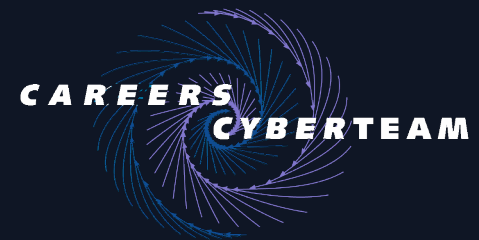# Parallel Analysis of Variants in Multiple Bear Genomes

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Mentor: Galen Collier, Rutgers University

Researcher: Dr. Andrey Grigoriev, Rutgers University

March 10, 2021

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Polar Bear/ Brown Bear Comparison

Figure 1 - comparison of brown bear (left) and polar bear (right) head and facial area.

Figure 2 - Comparison of brown bear (left) and polar bear (right) whole body, not to scale.
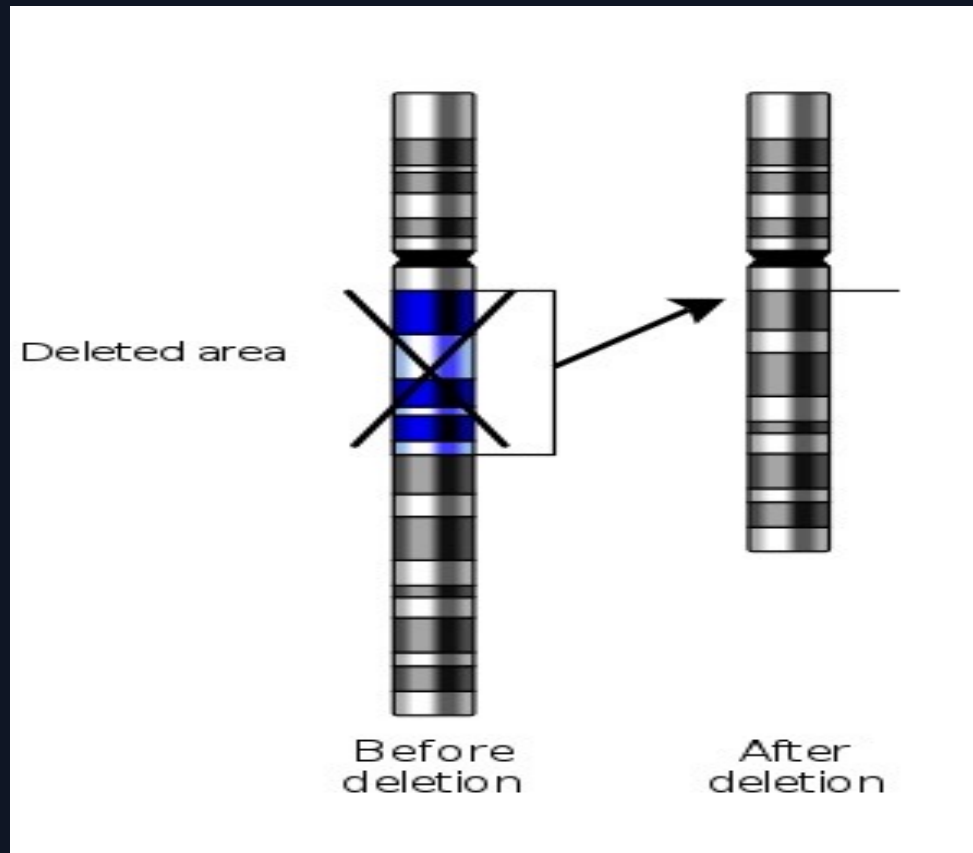
Objectives

- Exploit HPC approaches to analysis of gene sequencing of brown and polar bears
- Improve and speed detection of common variants in related genomes
- Establish evolutionary trajectory of corresponding species
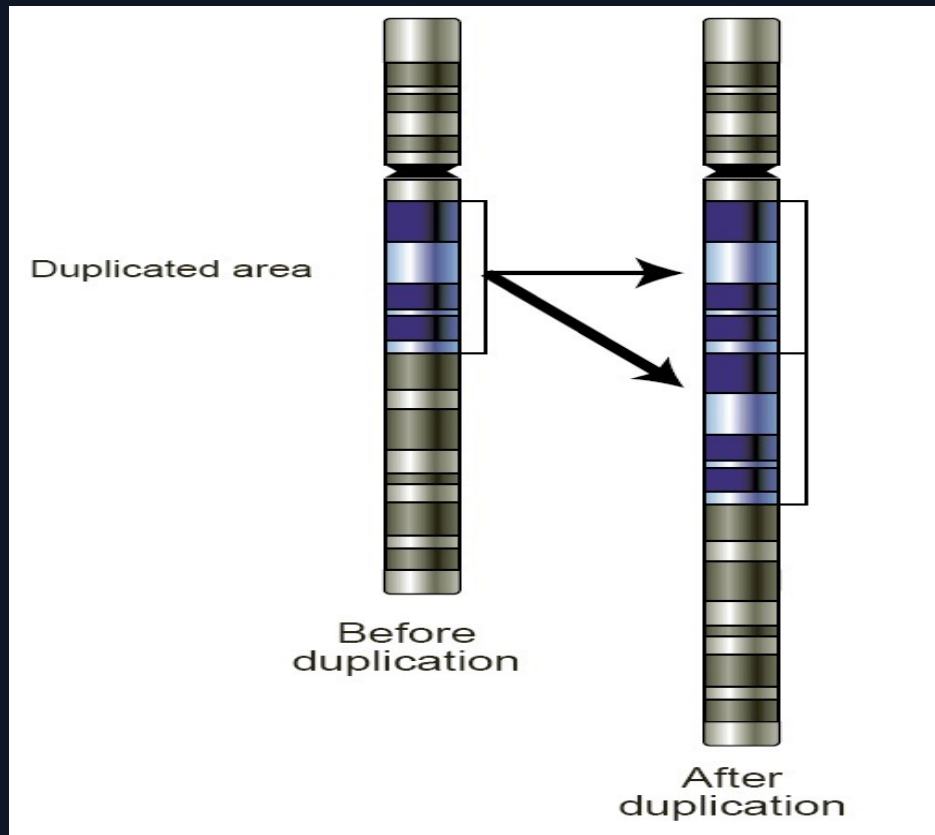
Single Nucleotide Polymorphism
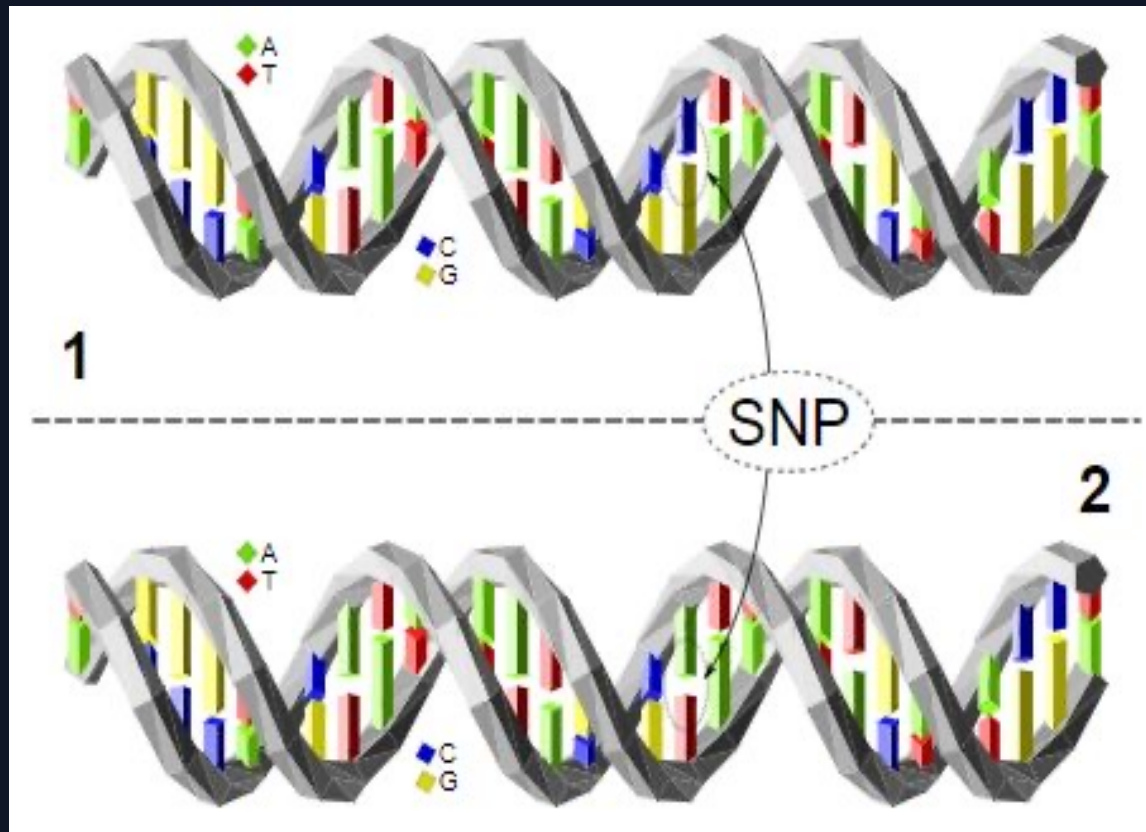
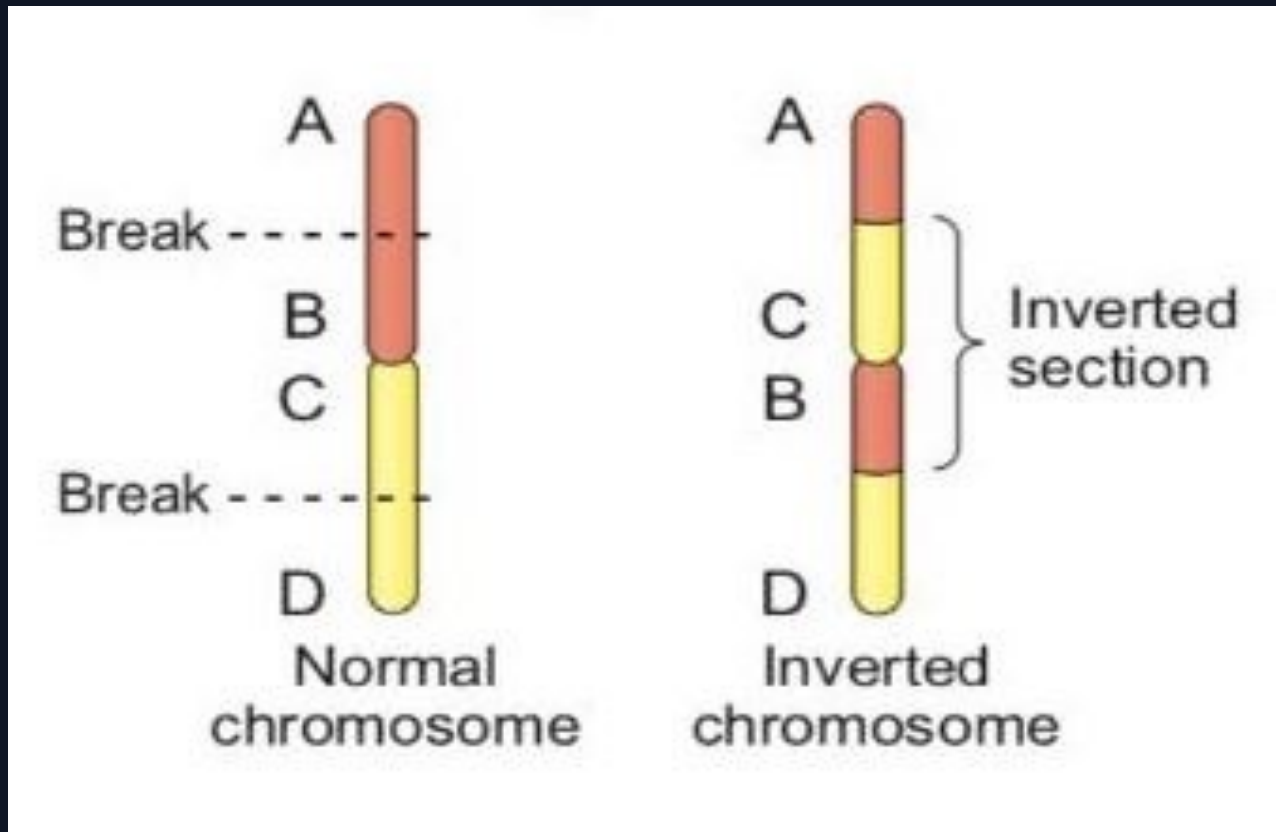# INDELs: Insertion/Deletion <50 bps

Deleted area

Before deletion

After deletion

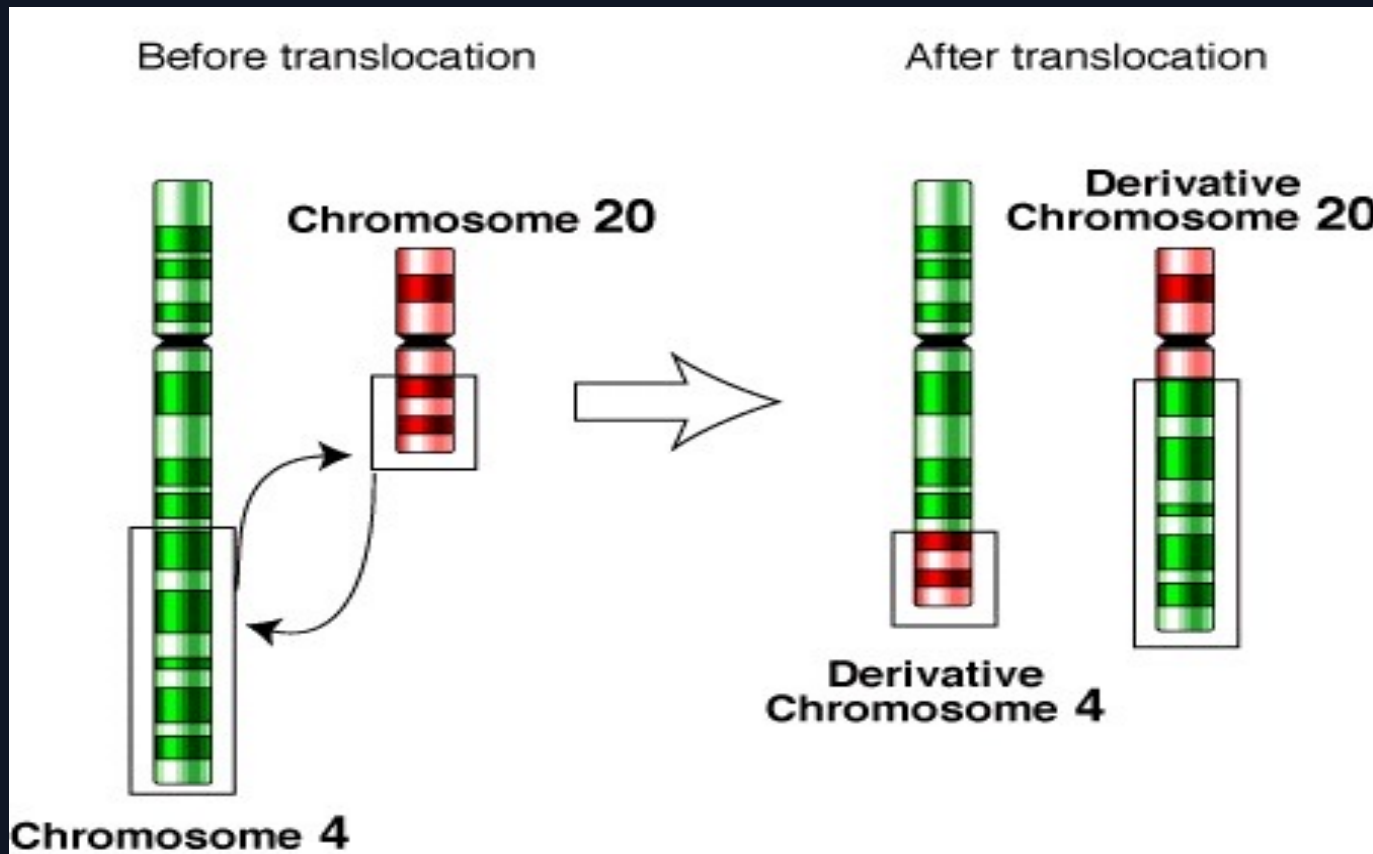# Structural Variant: Duplication >50 bps

Structural Variant: Inversion >50 bps

Structural Variant: Translocation > 50 bps

GROM

- GROM-Genome Rearrangement Omni-mapper
- Developed in Dr. Grigoriev's lab
- Comprehensive variant detection with 1 algorithm
- Superior speed and accuracy

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Goals

- Implement joint analysis of multiple samples

- Incorporate parallelization methods

- Investigate possibilities of incorporating machine learning methods

- Document code and results

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Parallel Analysis of Variants in Multiple Bear Genomes

- Timeframe
  - February 19, 2021
  - July 31, 2021

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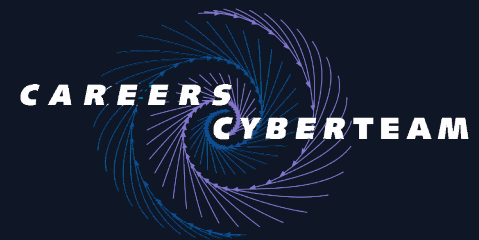
Parallel Analysis of Variants in Multiple Bear Genomes

- Goals for Next Month
  - Become familiar with GROM pipeline, data, and concepts
  - Expand GROM for joint analysis of multiple samples

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Parallel Analysis of Variants in Multiple Bear Genomes

- ## What I hope to learn
  - Improved understanding of programming in HPC environment
  - Better understanding of computational biology