日程: 2011 年 06 月 23 日 (木) 15:00〜
場所: 臨海副都心センター別館８階コラボレーションコーナー
講演者/発表者: Timo Lassmann (RIKEN OSC Senior Researcher)
主催チーム:　配列解析チーム

タイトル
Probabilistic Models in Next-Gen Sequence Analysis

概要
The functional annotation of genomes is being accelerated by high
throughput assays employing next generation sequencing. The readout of the
various -seq experiments are millions of short reads which have to be placed
back onto a reference genome. Avoiding mistakes at this stage is critical
as falsely placed reads can lead to false hypothesis. I developed the method
Delve to improve the interpretation of next-gen assays by modeling read
sequences, sequencing errors and local read densities on the genome. If
time permits I will also talk about a HMM based approach to classify
transcriptional start sites.