

## Modeling Probe-Specific Microarray Hybridizations for Diploid Resequencing

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Refreshments at 2:30, Talk from 3:00-4:00

Basecalling is a critical step of the analysis of DNA resequencing microarray data for SNP discovery and genotyping. For microarrays hybridized with DNA derived from diploid organisms, basecalling with high accuracy at high call rates is a challenging task. Current methods sometimes do not produce satisfactory results. We explored using physical models based on the sequences of the probe and the target to predict feature intensities in resequencing microarrays. Based on these intensity-predicting models, a new basecalling method (Model-P), which takes into consideration the expected feature intensities for different potential genotypes, was developed. Model-P is shown to have better performance at high call rates compared with ABACUS, the current state-of-the-art method, on a test dataset and on relatively AT-rich regions, in general.

### *Biography*

David Kulp received his Ph.D. in 2003 in Computer Engineering (Bioinformatics) from UC Santa Cruz. He was a Fulbright Scholar in Computer Science at the University of Canterbury in New Zealand. His primary research interest is bioinformatics. Currently active topics are genomic gene-finding, microarray designs for sequencing by hybridization and associated basecalling algorithms, fast sequence searching algorithms using physical models of hybridization, and the integration of quantitative expression and genetic markers.