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Designing Computational Biology Workflows with Perl - Part 1 & 2

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

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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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