NCBI Microbial Resources User Survey

We want to improve NCBI's products and services. We would like to learn more about how this site helps you with your work, and what we can do better. Please click "next" below to get started.

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Next

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Increasing utilization of next-generation sequencing, especially in bacterial pathogen surveillance, has resulted in tens of thousands to hundreds of thousands of genomes being submitted to the public archives. The NCBI Pathogen Detection project has analyzed (assembled, annotated, clustered) more than 100,000 *Salmonella* genomes to aid food safety. In a few short years that number will grow to over 1 million draft genomes, and with annotation, that will grow to billions of proteins, just for this particular species. As the scale of data grows, NCBI needs to evaluate how best to serve the research and public health needs by determining what critical features are needed when searching, browsing, downloading, and analyzing this much data so that we can build tools and interfaces to meet those needs.

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

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

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

- ○ College or University
- ○ Commercial / Industry
- ○ Non-profit Organization
- ○ Government
- ○ Other (please specify)

3. Do you currently or expect to work with large volumes of microbial sequences/genomes/assemblies on a regular basis?

- ○ Yes
- ○ No

4. Do you plan to use the data from next generation sequencing for routine pathogen surveillance? These data represent more than 100,000 genomes for some bacteria such as *Salmonella*.

- ○ Yes
- ○ No

If yes, what research problem/question can these data likely help you answer?

5. How would you select sequences to use out of these large datasets? Please check all that apply.

- ☐ Download only a set of pre-selected representative genomes (not all of them).
- ☐ Select genomes/genes/proteins based on the isolate metadata/attributes (geographic location, etc.)
- ☐ Search for sequences to work with using a sequence similarity search (BLAST) to identify genomes/genes/proteins.
- ☐ Select genomes/genes/proteins by text search for gene name/protein names or attributes.
- ☐ Download all of the genomes (assembled or reads in SRA) for a particular species, or for several species (no matter how many).
- ☐ Download all of the gene/protein sequences from all of the genomes for a single/multiple species (no matter how many).
- ☐ Other (please specify)

6. How often would you want to be notified, for example by an email alert, when new sequences are added to a dataset/search of interest?

- ○ Every day
- ○ A few times a week
- ○ About once a week
- ○ A few times a month
- ○ Once a month
- ○ Less than once a month
- ○ Never notify me
- ○ Other (please specify)

7. Once you have the microbial sequence data what will you do next? Please select all that apply.

- ☐ Map sequence reads to a reference genome to identify SNPs/variations or make a reference-guided assembly
- ☐ Create a local BLAST database of the sequences I downloaded
- ☐ Map RNAseq data to a reference genome for expression analysis
- ☐ Use the sequences to verify the identity of novel sequences, contamination, or classify/bin them taxonomically for further analyses
- ☐ Generate a multiple alignment/phylogenetic tree of the genes/proteins I found
- ☐ Determine primer sites for PCR
- ☐ Assemble sequence reads to generate *de novo* assemblies
- ☐ Compare assembled genomes to find **novel** sequences/regions/variations including genes/proteins/SNPs
- ☐ Compare assembled genomes to find **conserved** sequences/regions/variations including genes/proteins/SNPs
- ☐ Use the data in a separate analysis pipeline or as part of a tool I am building
- ☐ Determine synteny or genome organization
- ☐ Other (please specify)

8. If the sequence data for all isolates was not available, would it hinder your research?

- ○ Yes
- ○ No

If yes, how would the lack of availability hinder your research?

9. What other resources have you used to obtain microbial sequence data? Please select all that apply.

- ☐ UniProt
- ☐ The European Bioinformatics Institute (EBI)
- ☐ The DNA Data Bank of Japan (DDBJ)
- ☐ Integrated Microbial Genomes and Microbiomes site (IMG)
- ☐ NIAID BRC PATRIC site
- ☐ KEGG
- ☐ No resources other than NCBI
- ☐ Other (please specify)

10. What other tools do you routinely use for your analyses?

- ☐ Genome comparison tools (MUMmer, Mauve, etc.)
- ☐ Phylogenetic tree reconstruction (RAxML, PhyML, FastTree, etc.)
- ☐ Read mapping software (BWA, Bowtie, etc.)
- ☐ Assembly software (Velvet, SPAdes, etc.)
- ☐ Metagenomic/microbiome analyses tools (QIIME, mothur, Kraken, etc.)
- ☐ Multiple alignment programs (Clustal, Muscle, etc.)
- ☐ Annotation systems (Prokka, RAST, etc.)
- ☐ Other (please specify)

11. If there was one thing that you could change about existing NCBI microbial resources, what would it be?

12. What is the one critical thing you would like added to NCBI microbial resources?

13. Did you find what you were looking for today?

- ○ Yes
- ○ No

Additional comments.

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

Not at all likely — Extremely likely

0	1	2	3	4	5	6	7	8	9	10

Please note, you may contact us at the help-desk to provide additional feedback about the resources in this survey or any other NCBI resource.

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