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

End of Block: Default Question Block