



## Channing Network Science Seminar

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### Identification of key regulatory pathways in ovarian cancer subtypes

Conventional methods to analyze genomic data do not make use of the connectivity between different data types, such as transcriptional regulation and gene expression, thereby often failing to identify the cellular processes that are unique to cancer and cancer subtypes. An example of this are the four recently characterized high-grade serous ovarian cancer transcriptomic subtypes, which have not been associated with significant differences in survival and have not lead to the identification of subtype-specific therapies. Uncovering the regulatory mechanisms mediating differences in expression between these subtypes may identify new therapeutic interventions. We recently developed PANDA, a network inference approach that uses genomic data to search for an optimal network by modeling information flow between transcription factors and their target genes. Because microRNAs play an important role in gene regulation in cancer, we modified PANDA to account for the regulatory effects of microRNAs in addition to transcription factors (miR-PANDA). We used miR-PANDA to model gene regulation in each of the four ovarian cancer subtypes, and identified several cancer-related pathways that are highly targeted in specific subtypes. Our results may point to new therapeutic interventions and advance personalized treatments for ovarian cancer patients.

Hosted by Kimbie Glass