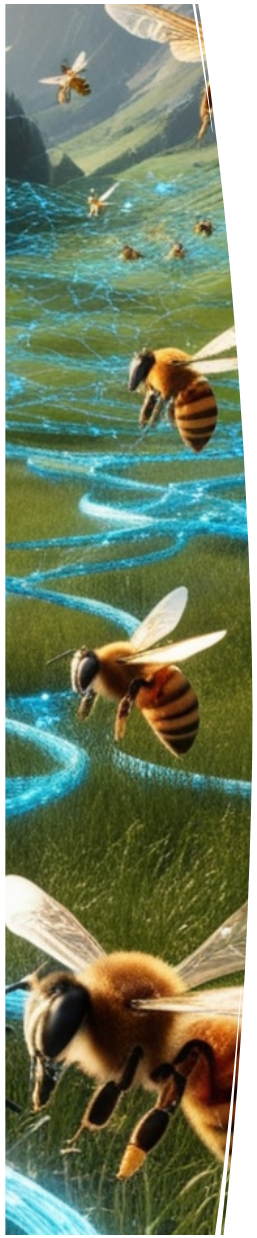

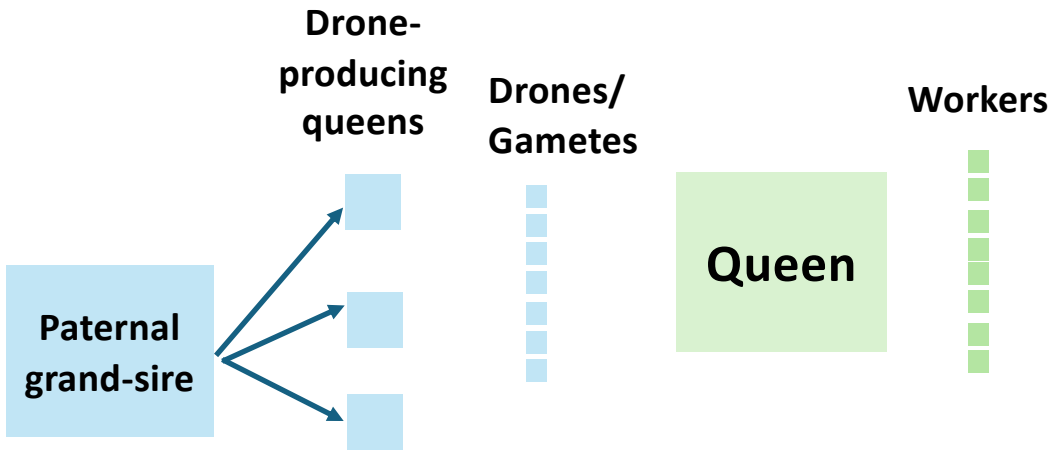

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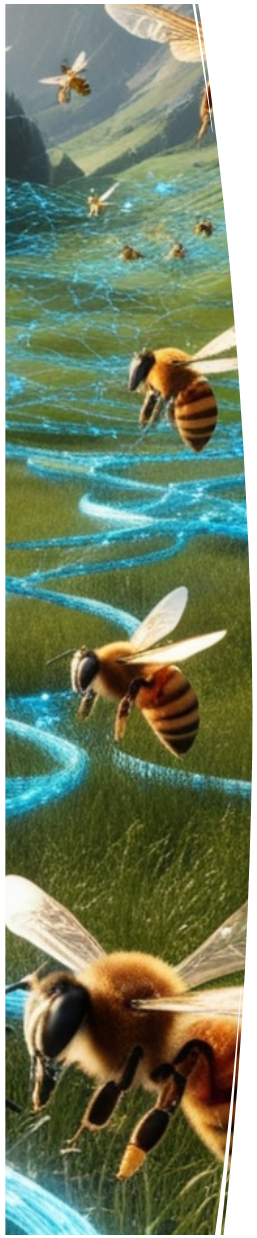

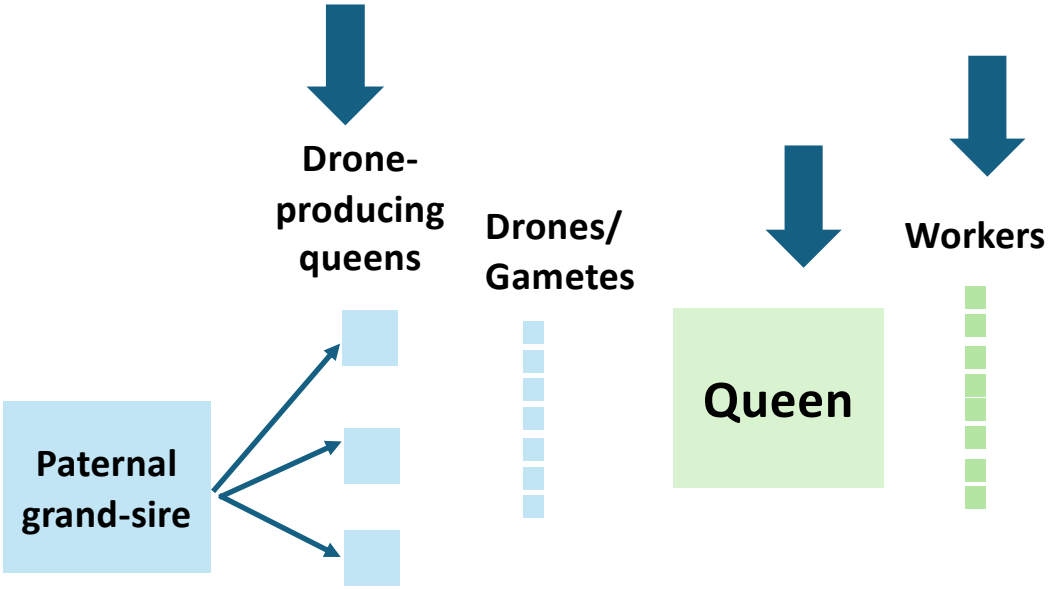

Genotype queen + brood/workers + drone producing queens

Evaluate success of mating control

Determine the number of patrilines

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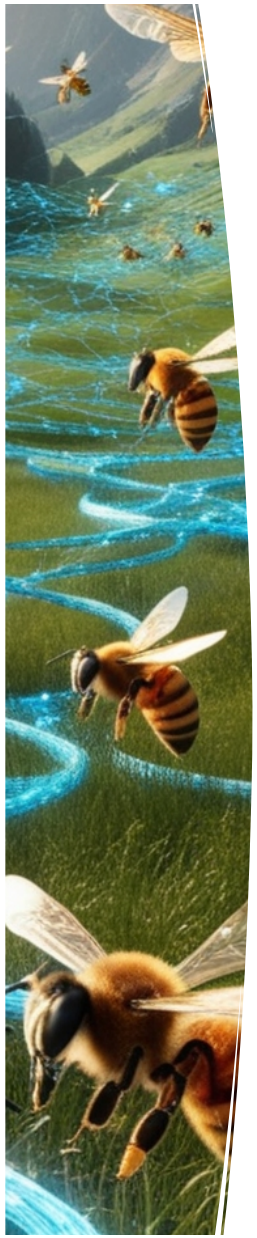

Reconstruct the pedigree
Bee | queen | drone-producing queen

Genotype queen + brood/workers +
drone producing queens

Evaluate success of mating control

Determine the number of patrilines

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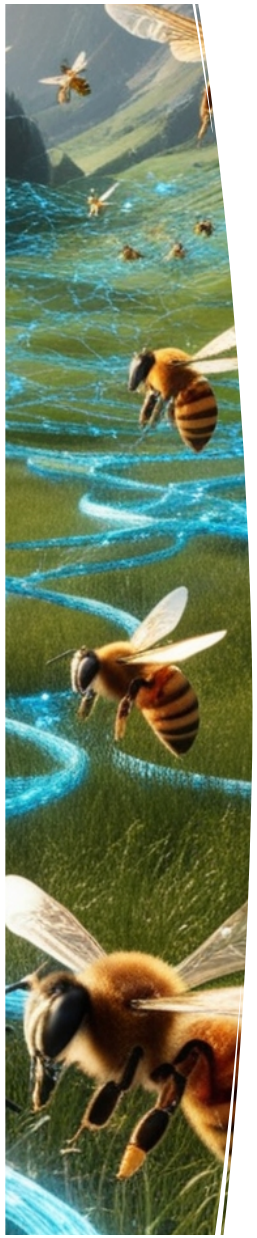

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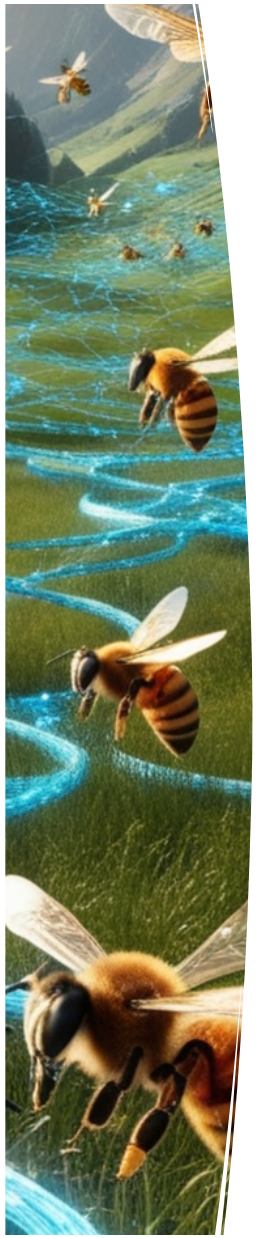

Reconstruct paternal haplotypes and count the number of unique ones in a colony

?

Reconstruct the pedigree
Bee | queen | drone-producing queen

Genotype queen + brood/workers + drone producing queens

Evaluate success of mating control

Determine the number of patrilines

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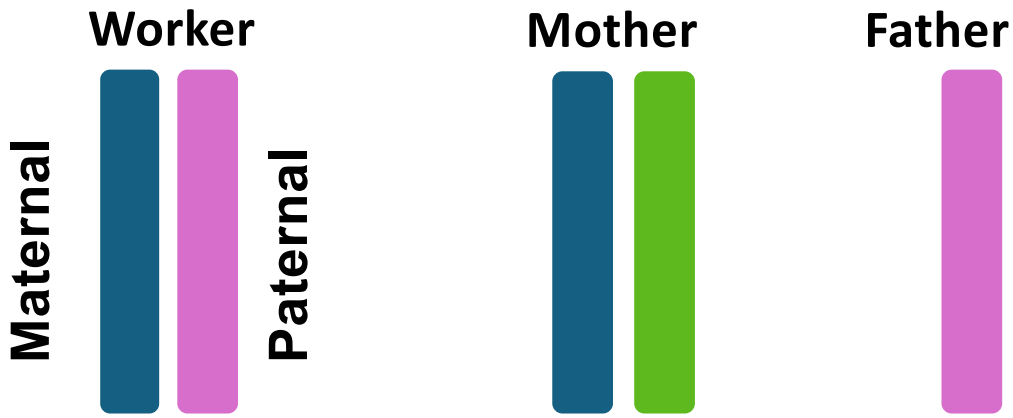
Reconstruct paternal haplotypes



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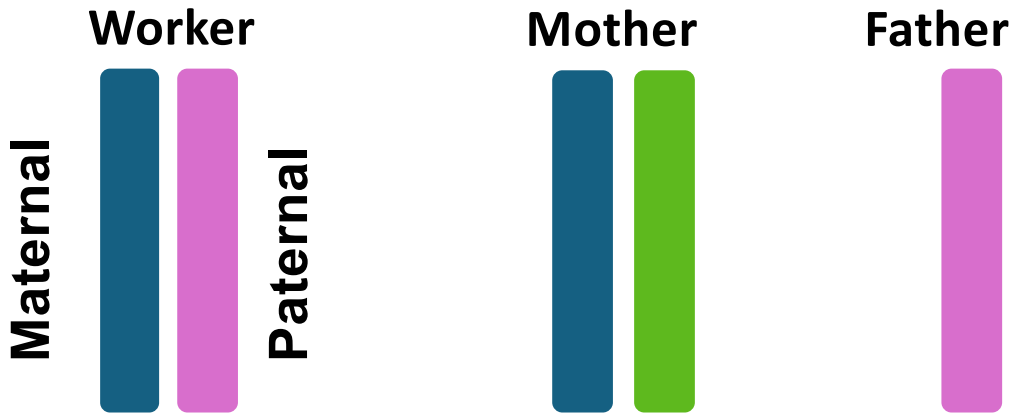
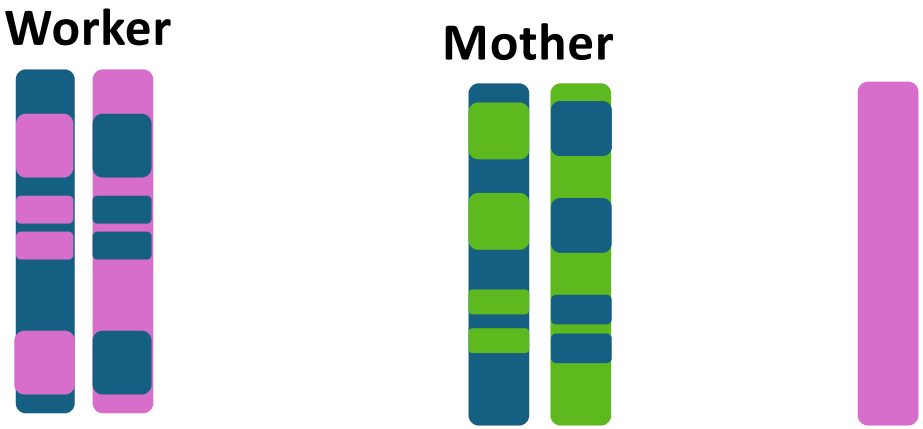
Reconstruct paternal haplotypes





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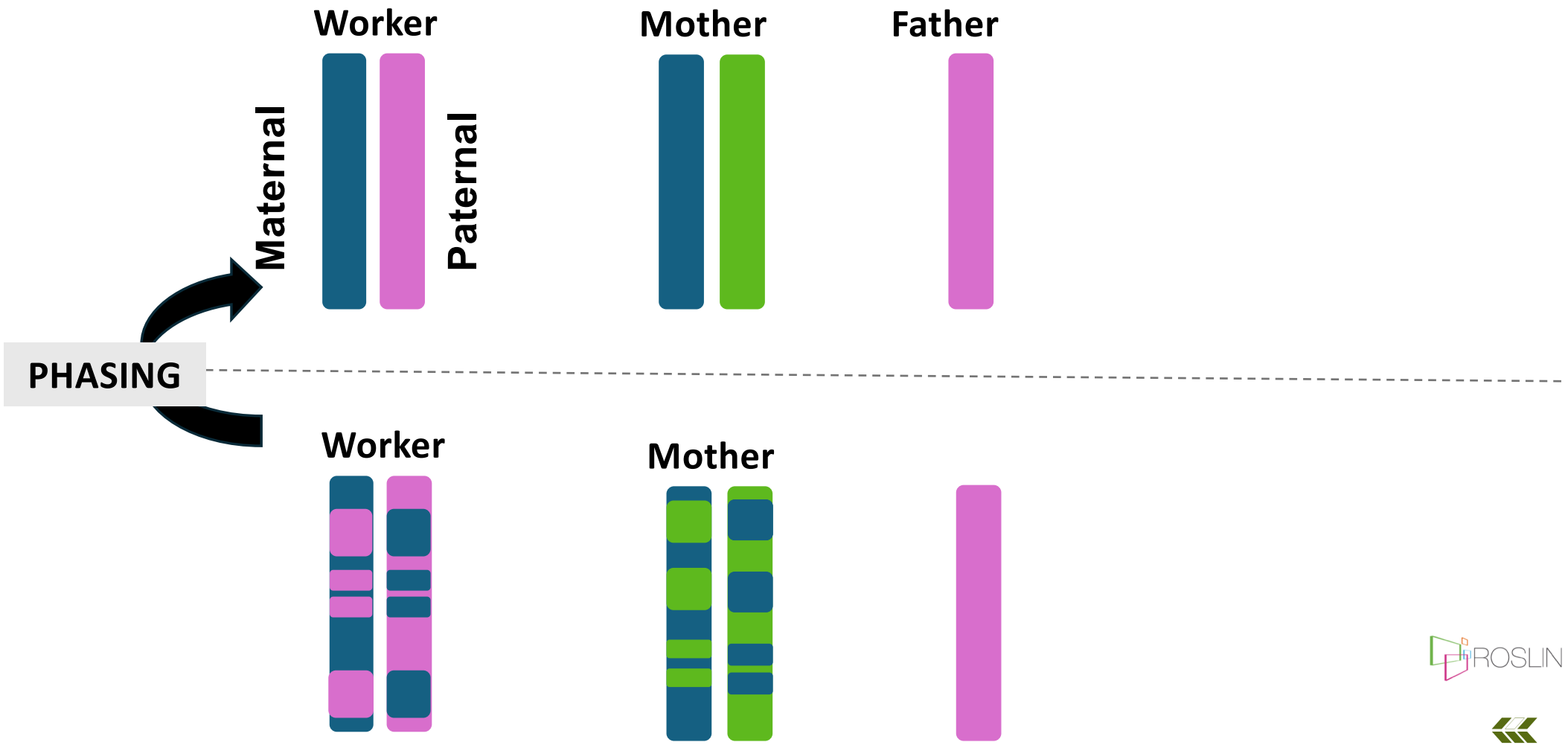
Reconstruct paternal haplotypes



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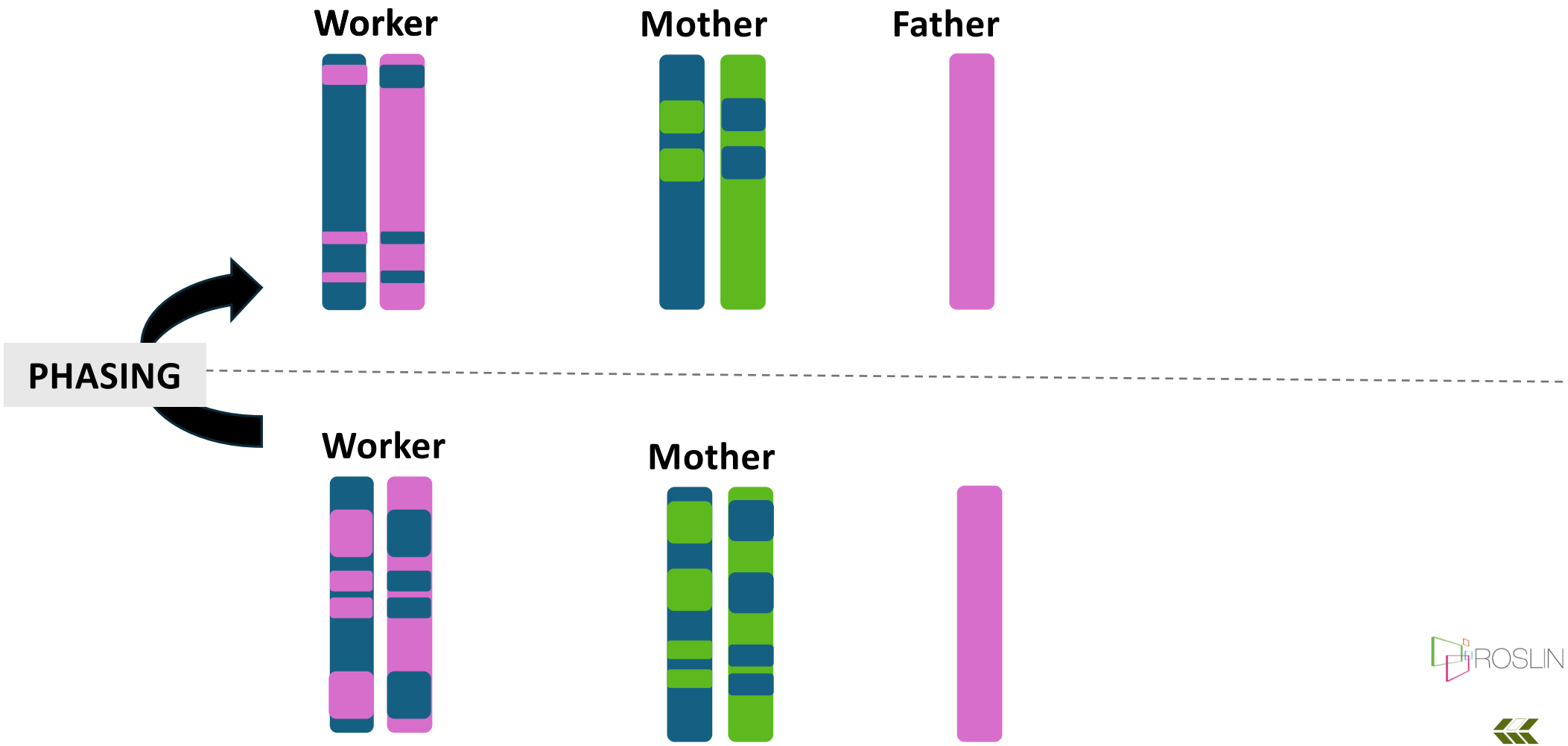
Reconstruct paternal haplotypes



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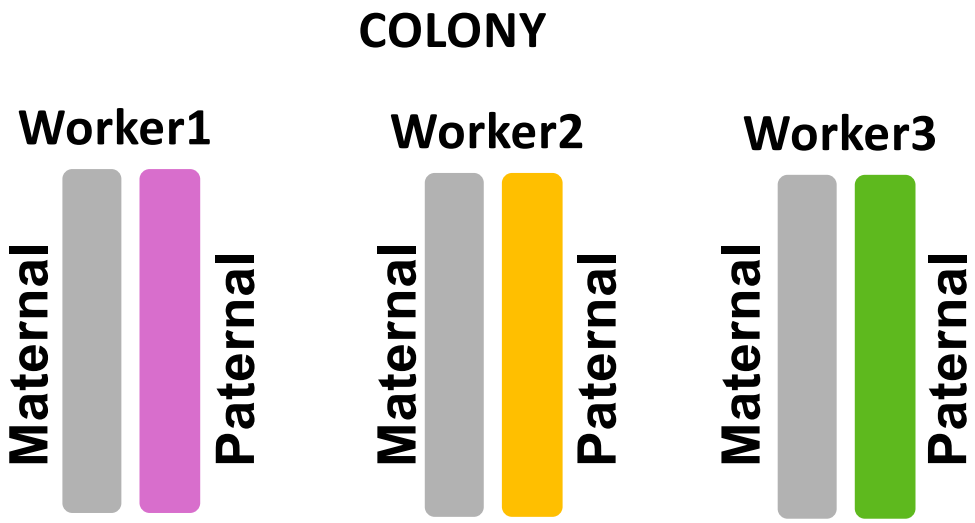
Count unique paternal haplotypes



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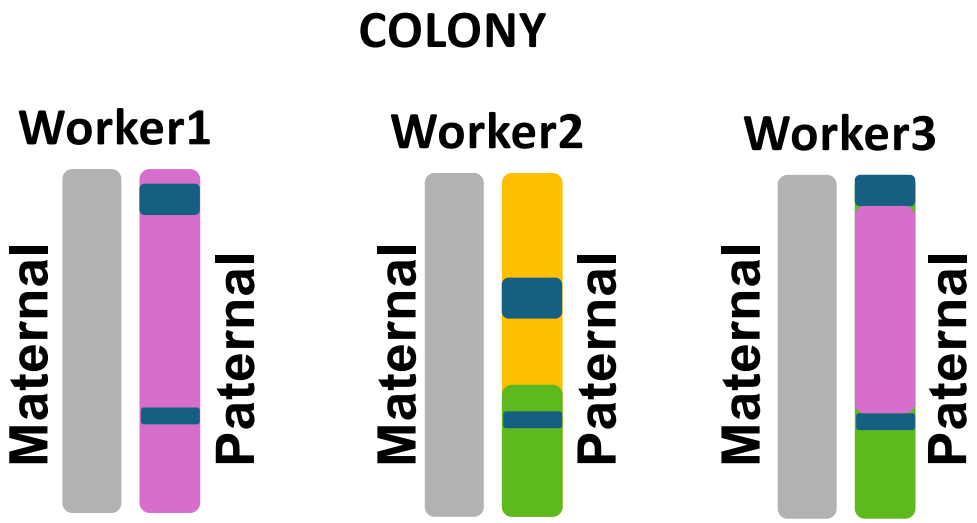
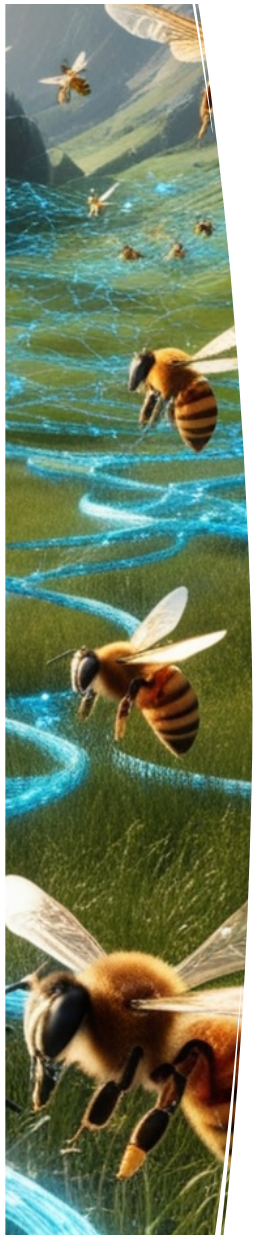
Count unique paternal haplotypes





Data

Real data

Genotyped **queens, workers + sister drones producing queens**

1.7K SNPs

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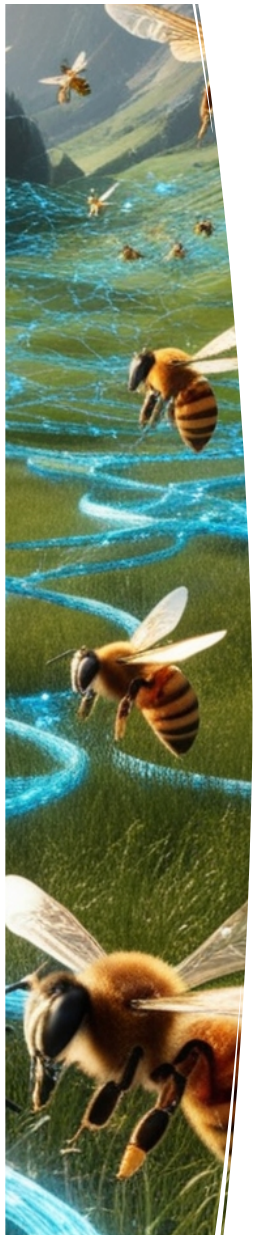


Data

Real data

Genotyped **queens, workers + sister drones producing queens**

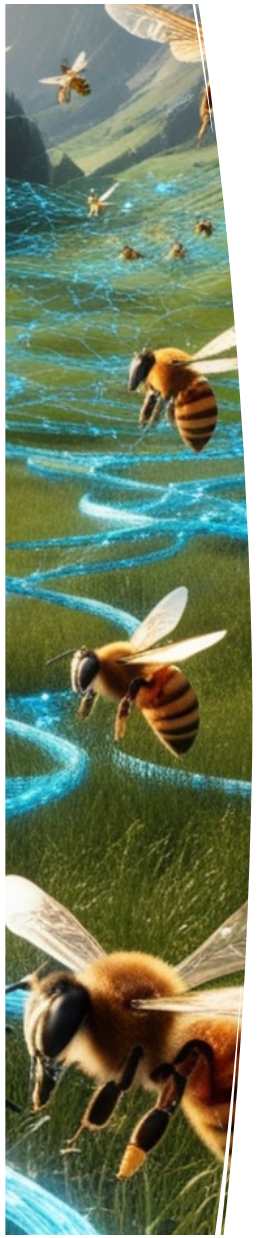
1.7K SNPs

Simulated data

SIMplyBee: genomic data (+ genotyping errors)

Mimicked real data

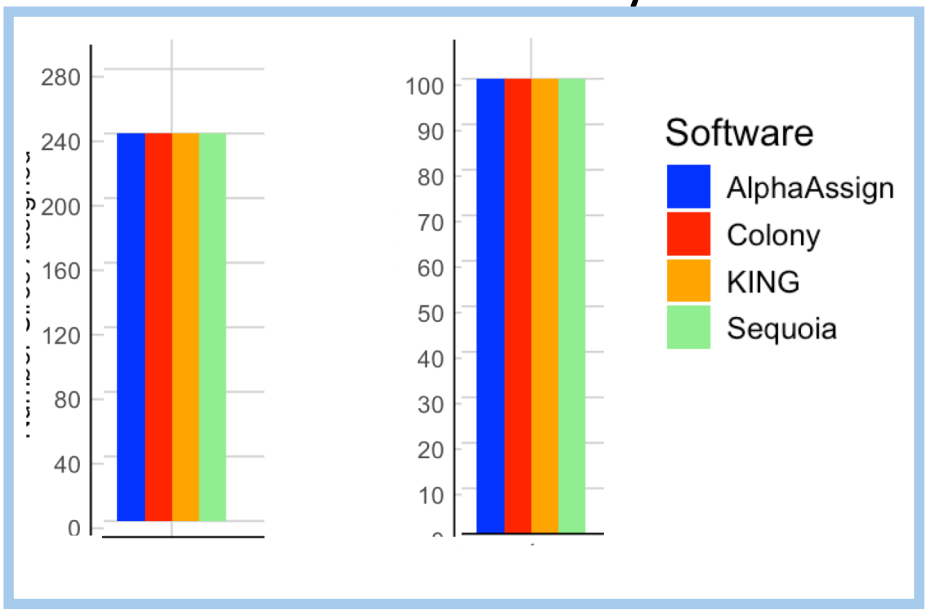
1.7K SNPs



Pedigree reconstruction

Number of sires assigned

Accuracy



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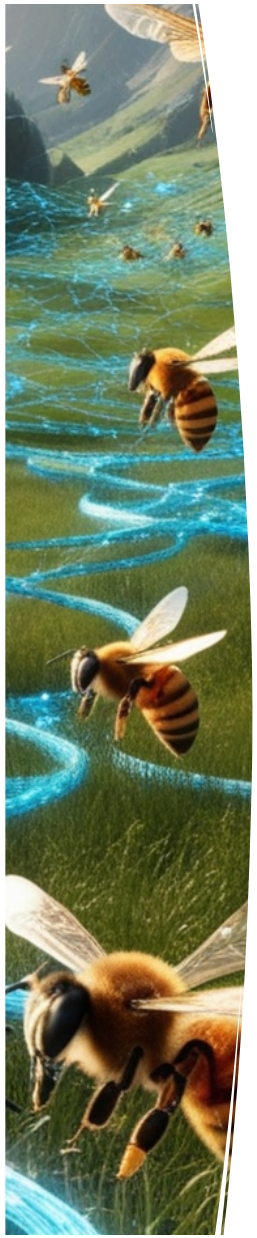

Pedigree reconstruction

Number of sires assigned

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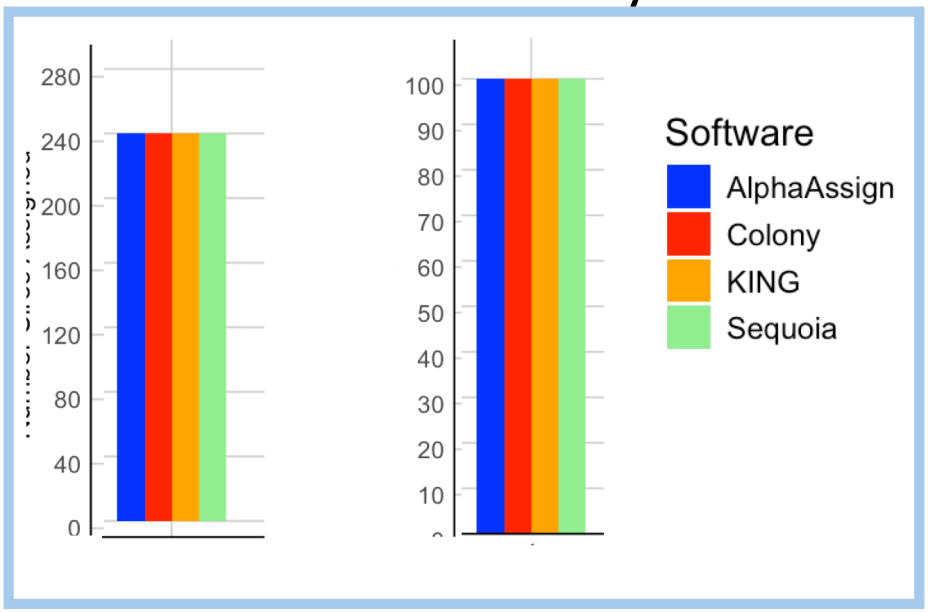
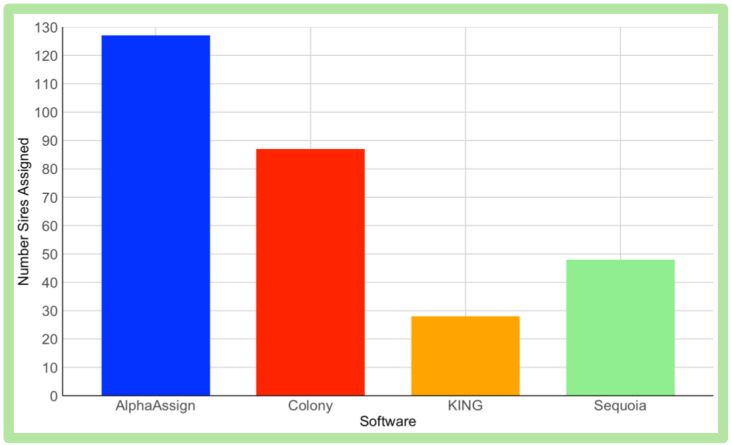


Number of sires assigned – real data



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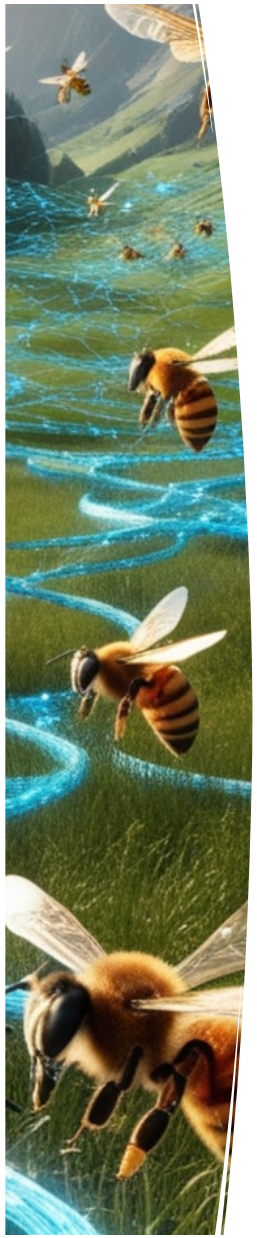

Phasing + haplotype parental origin

- Beagle + own code (runs of matches)

Offspring haplotype	1	0	0	1	0	1	1
Parent genotype	2	0	1	2	2	1	1

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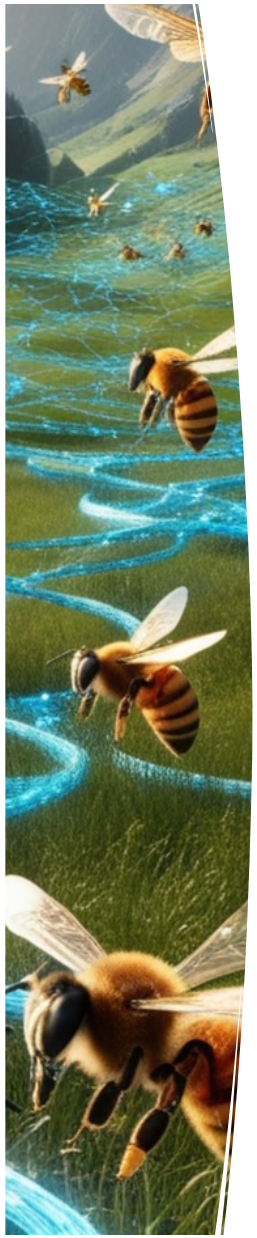
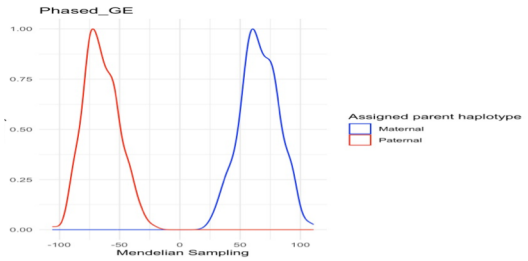
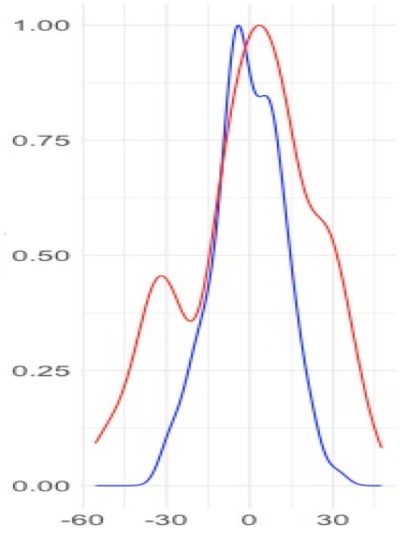


Phasing + haplotype parental origin

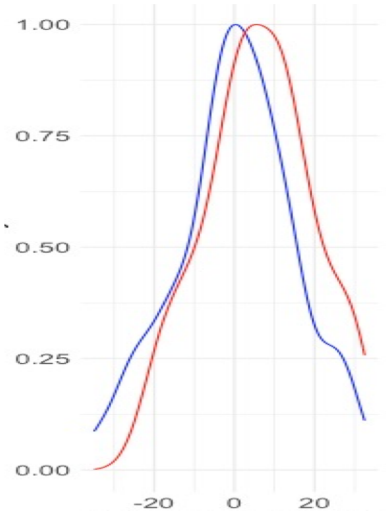


- Beagle + own code
- Success? Gametic Mendelian sampling terms

Simulated



Real



Maternally assigned

Paternally assigned

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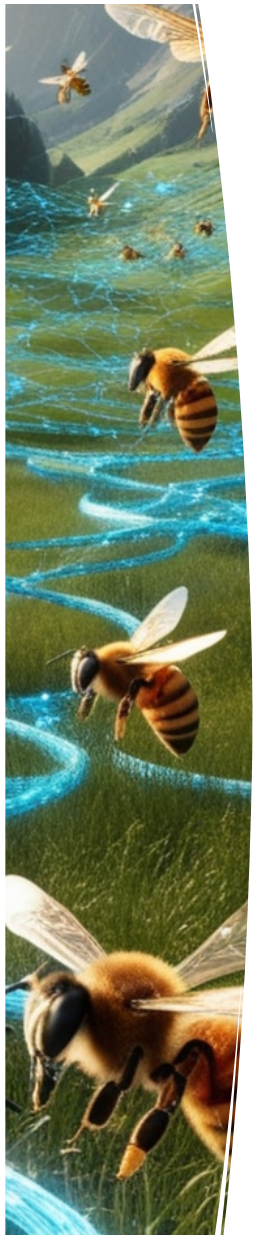
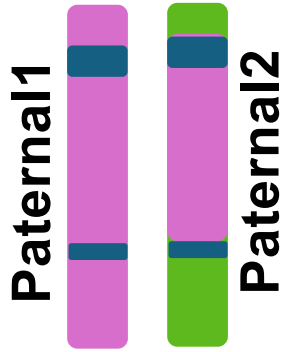
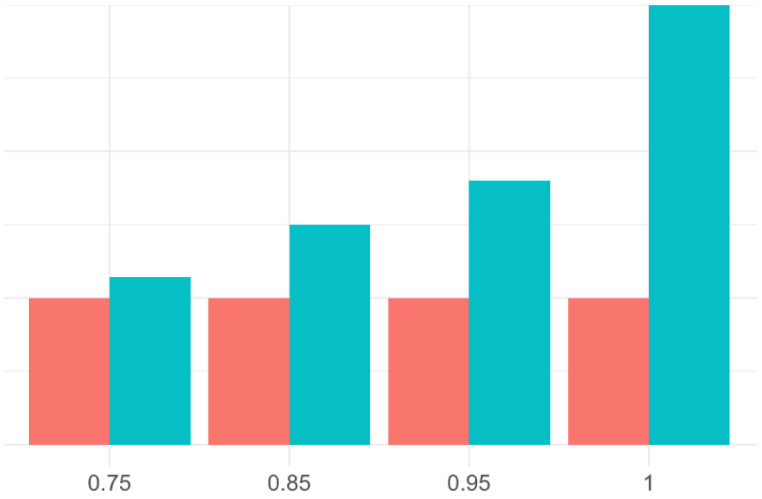


Number of patrilines

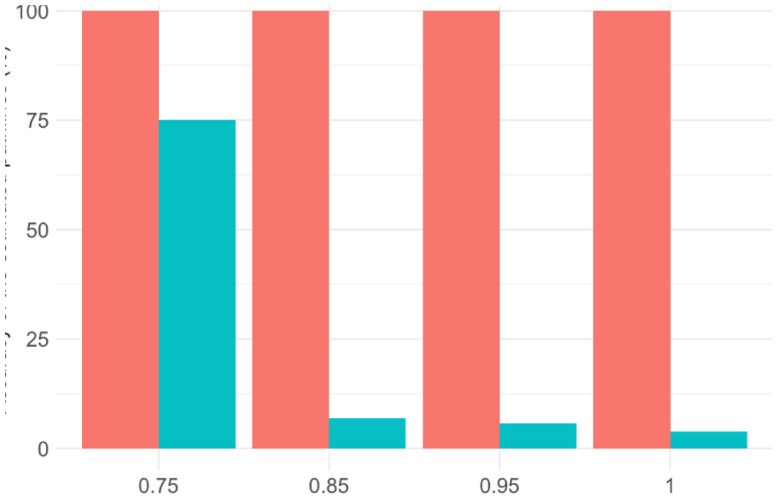
- #unique paternal haplotypes are in a colony
- Similarity metric 0.75 - 1



#PATRILINES



ACCURACY



SIMILARITY THRESHOLD

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