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The immunoSEQ REST API: example scripts

Adaptive provides a set of example scripts that show how the immunoSEQ REST API(/help?target=!The%20immunoSEQ%20REST%20API:%20documentation) can be used in scripts to simplify authentication and to automate querying and exports. These scripts are packaged for download in the Downloads section. This package contains a set of Bash scripts that simplify common immunoSEQ Analyzer API tasks into easy command line executables:

- iseq.sh: outputs the results of a query you provide against the workspace project you specify
- iseq_export: outputs configurable sample/sequence details for all samples in a project
- iseq_export_one: same as iseq_export, but for a single sample you specify

Each script uses a set of editable configuration files to securely query your Analyzer workspace project(s) using the command line within a Bash shell. Query results are output to your command line or as local files.

Installation

Download the scripts Download the iseq package(/globalDownloadRedirect?folderName=help&fileName=immunoSEQ+iSEQ+example+scripts.tar.gz) (also available on the Downloads page(/help?target=Download))

- Extract into a directory and note its path; you will run these scripts from within this directory. **Note:** Keep all files in the same directory, as they reference each other during execution.

Set Up Authentication

Each script looks for a special file to find your immunoSEQ API credentials. These credentials are the same ones you use when logging into the Analyzer website(/). In your home directory (~/.), create this file named ".iseq" and type the following text:

```
analyzer:YOUREMAIL:YOURPASSWORD:https://analyzer.adaptivebiotech.com
```

Where:

- YOUREMAIL = the email address you use to log into the Analyzer website
- YOURPASSWORD = the password associated with YOUREMAIL

Note: Terminate with a newline character before saving.

Using the iseq script: easy command-line querying

This script executes your query and returns results to the command line.

Usage: > **iseq {service_name} {workspace_name} {project_name} {sql}**

Example: > **iseq analyzer MyWorkspace-Name Summary "select sample_name, test_name, release_date, max_productive_frequency from samples where max_productive_frequency > 0.5"**

Inputs:

- {service_name}: "analyzer", as defined in your .iseq file by following the instructions above
- {workspace_name}: the name of your Analyzer workspace
- {project_name}: the name of the Project containing the samples you wish to query. Use the project name "Summary" to query all samples in the Workspace.
- {sql}: the SQL query you wish to execute. Query objects and their column definitions are found in the Column Info help section(/help?target=SQL).

Tip: try out your queries first using Analyzer. In Analyses 3.0, start a new Analysis in your target project. Use the Advanced Query view to edit your own SQL and customize results.

Output

- the results of your SQL query are returned to the command prompt

Using the iseq_export script: easy bulk download of project samples

(<http://www.adaptivebiotech.com/>)

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Example: `> iseq export analyzer MyWorkspace-Name Summary`

- {service_name}: "analyzer", as defined in your .iseq file by following the instructions above
- {workspace_name}: the name of your Analyzer workspace
- {project_name}: the name of the Project containing the samples you wish to query. Use the project name "Summary" to query all samples in the Workspace.

- **samples.tsv:** a list of all samples exported, by the columns you defined in export_samples.sql file
- **Output folder:** Workspace-Project (provided as inputs)
- **{sample_name}.tsv:** one file for each sample exported, by the columns you defined in export_rearrangements.sql file

Using the iseq_export_one script

```
Usage: > iseq_export_one {service_name} {workspace_name} {project_name} {sample_name}
{target directory}
```

Inputs:

- {service_name}: "analyzer", as defined in your .iseq file by following the instructions above
- {workspace_name}: the name of your Analyzer workspace
- {project_name}: the name of the Project containing the samples you wish to query. Use the project name "Summary" to query all samples in the Workspace.
- {sample_name} : the Sample Name to download.
- {target_directory} : optional; specifies the output directory. If it does not exist, it will be created in the current directory.

- **{sample_name}.tsv**: one file, named after the sample, including the columns you defined in export rearrangements.sql file

Tip: the `iseq_export_one` batch file is designed to download only sample results that have not previously been downloaded. It will check to see whether the sample file already exists in the Output folder and skip it if found.

Building Queries

Query formats expected in the body of certain immunoSEQ API endpoints use the same schemas as the Analyzer's Advanced Query view, with one exception: endpoints do not inherit any analysis filters, so will query all samples in the project.

To see exhaustive documentation on these fields, go to the Column Info help section(</help?target=SQL>).

Learn more about the immunoSEQ REST API(</help?target=!The%20immunoSEQ%20REST%20API:%20documentation>).