

# Mathematical & Computational Biology Seminar

Organizer: Lior Pachter

Wednesday, 2:00–3:00pm, 939 Evans

---

Mar. 11    **Rahul Satija**, University of Oxford

*Studying gene regulation with statistical alignment*

Despite the large quantity of genomic sequence data available in multiple related species, predicting sequences governing gene regulation in non-coding DNA remains an extremely challenging task. One difficulty arises from errors or biases present in sequence alignments, which may confound further comparative sequence analyses. Statistical alignment methods can be used to remove the traditional dependence of comparative sequence analysis on a single DNA sequence alignment, and we have developed new software tools which are robust to alignment uncertainty and error. I will also present a modification to the multiple alignment tool FSA that uses known information on transcription factor DNA binding specificity to significantly improve alignment accuracy in non-coding regions. Our results allow us to predict and analyze the evolution of binding sites on a genomic scale. This is joint work with Lior Pachter, Robert Bradley (Berkeley), Jotun Hein and Gerton Lunter (Oxford).