2020 NCBI CoLab Dataset Survey

Page Break

Q1 Select a professional category that best describes you.

○ Life Science Researcher

○ Clinical Testing Laboratory Staff

○ Health Professional / Clinician

○ Bioinformatics Professional

○ Computer Scientist / Software Developer

○ Educator

○ Student

○ Librarian / Information Specialist

Q2 Select a category that best describes your organization.

○ College or University

○ Commercial or Industry

○ Non-Profit Organization

○ Government

○ Clinical diagnostics

○ Clinical research

Q3 What is your preferred way of accessing sequence data? Select one.

○ Command line

○ API

○ Web interface

○ Other (please list below) _____

Q4 Which programming languages do you use?

☐ Python

☐ R

☐ C++

☐ Perl

☐ JavaScript

☐ Other (please list below)

_____

Q5 What type of data are you looking for?

☐ Gene sequence

☐ Gene expression

☐ Genome sequence

☐ Genetic variation

☐ Associated metadata for sequences

☐ Other (please list below)
_____

Q6 How do you query for data?

☐ Taxonomy

☐ Gene symbol

☐ NCBI accession

☐ Ensembl accession

☐ Other (please list below)
_____

Q7 What metadata format(s) do you prefer for your workflow? Select all that apply.

☐ CSV

☐ TSV

☐ JSON

☐ YAML

☐ Other _____

Q8 What annotation format(s) do you prefer for your workflow? Select all that apply.

☐ GFF

☐ GTF

☐ Other (please list below)

_____

Q9 Do you have any recommendations on how we can improve NCBI Datasets?

_____

_____

_____

_____

_____

Q10 On a scale from 0-10, how likely are you to recommend NCBI Datasets to a friend or colleague?

- ○ 0
- ○ 1
- ○ 2
- ○ 3
- ○ 4
- ○ 5
- ○ 6
- ○ 7
- ○ 8
- ○ 9
- ○ 10