service-ars documentation

Release 0.1

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Getting started

1.1 Overview

1.1.1 Antigen Recognition Site

1.1.2 ARS Groups

1.1.3 ARS Reduction

1.2 Service UI

1.2.1 Options

hml	• HML file
	Required parameter
output	Output directory
	Required parameter
imgtdir	• Location of where the BLAST IMGT database is located
	• Default location is /opt/html on the docker container
imgt	IMGT database version
	• Default is 3200
report	Binary flag for generating HTML validation report
	• default is 1

1.2.2 Advanced options

hml	• HML file
	Required parameter
output	• Output directory
	Required parameter

imgtdir	• Location of where the BLAST IMGT database is located
	• Default location is /opt/html on the docker container
imgt	IMGT database version
	• Default is 3200
report	Binary flag for generating HTML validation report
	• default is 1

1.2.3 Submit HML File

Service API

2.1 RESTful Interface

2.1.1 Parameters

- IMGT/DB
- Glstring
- ARS Type
- MAC Url
- Expand Genotypes
- Expand Genomic Typing

2.1.2 Convert HLA Typing

2.1.3 Convert Subject Typing

2.1.4 Get ARS Data

```
./nextflow run nmdp-bioinformatics/flow-blast-hml -with-docker \
    nmdpbioinformatics/docker-blast-hml \
    --hml test_file.hml --outdir /path/to/output/dir
```

2.2 Clients & Tools

2.2.1 Java

• hml-typing-resolution *

hml	• HML file
	Required parameter
output	Output directory
	Required parameter
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	• Default location is /opt/html on the docker container
imgt	• IMGT database version
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2.2.2 Perl

hml	• HML file
	Required parameter
output	Output directory
	Required parameter
imgtdir	Location of where the BLAST IMGT database is located
	• Default location is /opt/html on the docker container
imgt	• IMGT database version
	• Default is 3200
report	• Binary flag for generating HTML validation report
	• default is 1

Developers

3.1 Contributing

- 1. Log into Github web interface with your username-nmdp account
- 2. Browse to the repo at https://github.com/nmdp-bioinformatics/flow-blast-hml, hit the Fork button.
- 3. Copy the clone URL from the Github web page for the fork (something like https://github.com/usernamenmdp/pipeline.git)
- 4. Clone the fork

```
git clone https://github.com/username-nmdp/flow-blast-hml.git
cd flow-blast-hml
```

5. Add upstream as remote

git remote add upstream https://github.com/nmdp-bioinformatics/flow-blast-hml

6. Pull and merge latest changes from upstream master to your local master branch

```
git checkout master
git pull upstream master
git push
```

7. Create a new local feature branch

git checkout -b new-feature-branch

- 8. Edit files locally
- 9. Commit changes to local feature branch

git commit -m "made changes"

10. Push changes from local feature branch to remote feature branch on your fork

git push origin new-feature-branch

- 11. Browse to the Github web page for your fork repo (something like https://github.com/username-nmdp/flowblast-hml) and hit the new pull request button.
- 12. Edit the pull request description and hit create new pull request button.
- 13. Other contributors will review the changes in the pull request.
- 14. When the pull request looks good, it will be merged into the master branch.

- 15. Hit the delete branch button to delete your remote feature branch (the commits have been merge upstream, so it is no longer necessary).
- 16. Delete your local feature branch

git branch -d new-feature-branch

3.2 Installation

3.3 Docker