**Introduction session- key steps: Setting up the IgBlast job in VDJServer**

1. Create a new directory on your desktop.
2. Download all files from <https://github.com/initoby/VDJServer_Nanocourse>.
3. Extract all content from the zip folders and place them into the new directory on your desktop. As a suggestion, you should keep the name of the unzipped directory the same as the name of the original zip file minus the .zip extension.
4. In VDJServer, create a new project.
5. Upload all fasta files (9 total), labeled “Demo data fasta files”, and all metadata files (4 total), labeled “metadata for demo data”.
6. Confirm that VDJServer set the appropriate file types, and if not, set them manually. The fasta files should have type Read-Level Data, and the metadata files should have type TAB-separated Values.

**Data digest session- key steps: Setting up RepCalc;**

***(Complete steps 1 – 6 above if you didn’t do so during the introduction session)***

1. You should have 4 total metadata files uploaded and specified as “TAB-separated values” in the Upload and Browse Project Data screen.
2. Go to the Metadata Entry screen and confirm the entries for Project / Study Metadata.
3. Next, import each of the 4 metadata files into the appropriate sections Subject Metadata, Sample Metadata, Cell Processing Metadata, and Nucleic Acid Processing Metadata.
4. Define the following Sample Groups (using “sample fields” options to group):
   1. Tissue (group by “tissue”), Sample type (group by “sample\_type”), and Disease state (group by “disease\_state\_sample”)
5. Define additional Sample Groups if you would like.
6. Run repcalc.
   1. For now, you will use the default options that have been pre-selected for you on vdjserver. In the next session, we will go over the various options for calculations that you can choose from within the repcalc application.

**IgBlast web application demo key steps**

1. If you’ve not already done so, download the file labeled “IgBlast web test seqs.fasta” from <https://github.com/initoby/VDJServer_Nanocourse> and extract the contents.
2. You should see 3 sequences total.
3. Go to the IgBlast web application @ NCBI, <https://www.ncbi.nlm.nih.gov/igblast/>
4. Copy the sequences and paste them directly into the web browser window for the sequence search.
5. Leave the blast default parameters as they’ve been set but be sure to select organism database option as “human” and analyze using the “Analyze immunoglobulin (IG) sequences” option.