11
JUIN.
2015

de 11h à 12h

SÉMINAIRE

Phylogenetic Fate Mapping

Joanna Hård
Institutionen för cell- och molekylärbiologi, Karolinska Institutet

We are exploring techniques using single cell genomic sequencing in human beings for the purpose of defining phylogenetic trees to explain the relationship of cells within defined human tissues. I will discuss how we used single cell exome and whole genome sequencing to identify patient and donor adipocytes in human white adipose tissue biopsies taken from bone marrow recipients and discuss future projects using similar methods to explore cellular identities in human tissue samples.