

1116-00-2976

**Bin Yu\*** ([binyu@stat.berkeley.edu](mailto:binyu@stat.berkeley.edu)), Department of Statistics and EECS, UC Berkeley, 367 Evans Hall #3860, Berkeley, CA 94720. *The multi-facet of a data science project to answer: how are organs formed?*

Genome wide data reveal an intricate landscape where gene actions and interactions in diverse spatial areas are common both during development and in normal and abnormal tissues. Understanding local gene networks is thus key to developing treatments for human diseases. In this talk, I present results from a project co-led by biologist Dr. Frise from LBNL to answer the fundamental systems biology question in the talk title. My group (Wu, Joseph, Kumbier) collaborates with Dr. Erwin and other biologists (Hommands) of Celniker's Lab at LBNL that generate the Drosophila spatial expression embryonic image data. We develop a novel image representation decomposing spatial data into building blocks (or principal patterns). These principal patterns provide an innovative and biologically meaningful approach for the interpretation and analysis of large complex spatial data. They are the basis for constructing local gene networks, and we have been able to reproduced 10 out of the 12 links in the famous (local) gap-gene network. Moreover, we are collaborating with the Celniker Lab to verify possible new members of the gap gene network through knock-out experiments and with Dr. Xu.s group at Hsinghua University for software development based on SPARK. (Received September 28, 2015)