



Genomics of Human Diseases

2019 Dragon Star Bioinformatics Course

Housekeeping issues

- **Course date: July 29 – August 2, 2019**
- **Theme: Genomics of Human Diseases**
- Morning (9am-12pm with break): lecture session on basic concepts and bioinformatics methods to study the genomics of human diseases
- Afternoon (2pm-4pm): computing exercise to practice software tools discussed in the morning
- Lecture notes and computing exercises in English
- The lecture slides and exercises are shared to students. The computing exercise instructions are also available at GitHub: <https://github.com/WGLab/dragonstar2019>

Housekeeping issues (continued)

- The afternoon computing exercise session will be split into four rooms, with maximum capacity of 110, 110, 55 and 55 students, respectively.
- We will have teaching assistants in each room to address questions and troubleshoot problems.
- Each student will be assigned a separate IP address to connect to a cloud server by SSH.
 - The username and password are `biouser` and `biouser`, respectively.
 - You should change your password using `passwd` command upon logging into the server.
- Each cloud server is only used by one student, and is not shared with the rest of the class.

Acknowledgements

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Outline of the five days

- Day 1: genomic technologies, typical file formats
- Day 2: alignment of sequencing data and genome assembly
- Day 3: detection of structural variants, phenotype-driven variant annotation/interpretation
- Day 4: SNP and sequencing based association studies, rare or de novo variants in human diseases
- Day 5: RNA-Seq and other advanced topics (artificial intelligence, somatic mutation, etc)

For questions and comments before and after class, contact me at kaichop@gmail.com