**QUESTIONNAIRE**

*We would like to know a little about your background knowledge of influenza and bioinformatics. Please do not worry if you have not used any of the programs we mention.*

**QUESTIONS ABOUT YOU**

1. Please describe your background.

* Molecular Biologist
* Molecular Epidemiologist
* Epidemiologist (*not molecular*)
* Biology (*not molecular*)
* Microbiology
* Computer Scientist
* Bioinformatician
* Other

Please specify:

1. Please describe your current title and a brief description of what you do:
2. Please describe how long you have worked in the influenza field.

* Never
* Less than 1 year
* More than 1 year
* 2-5 years
* More than 5 years

If you did not choose “Never”, please provide some details of your influenza related projects:

**LAB AND INSTITUTION**

1. How many flu positive specimens does your laboratory receive each month?
2. Does the laboratory isolate influenza viruses? Y/N

If yes, approximately how many viruses are isolated per month?

1. Does the laboratory perform a neuraminidase inhibition assay for drug susceptibility assessment? Y/N
2. Does the laboratory have a plate reader to measure fluorescence? Y/N Luminescence? Y/N

Which model?

**SANGER SEQUENCING CAPABILITY**

1. Does the laboratory have Sanger sequencing capabilities? Y/N

If YES, what sequencing platform are you currently using?

* 1. Model?
  2. Number of capillaries?

1. Can you share/send your current Sanger Sequencing protocol for processing your sample, from RNA extraction to sequencing/assembly? Y/N
2. How many samples/isolates do you sequence by Sanger each month?
3. What gene(s) do you sequence by Sanger?
   * Partial HA
   * Full HA
   * Full NA
   * Three genes HA/NA/M (full/partial)
   * Three genes HA/NA/NS (full/partial)
   * Full Genome
4. What software are you currently using for assembling data from your Sanger sequencing?

**LABORATORY EQUIPMENT**

1. What do you use to quantitate DNA?

* Qubit Fluorometer
* **Fluorescence** Microplate **Reader**
* **NanoDrop**
* **Other: specify**

1. **What do you use to visualize PCR fragments?**

* Agarose gel. Precast E-gels?
* Agilent Fragment analyzer
* Agilent Bioanalyzer or Tape Station
* Qiagen QIAxcel
* Other: specify

**NEXT-GENERATION SEQUENCING CAPABILITY**

1. Does the laboratory have NGS capabilities? Y/N

If Yes,

1. What NGS instrument do you have/have access to?
2. What chemistry are you currently using for the NGS sequencing reaction?
3. How frequently do you run NGS sequence reactions on your sequencer?
4. What influenza subtype and what genes are you currently sequencing on this NGS instrument?
5. Are you using random priming or a targeted amplification scheme?
6. Can you share/send your current NGS protocol for processing your sample, from RNA extraction to sequencing/assembly?
7. What software are you currently using for NGS data assembly?

**DATA MANAGEMENT AND ANALYSIS**

1. How to you store your compiled sequence data?
   * Separate files and folders
   * In-house database
   * On-line database (such as NCBI, IRD, GISAID)
2. Which of the following online databases have you used previously? (*select all that apply*)

* NCBI Influenza Virus Resource
* BioHealthBase
* LANL Influenza Sequence Database
* GISAID EpiFluDB
* None of them

1. Which of the following online databases do you currently submit your sequence data? (*select all that apply*)

* NCBI Influenza Virus Resource
* BioHealthBase
* LANL Influenza Sequence Database
* GISAID EpiFluDB
* None of them

1. What type of computers does your laboratory have?
   * PC
   * MAC
   * LINUX/UNIX
   * High Performance Computing Cluster

**PHYLOGENETICS**

1. How often do you build phylogenetic trees?

* Never
* 1-10 times
* Weekly
* Daily

1. If you did not choose “Never”, please describe what method(s) you have used

* Neighbor Joining
* Maximum Parsimony
* Maximum Likelihood
* Bayesian
* Using Clustal
* Other

Please specify:

1. If you did not choose “Never” in #18 above, what programs are you currently using for bioinformatics/phylogenetic analysis? Please choose all that you currently have available:
   * BioEdit
   * MEGA
   * Geneious
   * GARLI
   * FastTree
   * RaxML
   * TreeSub
   * DNAStar
   * BEAST
   * MrBayes
   * PAML
   * PAUP\*4.0
   * PhyML
   * RAxNL
   * TNT
   * HYPHY
   * R
   * BioPerl
   * BioPython
2. Please list other bioinformatics tools you are currently using not listed above.
3. Do you have programs to edit PDFs such as Adobe Illustrator, Adobe Acrobat Professional or other (please specify)?
4. How often will you build phylogenetic trees after taking this workshop?

* Never
* 1-10 times
* Monthly
* Weekly
* Daily

1. Please describe briefly what you would like to learn from this workshop and how it applies to your current work?