Cheat sheet for uploading your DIPnet data to the NCBI Short Read Archive (SRA)

After submitting your metadata to DIPnet two files will be produced the bioSample-attributes.tsv and the sra-metadata.tsv files and you will be directed to SRA to upload your data. There are several steps but the creation of those two files will streamline the process significantly!

Step 1: Submitter
  You will enter your personal information and create an account (or login if you already have an account)

Step 2: General Info
  You will be asked two important questions here:

  1. Do you want to create a new BioProject?
  2. Do you want to create new BioSamples for this submission?

  In the majority of cases the answer to both questions will be yes.

  The following instructions are based on the user answering "yes" to both of the above questions.

Step 3: Project Info
  Fill in project information. For example:
        Project Title: Acanthurus_reversus_RADSeq_data
        Project Description: RADSeq data for the reef fish Acanthurus reversus
        Relevance: Evolution
        Is your project part of a larger initiative that is already registered with NCBI?-No
        External links: Add if relevant
        Select your grants: If relevant

Step 4: Publications
   Add details of relevant publications

Step 5: Biosample type
  Here you choose your sample type. Most DIPnet members will check either "Invertebrates" OR "Model organism or animal sample" for vertebrates.

Step 6: Biosample attributes
  Upload the bioSample-attributes file (tab-delimited format) produced by the FIMS system

Step 7: SRA metadata
  Upload the sra-metadata file (tab-delimited format) produced by the FIMS system

Step 8: Files
  Follow the directions on SRA and upload your files. You will be asked to download the latest version of Aspera Connect. This will speed upload tremendously. Once Aspera is installed go directly to the Choose Files option, choose your zipped folder, and Aspera will automatically open.

Step 9: Overview
  Submit!