NCBI 2018 Population Frequency Survey

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2018 Population Frequency Survey

1. Which professional category best describes you? Please select only one.

- ( ) Bioinformatics professional
- ( ) Educator
- ( ) Healthcare professional
- ( ) Librarian / Information Specialist
- ( ) Other (please specify)
- ( ) Life Science Researcher
- ( ) Student
- ( ) Technician
- ( ) Computer Scientist / Software Developer

2. Please pick one category that best describes your organization.

- ( ) College or University
- ( ) Commercial / Industry
- ( ) Non-profit Organization
- ( ) Other (please specify)
- ( ) Research Institute
- ( ) Government
- ( ) Hospital/health care organization

3. Which of these is the most frequent kind of search you perform for a variant with allele frequency information?

- ( ) Using a variant genomic or sequence position or region
- ( ) Using a gene name or symbol
- ( ) Using an HGVS name
- ( ) Using a dbSNP Reference SNP (rs) ID
- ( ) Using a disease or phenotype name/description
- ( ) Other (please specify)

4. How many variants do typically want to search or retrieve?

- ( ) 1-100
- ( ) 100-1,000
- ( ) 1000-1,000,000
- ( ) > 1,000,000

5. How often do you perform searches for variants at the NCBI site?

- ( ) Daily
- ( ) Weekly
- ( ) Monthly
- ( ) Yearly

6. How would you like to filter your results? Please check all that apply.

- [ ] By allele frequency
- [ ] Ethnicity
- [ ] Continent of origin (Asia, Africa, Europe, North America etc.)
- [ ] Functional consequences (Missense, Nonsense, Frame shift)
- [ ] Variant type (Single Nucleotide Variation, Deletion, etc)
- [ ] ClinVar clinical significance
- [ ] Variants cited in publications
- [ ] Other (please specify)

7. Are you interested in frequency aggregated by asserted/reported ethnic population?

- ( ) Yes
- ( ) No
- ( ) No preference

8. Are you interested frequency aggregated by computed population (PCA, GRAF, etc.) based on genotype?

- ( ) Yes
- ( ) No
- ( ) No preference

9. How do you use allele frequency data? Please check all that apply.

- [ ] Classify or prioritize variants for research
- [ ] Identify cancer or disease-causing variants
- [ ] Identify ancestry markers
- [ ] Clinical interpretation
- [ ] Variant quality control or validation
- [ ] Other (please specify)

10. Are global allele frequencies useful to you?

- ( ) Yes
- ( ) No

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11. How likely is it that you would recommend NCBI variation resources to a friend or colleague?

Not at all likely — Extremely likely

0	1	2	3	4	5	6	7	8	9	10

12. If there was one thing you could change about NCBI variation resources, what would it be?

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2018 Population Frequency Survey, Contact us

We welcome your input! Please contact us at suggest@ncbi.nlm.nih.gov if you would like to provide additional feedback about NCBI variation resources and populationfrequency data.

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