Universität Münster

Assessing Assembly Quality's Impact on *De novo* Gene Identification

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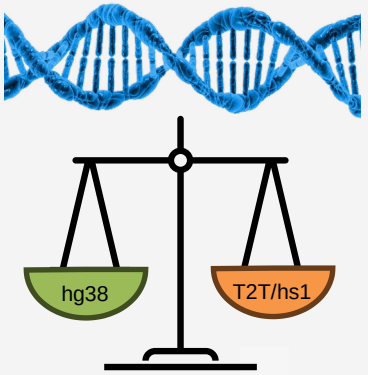
Background: With the advancement of new sequencing technologies, more complete genomes are available for us to ask and answer biological questions. Because of this enhanced completeness, we expect this would allow greater power to detect *de novo* genes compared to older assemblies. This has not yet been formally evaluated.



Aim: For one chromosome in hg38 and hs1, compare how many *de novo* genes are identified using DENSE.

Methods: The student will learn some of the comparative genomic techniques including file manipulation, use of phylostratigraphy for *de novo* gene identification using DENSE, and if time permitting, methods to characterize the new *de novo* genes.

Requirements: Some experience with command line/bash or willingness to learn. Interest in genomics and bioinformatics.

Literature: De Novo Genes – Zhao Annual Review of Genetics 2025; DENSE – Roginski GBE 2024; Human T2T - Nurk Science 2022; Ape T2T - Yoo Nature 2025

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