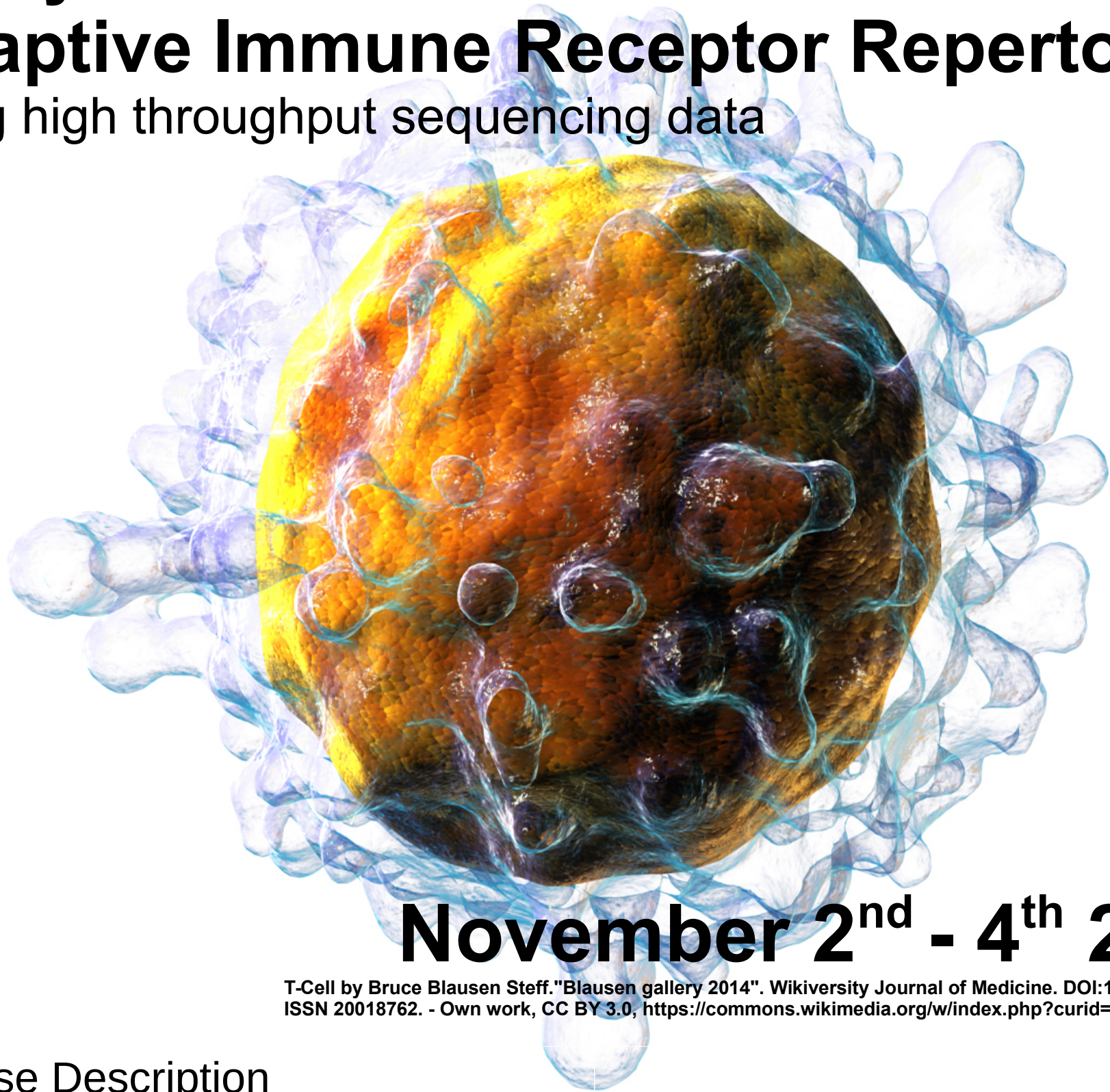


AAIRR16

Analysis of Adaptive Immune Receptor Repertoires using high throughput sequencing data



November 2nd - 4th 2016

T-Cell by Bruce Blausen Steff. "Blausen gallery 2014". Wikiversity Journal of Medicine. DOI:10.15347/wjm/2014.010. ISSN 20018762. - Own work, CC BY 3.0, <https://commons.wikimedia.org/w/index.php?curid=28761827>

Course Description

This course will cover the analysis of B and T cell repertoires (adaptive immune receptor repertoires, or AIRR) from high-throughput sequencing data using bioinformatics workflows. Topics include germline allele assignment, identification of clones, and visualisation/analysis of clonal frequencies. The course will also cover emerging standards (VDJML, Change-O) in the analysis and reporting of Adaptive-immune Receptor Repertoire (AIRR) data. In addition to an introduction to software used, such as IgBLAST, pRESTO, Change-O, etc., the course will also provide an introduction to the use of Jupyter notebooks for conducting exploratory analyses and the Common Workflow Language to automate analyses.

Instructor:

Simon D. Frost

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Course website:

<http://gtpb.igc.gulbenkian.pt/AAIRR16>

