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### Designing Computational Biology Workflows with Perl - Part 1 & 2

Esma Yildirim

*CUNY Queensborough Community College*

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<b>Title:</b> Designing Computational Biology Workflows with Perl – Part 1 & 2
<b>Author/Affiliation:</b> Esma Yildirim / Queensborough Community College
<b>Date:</b> 05/15/2019
<b>Material Type:</b> Virtual Machine Image
<b>CS + Computational Biology</b>
<b>Software/Equipment Dependencies:</b> Terminal program
<b>Prior Knowledge Needed (if any):</b> None
<b>Keywords:</b> virtual machine image, cloud computing
<b>Approximate time needed:</b> 1 hour
<b>Description:</b> This manual guides the instructor to combine the parts of the virtual machine image and construct .ova file.

## Designing Computational Biology Workflows with Perl – Part 1 & 2

The virtual machine image **sequencer.ova** is a very large file (approximately 12GBs). Therefore it is split into six 2GB parts before being uploaded to CUNYAcademicWorks. To combine these files, and create **sequencer.ova** to be used in the lab exercises, the following steps must be followed:

Step 1: Download all parts starting with the prefix **sequencer\_broken** into a Linux/UNIX file system directory.

Step 2: Launch your Terminal program and use **cd** command to go into the directory where the parts exist.

Step3: Run the following command to combine the parts:

```
$ cat sequencer_broken* > sequencer.ova
```

Step4: Check if your file is created with **ls** command:

```
$ ls -l sequencer.ova
```

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