New Sequence Features

IRD curates the location of regions of influenza virus proteins with specific characteristic from scientific literature, public archives, and direct submission termed “Sequence Features” (SF). For each SF, IRD calculates sequence variations for the defined region using all relevant protein sequences in IRD and provides this as “Variant Type” (VT) grouping information.

The SFVT component has been extended by the addition of seven new SFs contributed by the New York Influenza Center of Excellence (NYICE) at the University of Rochester and five expanded Caton immune epitope SFs curated by IRD. To access the data, “Sequence Feature Variant Type” under the “Search Data” dropdown menu. For a detailed description of the application of the SFVT approach for the study of influenza virus, see PMID 22398823. IRD also invites the community to recommend new SFs, thereby sharing them with the wider research community.

Compare flu strains from different seasons

The metadata-driven Comparative Analysis Tool (meta-CATS) is a unique statistical analysis tool in IRD/ViPR, providing the capability of comparing user-defined groups of sequences and identifying positions that significantly differ between the groups. Meta-CATS can be used, for instance, to find specific genetic changes that enable an animal virus to infect humans or cause resistance to antiviral drugs. Sequences can be assigned into groups manually, or automatically by using one of the sequence metadata fields, including host information, geographic region, isolation year, virus type, etc. In this release, the meta-CATS tool has added a new auto grouping field - flu season, which allows you to easily compare influenza strains from different flu seasons.

Choose Sequence Type for Analysis

IRD provides an integrated pipeline for retrieving sequences through tailored sequence search interfaces and subsequently feeding desired sequences to a suite of analytical tools. For this release, we have added a sequence type selection option to better support the sequence analysis workflows. Specifically, when you select sequences from a Sequence Search Results page and choose one of the analysis options from the “Run Analysis” dropdown menu, a “Select Sequence Type” lightbox will pop up, where you will have the option to choose nucleic acid (NA), nucleic acid (CD), or amino acid (AA) sequences as input to your desired analysis tool.

Select Sequence Type

Choose your desired sequence type for downstream analysis.

A PA Sequence Feature responsible for enhanced polymerase activity in mammalian cells.

The May 2014 release of IRD is now available, visit www.fludb.org

Metadata-driven Comparative Analysis Tool (meta-CATS)

The meta-CATS tool provides the ability to perform statistically rigorous comparisons of aligned and unaligned sequences and is available by selecting an alignment method from the “Alignment” dropdown menu. For each input sequence, the meta-CATS tool will calculate all possible pairwise alignments and compare data from user-defined groups to determine which residues significantly correlate with one or more metadata fields. The P-value threshold is used as the confidence level to determine positions that are significantly different between user-defined groups of sequences. However, statistical testing to confirm actual immune epitopes from a meta-CATS analysis should be performed using advanced statistical methods. Click here to view meta-CATS tutorial. See the SOP for a detailed description of the application of the SFVT approach for the study of influenza virus, see PMID 22398823. IRD also invites the community to recommend new SFs, thereby sharing them with the wider research community.

Compare flu strains from different seasons

The metadata-driven Comparative Analysis Tool (meta-CATS) is a unique statistical analysis tool in IRD/ViPR, providing the capability of comparing user-defined groups of sequences and identifying positions that significantly differ between the groups. Meta-CATS can be used, for instance, to find specific genetic changes that enable an animal virus to infect humans or cause resistance to antiviral drugs. Sequences can be assigned into groups manually, or automatically by using one of the sequence metadata fields, including host information, geographic region, isolation year, virus type, etc. In this release, the meta-CATS tool has added a new auto grouping field - flu season, which allows you to easily compare influenza strains from different flu seasons.

Choose Sequence Type for Analysis

IRD provides an integrated pipeline for retrieving sequences through tailored sequence search interfaces and subsequently feeding desired sequences to a suite of analytical tools. For this release, we have added a sequence type selection option to better support the sequence analysis workflows. Specifically, when you select sequences from a Sequence Search Results page and choose one of the analysis options from the “Run Analysis” dropdown menu, a “Select Sequence Type” lightbox will pop up, where you will have the option to choose nucleic acid (NA), nucleic acid (CD), or amino acid (AA) sequences as input to your desired analysis tool.

Select Sequence Type

Choose your desired sequence type for downstream analysis.

A PA Sequence Feature responsible for enhanced polymerase activity in mammalian cells.

The May 2014 release of IRD is now available, visit www.fludb.org

Metadata-driven Comparative Analysis Tool (meta-CATS)

The meta-CATS tool provides the ability to perform statistically rigorous comparisons of aligned and unaligned sequences and is available by selecting an alignment method from the “Alignment” dropdown menu. For each input sequence, the meta-CATS tool will calculate all possible pairwise alignments and compare data from user-defined groups to determine which residues significantly correlate with one or more metadata fields. The P-value threshold is used as the confidence level to determine positions that are significantly different between user-defined groups of sequences. However, statistical testing to confirm actual immune epitopes from a meta-CATS analysis should be performed using advanced statistical methods. Click here to view meta-CATS tutorial. See the SOP for a detailed description of the application of the SFVT approach for the study of influenza virus, see PMID 22398823. IRD also invites the community to recommend new SFs, thereby sharing them with the wider research community.