**Online Assembly Exercise**

1. **Access the BV-BRC Assembly Service**

* Go to [BV-BRC Assembly Service](https://www.bv-brc.org/app/Assembly2) website.
* Sign in or register for an account.
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  Description automatically generatedClick on Assembly to go to the genome assembly service.

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**2. Upload Illumina Raw Reads**

* Upload the **Illumina fastq files**.
* Run the **assembly**.
* Run the illumina-only **assembly**.

**3. Upload ONT (Oxford Nanopore) Raw Reads**

* Go back to the BV-BRC Assembly Service.
* Upload the **ONT fastq file**.
* Run the **ONT-only assembly**.

**4. Hybrid Assembly: Combining Illumina and ONT Reads**

* After running the individual assemblies, go back to the Assembly Service.
* Upload both the **Illumina** and **ONT reads**.
* Run the **hybrid assembly**.

**5. Download Assembled Genomes**

* Once all assemblies (Illumina, ONT, and Hybrid) are complete, download the assembled genome files from the results page.
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  Description automatically generatedThese files will usually be in **FASTA format**.

**6. Visualizing Assemblies with Bandage**

* Download and install **Bandage** if not already installed: [Bandage Download](https://rrwick.github.io/Bandage/).
* Open Bandage on your computer.

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**7. Viewing the Assemblies:**

* Open the **assembled genome files** (FASTA files) in Bandage.
* Explore the assembly graph:
  + **Examine contigs**: Look at how contigs are connected.
  + **Compare assembly quality**: Note any differences in the assembly structure between Illumina-only, ONT-only, and Hybrid assemblies.
  + Look at the **gaps**, structural features, or possible **misassemblies** and see which assembly seems more complete or accurate.

**8. Questions:**

* Are there differences between the Illumina-only, ONT-only, and Hybrid assemblies?
* Do you see a lot of contigs or few contigs?
* Are there any plasmids?
* Did you notice any regions better resolved in one assembly type versus the other?
* How does the hybrid assembly improve or change the genome structure? Is it more contiguous than the individual assemblies?
* What challenges did you face when visualizing the genomes in Bandage? How do different assemblies affect the clarity of the graph?