**EXIT SEMINAR**

**Emily Hindalong**

**B.Sc., University of British Columbia, Canada, 2011**

**Friday, August 7th, 2015 at 11 AM**

**LOCATION: Gordon & Leslie Diamond Lecture Theatre, BCCRC**

**A Study of Methods for Learning Phylogenies of Cancer Cell Populations from Binary SNV Profiles**

**Abstract:**

An accurate phylogeny of a cancer tumour has the potential to shed light on numerous phenomena, such as key oncogenetic events, relationships between clones, and evolutionary responses to treatment. Most work in cancer phylogenetics to-date relies on bulk tissue data, which can resolve only a handful of genotypes unambiguously. Meanwhile, single-cell technologies have considerably improved our ability to resolve intra-tumour heterogeneity. Furthermore, most of these methods rely on classical phylogenetic approaches such as Neighbor-Joining, which puts all extant species on the leaves of the tree. But in cancer, ancestral genotypes may be present in extant populations. There is a demand for scalable methods that can capture this phenomenon.

We have made progress on this front by developing the Genotype Tree representation of cancer phylogenies, implementing three methods for reconstructing Genotype Trees from binary SNV profiles, and testing these methods under a variety of conditions. Additionally, we developed a tool that simulates the evolution of cancer cell populations, allowing us to systematically vary evolutionary conditions and observe the effects on tree properties and reconstruction accuracy.

Of the methods we tested, Recursive Grouping and Chow-Liu Grouping appear to be strong candidates for learning phylogenies over hundreds and potentially thousands of cancer genotypes. Of the two, Recursive Grouping has the strongest and most stable overall performance, while Chow-Liu Grouping has a superior asymptotic runtime that is competitive with Neighbor-Joining.

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