Reviewer Report

Title: IDseq â€“ An Open Source Cloud-based Pipeline and Analysis Service for Metagenomic Pathogen Detection and Monitoring

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Reviewer Comments to Author:

Summary:
The goal of this study is to provide an open source cloud-based metagenomics pipeline and service for global pathogen detection and monitoring from raw next-generation sequencing (NGS) reads. Their platform is optimized for scalable Amazon Web Services (AWS) cloud deployment. The authors provided a portal, IDseq portal to get raw mNGS data as input and to generate the assignment of reads and contigs to taxonomic categories.
This paper mainly presents two key contributions:
1. Providing an open source portal for pathogen detection from raw next-generation sequencing (NGS).
2. Providing open source Github repos.

Comments:
The paper makes a good effort to introduce an open source platform for pathogen detection. However, the provided Github is not working on a cloud platform other than AWS. I chose two platform to test the Github code on powerful cloud severs, however, the coded seems not working. These are the samples of errors:

```
ERROR: test_many_samples (tests.test_samples_on_local_steps.TestSamplesOnLocalSteps)
tests/test_utils.py", line 84, in run_step_and_match_outputs
  test_bundle, output_dir_s3)
idseq-dag/tests/idseq_step_setup.py", line 82, in get_test_step_object
  command.make_dirs(result_dir_local)
mkdir(name, mode)
PermissionError: [Errno 13] Permission denied: '/mnt/idseq'
```

We highly suggest the authors to fix these issue, and make their Github repo easy to work and install.

Level of Interest

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Quality of Written English

Please indicate the quality of language in the manuscript: Choose an item.

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