“Faster, Smaller, Better : How improved methods can facilitate better biology”

As the cost of high-throughput sequencing has plummeted, the variety of different sequencing assays available, the frequency with which we perform sequencing, and the volume of data being generated, has increased exponentially. At the same time, many biological systems are notoriously complex, and the experimental assays we use to measure them are often noisy and biased. Thus, we are quickly approaching a regime in which the bottleneck will cease to be our ability to acquire data, and will instead become the computational costs associated with analyzing this data, and trying to derive precise, robust, and interpretable answers to the biological questions we wish to ask.

I will talk about the methods that my lab, along with our collaborators, have been developing, which center around the concept of analysis-efficient computing. I will explain how new approaches to certain analysis tasks can be made simultaneously much faster and more accurate than traditional methods. Specifically, I will discuss our recent work in fast, accurate and bias-aware methods for transcript quantification, as implemented in our tool Salmon. I will also describe the subsequent improvements we have made to this method, including the derivation and use of a data-driven approach to likelihood factorization to improve inferential accuracy and the development of a hybrid read-mapping approach called selective alignment. Finally, I will discuss our current work on a scalable, memory-efficient, and fast graph-based index for aligning reads to a collection / population of genomes and transcriptomes, and how this might help improve both the speed and accuracy of a number of genomics tasks.

Date:  Monday, November 6th, 2017
Time:    16:00 h
Room:    Lounge (level 13), Klingelbergstrasse 61
         (vis-à-vis Pharmazentrum)
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