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1. CHECK ALL THAT APPLY IN THE FOLLOWING STATEMENTS

I (and my team) currently:

Work with non-human data in the cloud on the following platforms:

AWS  GCP  Azure other \_\_\_\_\_

Work with human data in the cloud on the following platforms:

AWS  GCP  Azure other \_\_\_\_\_

Plan to start working in the cloud within the next 12 months.

2. NCBI is planning additional cloud-based data services to complement the Sequence Read Archive. Rank your likelihood to use the following data services in the next 12 months.

(1=MOST INTERESTED, DELIVER IT NEXT, 2= SECOND PREFERENCE, .... , 9=LEAST INTERESTING.)

\_\_\_\_\_ **BLAST cloud service** e.g. with an opportunity to build and search private custom databases that include your local sequence data.

\_\_\_\_\_ **SRA sequence search** e.g. to find accessions similar to a query string perhaps 1+ kilobases in length.

\_\_\_\_\_ **SRA metadata query** e.g. using BigQuery or other cloud-native database query tools to generate worklists of SRA accessions for downstream processing.

\_\_\_\_\_ **GenBank / RefSeq** e.g. quickly retrieving sequence data and annotations for large datasets.

\_\_\_\_\_ **dbSNP annotations** e.g. to mark-up VCF genotype files containing genomic coordinates and alleles with dbSNP functional and allele frequency information.

\_\_\_\_\_ **ClinVar** e.g. to filter human called variants into subsets according to their clinical significance and validation properties.

\_\_\_\_\_ **dbGaP genotype data** e.g. as VCF file objects for use in cloud-based analysis workflows.

\_\_\_\_\_ **dbGaP phenotype data** e.g. queried as observations via FHIR service.

\_\_\_\_\_ Other (specify): \_\_\_\_\_