JHU BOLOGY DEPARMENT SPECIAL SEMINAR Neural crest development, cell fate, in

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Host: Bob Johnston

Abstract:

The maturation of single cell transcriptomic technologies has facilitated the generation of comprehensive cellular atlases from whole embryos. A majority of this data, however, has been collected from wild-type embryos without an appreciation for latent variation present in development. I will present our new approach for deep molecular, cellular and temporal phenotyping of developmental perturbations at whole-organism scale. Deploying this approach to study zebrafish development, we measure the effect of 23 genetic perturbations on cell type composition and gene expression, as well as the variance in cell type abundances during normal development. In one case, time-series profiling of individual mutants identified a group of brachyury-independent cells with strikingly similar transcriptomes to notochord sheath cells, leading to new hypotheses about the origins of the skull. We anticipate that standardized collection of high-resolution, organism-scale single cell data from large numbers of individual animals will enable mapping the genetic dependencies of cell fate decisions, while also addressing long-standing challenges in developmental genetics, including the cellular and transcriptional plasticity underlying phenotypic diversity across individuals.



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