1) Abstract:

Background: The ENCODE consortium produced functional genomics data in many cell types. Our goal is to annotate the active genomic functional elements in this diverse set of cell types. The challenge is that many of these cell types have little data available. We aim to leverage existing high quality annotations from six well-studied cell types in the production of annotations for the remaining cell types.

Approach: We use the genome annotation software Segway to perform annotations, augmented with *entropic graph-based regularization* (EGBR) to leverage existing annotations. We chose cell types that had at least two out of four distinct types of assays (DNase-seq, RNAseq, histone modification ChIP-seq and transcription factor ChIP-seq).

Results: We will produce functional annotations of 73 cell types. These annotations will be made publicly available on the UCSC Genome Browser. In addition, the project has successfully migrated the Segway+EGBR annotation software to the DNAnexus cloud computing platform.