Prokaryotic Representative Genome Assemblies 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.

OMB Control Number: 0925-0648

Expiration Date: 03/31/2018

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NCBI maintains a set of ~5700 bacterial and archaeal genome assemblies, which are designated as ***representative*** and that represent the diversity of the prokaryotes. In this survey we ask you to tell us how you use these assemblies, so we can continue improving how they are selected.

1. Which professional categories best describe 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. Which of the following categories best describes your organization?

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

3. Please select the reasons you use representative assemblies. Check all that apply.

- ☐ Verify the identity of a query sequence
- ☐ Identify organisms (taxa) in environmental / metagenomic samples
- ☐ Detect contamination in query sequence(s)
- ☐ Help assemble new genomes based on a reference
- ☐ Identify single-nucleotide variation in the sample compared to a reference sequence
- ☐ Align Next Generation Sequence read data
- ☐ Work with annotation from a reduced set of assemblies, corresponding roughly to one per species
- ☐ Calculate orthologous proteins or orthologous protein groups
- ☐ Find structural re-arrangements in query assemblies compared to reference(s)
- ☐ Teach microbial genetics / genomics
- ☐ I do not use currently use representative assemblies, but I am interested in a reduced set of assemblies.
- ☐ I have no need for representative assemblies.
- ☐ Other (please specify)

4. Please rank the following characteristics of a representative assembly in order of importance to you from most important (1) to least important (8).

- ⠿ ☐ Accurate sequence
- ⠿ ☐ Complete set of expected genes for the species
- ⠿ ☐ Sequence from type material
- ⠿ ☐ Complete sequence, no gaps
- ⠿ ☐ High quality annotation (low number of frameshifted or partial genes).
- ⠿ ☐ Reported in a publication
- ⠿ ☐ Considered to be the reference by the research community
- ⠿ ☐ Contains all virulence genes of the species

5. Please list any other characteristics you think are important for a representative assembly to have that are not in the list in the previous question.

6. Please rank the characteristics of a SET of representative assemblies in order of importance to you (1 most important, 6 least important).

- ⠿ ☐ One assembly per species, or for highly diverse and well-characterized species a few assemblies
- ⠿ ☐ One assembly per clade (monophyletic), or for the few highly-populated clades a few assemblies
- ⠿ ☐ Low sequence redundancy
- ⠿ ☐ Represents all prokaryotes, including poorly known organisms where assembly quality cannot be guaranteed
- ⠿ ☐ Small total number of assemblies included – less than 6000 assemblies
- ⠿ ☐ Stable overtime (rarely updated)

7. Please list any other characteristics you think are important for a SET of representative assemblies to have that are not in the list in the previous question.

8. There are currently about 5,700 representative assemblies in the NCBI set. This number is:

- ◯ Too small
- ◯ Too large
- ◯ Just right
- ◯ The number of assemblies is not important.

Comments

9. Do you use the annotation provided by on representative assemblies?

- ◯ No
- ◯ Yes

If yes, please describe how you use the annotation.

10. Is it important that annotated genes are available in NCBI's Gene resource, with unique GeneID identifiers for each gene feature, and/or that they have gene symbols (e.g. recA)?

- ◯ No
- ◯ Yes

If yes, please describe how you use the gene identifiers and names.

11. If there was one thing that you could change about how representative assemblies are selected what would it be?

12. Which of these other sets of representative assemblies or proteins do you use? Please select all that apply.

- ☐ UniProt reference proteomes
- ☐ proGenomes
- ☐ MIDAS representative genomes
- ☐ FDA-ARGOS
- ☐ GEBA-I
- ☐ I do not use other sets of representative assemblies.
- ☐ Other (please specify)

13. How easy was it to find what you were looking for on our website?

- ◯ Extremely easy
- ◯ Very easy
- ◯ Somewhat easy
- ◯ Not so easy
- ◯ Not at all easy

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

Not at all likely — Extremely likely

0	1	2	3	4	5	6	7	8	9	10

15. May we contact you to get additional feedback?

- ◯ Yes
- ◯ No

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16. Please enter your email address below.

Prev Done