

**Seminar Presentation:**

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The University of Arizona

**June 15, 2017**

2:00-3:00 PM

Shantz Bldg. 440

**A Case Study on the Application of Bioinformatics:
Building gap-free reference genome assemblies with new technologies and multiple datatypes**

**Abstract**

New sequencing technologies have revolutionized our ability to rapidly and affordably generate vast quantities of sequence data. Once generated, raw sequences are assembled into contigs or scaffolds. However, these assemblies are mostly fragmented and inaccurate at the whole genome scale, largely due to the inability to integrate additional informative datasets (e.g. physical, optical and genetic maps). To address this problem, Dr, Zhang developed a semi-automated software tool—Genome Puzzle Master (GPM)—that enables the integration of multiple genomic signposts to edit and build ‘new-gen-assemblies’ that result in high-quality ‘annotation-ready’ pseudomolecules. GPM is a web-based pipeline and an important part of a Laboratory Information Management System (LIMS) which can be easily deployed on local servers for any laboratory. Dr. Zhang will present how to apply bioinformatics tools to build Platinum Standard reference genome assemblies with the integration of new technologies and multiple datasets.

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