

CIRM DCM



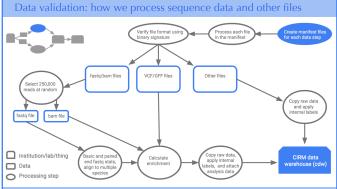
Purpose

Obtain metadata from labs, data set from CESCG Centers

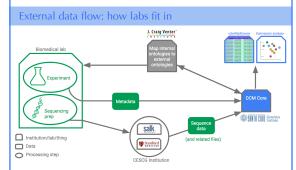
Unify data and metadata for internal consistency, perform validation and analysis QA on sequence data/files

Make submissions available to researchers though cdw

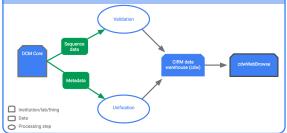
- Submission analysis for individual labs
- Download data from one or more labs . (restricted access prior to publication)
- Some data types can be visualized on the genome browser ٠



Data flow

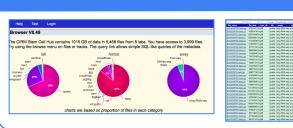


Internal data flow: how data moves to the data warehouse

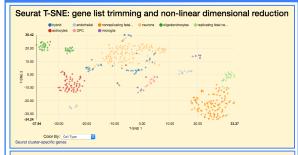


Convert to tag storm format Categorize tag Tags with 1:1 mapping to internal flags Tags with values that have no internal mapping Tags with 1:1 mapping values with biomedic lab to ensure tac nappings ar . Jodate inter Flag as tags to lab-specific tags represent nev data valu omed lat Institution/lab/thing pdate tag to b internally consistent Combine into comprehensiv tagStorm file 🗖 Data arehouse (cdw Processing step

cdw: CIRM Data Warehouse



Individual submission analysis



Seurat T-SNE: gene list trimming and non-linear dimensional reduction



Darmanis S, Sloan SA, Zhang Y, Enge M, Caneda C, Shuer LM, Hayden Gephart MG, Barres BA, Quake SR. (2015). A survey of human brain transcriptome diversity at the single cell level. Proceedings of the National Academy of Sciences. 112(23):7285-90.

Funding and Acknowledgements

We would like to thank the California Institute for Regenerative Medicine for providing grant GC1R-06673-C. DCM staff involved: Josh Stuart, Jim Kent, Chris Eisenhart and Clay Fischer. SANTA CRUZ Genomics





Data unification: how we process metadata