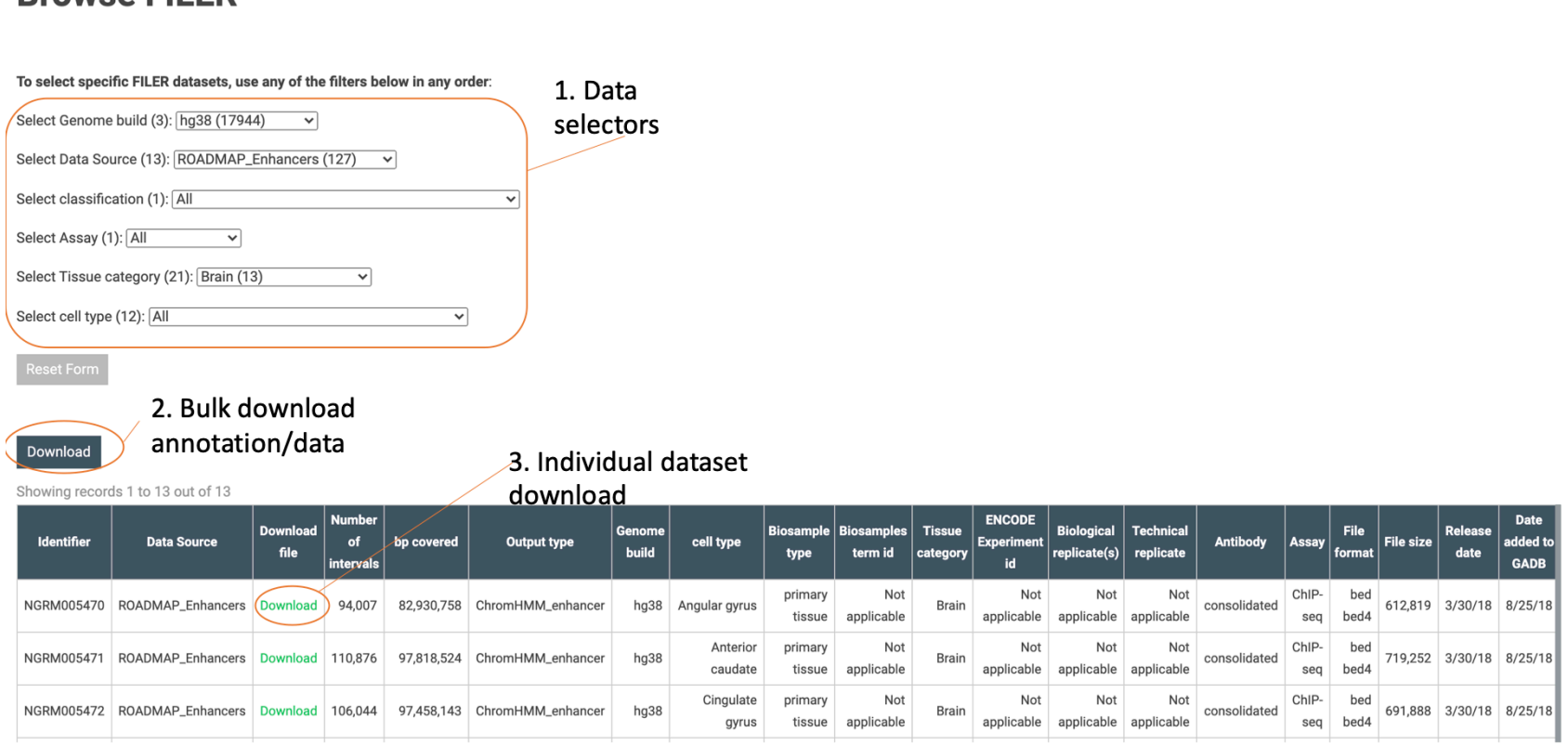
FILER tutorial

- Webserver: https://lisanwanglab.org/FILER. Three main functions:
  - Browse/download: identify and retrieve relevant FILER tracks for your downstream analyses
  - Search FILER tracks/genomic records using genomic coordinates
  - Analyze/annotate your own experimental data/loci:
    - Upload local file
    - Provide a data URL
- FILER stand-alone version, API (https://bitbucket.org/wanglab-upenn/FILER)

FILER webserver: browse/download

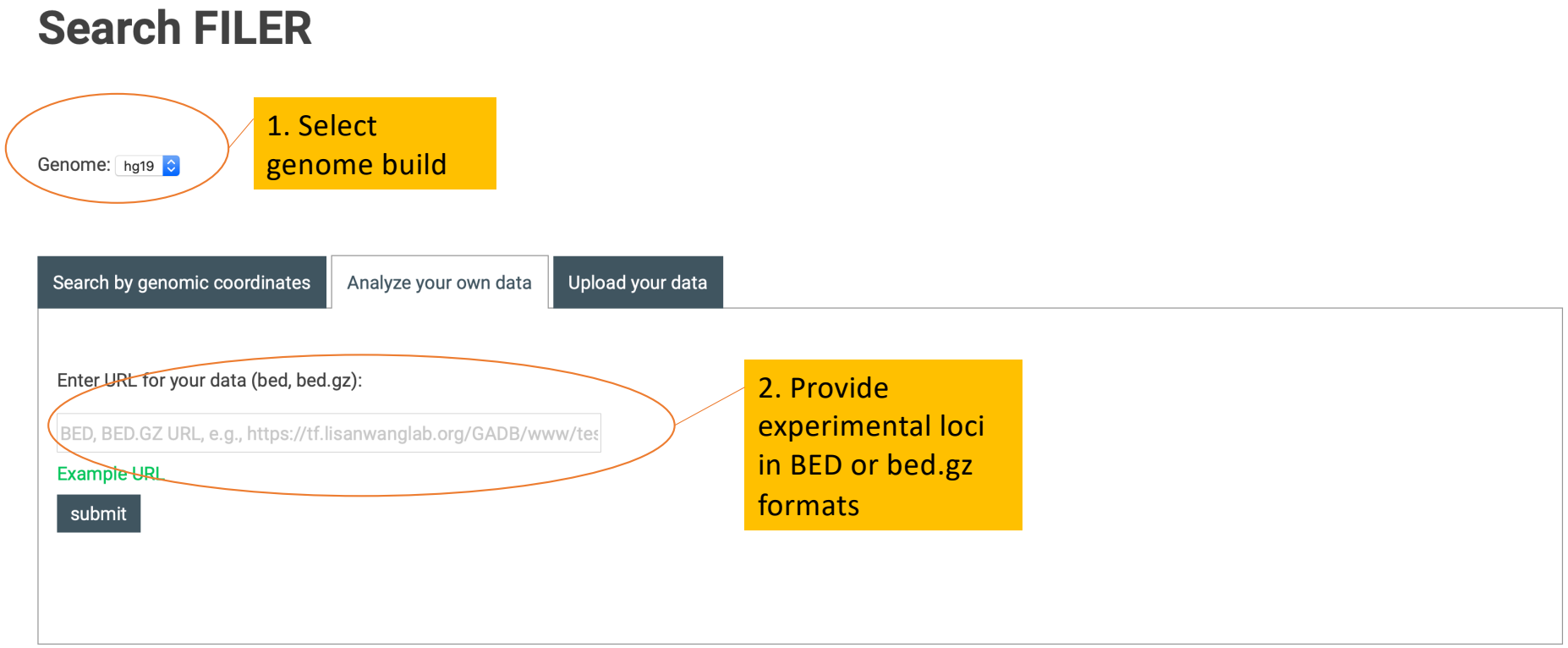
A) quickly identify and retrieve relevant experiments and data in specific tissue contexts for downstream analyses



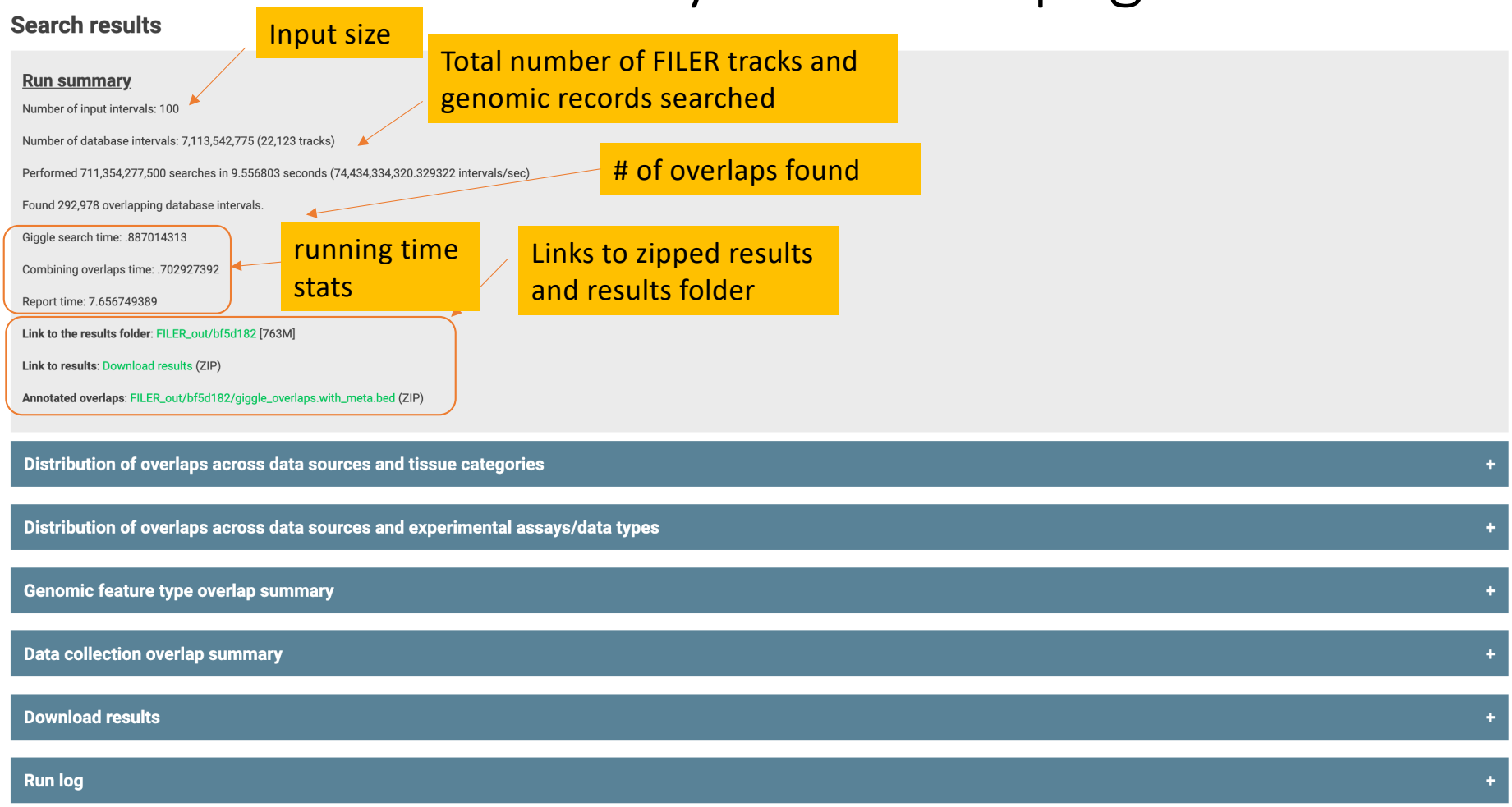
Identifier	Data Source	Download file	Number of intervals	bp covered	Output type	Genome build	cell type	Biosample type	Biosamples term id	Tissue category	ENCODE Experiment id	Biological replicate(s)	Technical replicate	Antibody	Assay	File format	File size	Release date	Date added to GADB
NGRM005470	ROADMAP_Enhancers	Download	94,007	82,930,758	ChromHMM_enhancer	hg38	Angular gyrus	primary tissue	Not applicable	Brain	Not applicable	Not applicable	Not applicable	consolidated	ChIP-seq	bed bed4	612,819	3/30/18	8/25/18
NGRM005471	ROADMAP_Enhancers	Download	110,876	97,818,524	ChromHMM_enhancer	hg38	Anterior caudate	primary tissue	Not applicable	Brain	Not applicable	Not applicable	Not applicable	consolidated	ChIP-seq	bed bed4	719,252	3/30/18	8/25/18
NGRM005472	ROADMAP_Enhancers	Download	106,044	97,458,143	ChromHMM_enhancer	hg38	Cingulate gyrus	primary tissue	Not applicable	Brain	Not applicable	Not applicable	Not applicable	consolidated	ChIP-seq	bed bed4	691,888	3/30/18	8/25/18

FILER webserver: analyze/annotate your own data

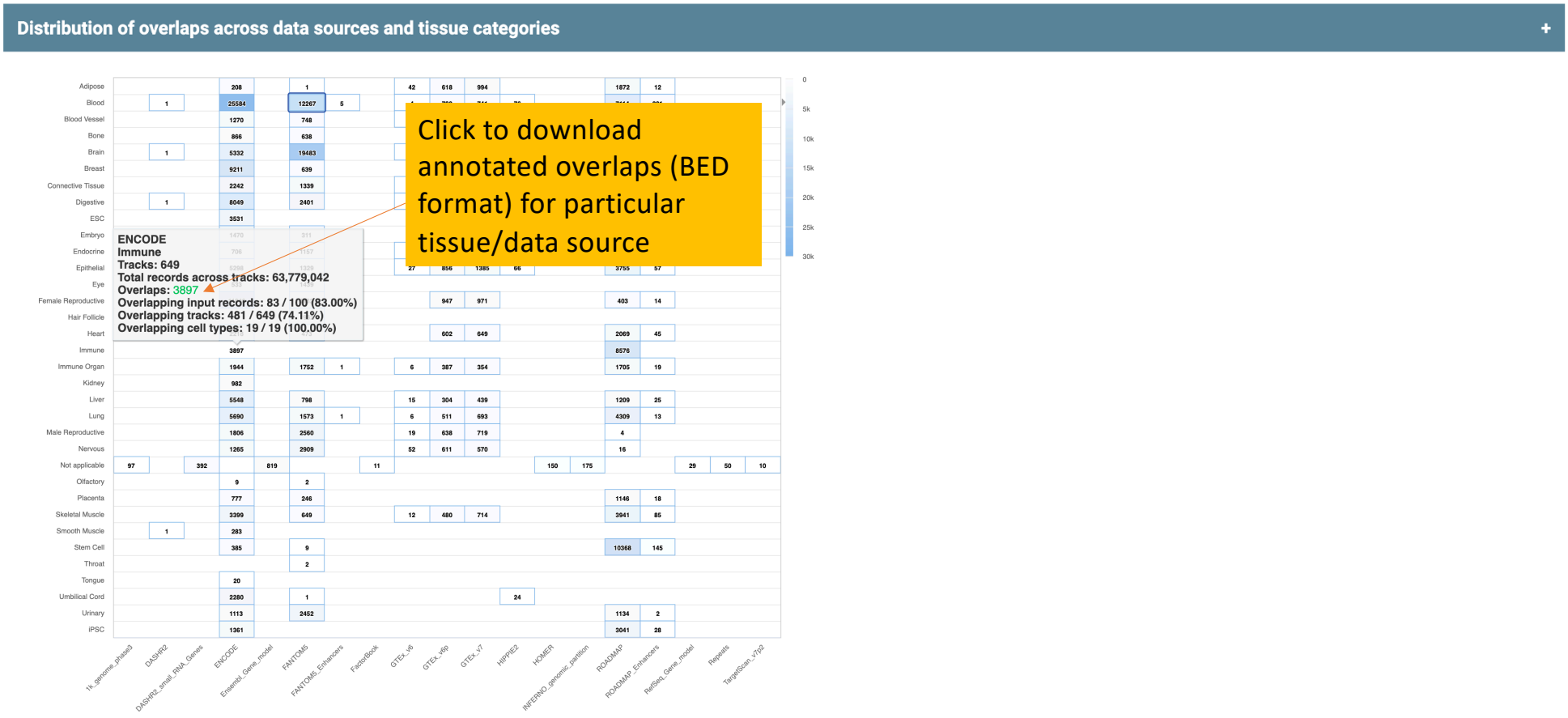
B) quickly search and retrieve all genomic intervals within the genomic regions of interest



FILER webserver: analysis results page



Interactive browsing/download of overlap results



FILER: stand-alone usage and API

- FILER code repository: https://bitbucket.org/wanglab-upenn/FILER
- Scripts for installing a stand-alone FILER instance (use FILER in your own cluster/cloud computing environment)
- Command line CLI scripts for accessing/querying FILER data: query, retrieve genomic data at scale
- Scripts for genomic data indexing and pre-processing (prepare data for adding to FILER)