

Combi Seminar

Wednesday, 11.7.18 | 1:30 | Foege Auditorium



Dr. Jesse Bloom

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“Single-cell virus sequencing of influenza infections that trigger innate immunity”

abstract:

Single-cell transcriptomics has revolutionized the study of cellular processes that are driven by changes in gene expression. But during viral infection, much of the variation in outcome may be due to mutations in viral genes that are not captured simply by using 3'-end sequencing to quantify the levels of transcripts. To determine if this is the case, we have developed an approach to combine 3'-end based single-cell transcriptomics with full-length PacBio sequencing of viral genes in single influenza-infected cells. Our results show that viral genetic variation makes a significant contribution to heterogeneity in infection outcome and innate-immune induction.

Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Combi website at <http://www.gs.washington.edu/news/combi.htm>

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