

Sequencing results from another library

aliquot can be **merged if** it originates from the **same barcoded cell sample** 

Seq Core

NeMO

Cell x fragment
matrix

Lydia Ng, Kimberly Smith (Allen Institute for Brain Science)

SnapATAC file

**N**: Multiple inputs possible WITHIN AND ACROSS species n: Multiple inputs possible WITHIN the SAME species

Object w metadata Digital data asset

Process w

resent in all methods