



Usage Guide for cmd_bio

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Overview

cmd_bio is a command line interface for BioGears. It was designed to facilitate usage and validation.

This presentation is for BioGears version 7.3.0, using git hash e4235759.

Acceptable Inputs

- Options
 - HELP – H
 - GENDATA
 - GENSEPSIS
 - GENSTATES
 - VERIFY
 - VERSION
- Keywords
 - THREADS – J
- MultiWords
 - TEST
 - CONFIG
 - SCENARIO
 - VALIDATE
 - GENTABLES

Help Dialog

Usage cmd_bio

[HELP, GENDATA, GENSTATES, GENSEPSIS, VERIFY, VERSION]

[THREADS N]

[CONFIG FILE [FILE]...]

[SCENARIO FILE [FILE]...]

[TEST cdm|bge]

[VALIDATE patient|drug|system|all]

[GENTABLES html|md|xml|web|all]

Options 1

- **HELP – H**
 - Provides simple guidelines for use of cmd_bio.
- **VERSION**
 - Provides a full version string of BioGears.

If either **HELP** or **VERSION** is given, no other command line inputs will execute and the current run will terminate after printing the help dialog or version string respectively.

Options 2

- GENSEPSIS
 - Queues run using GenSepsisStates.config.
- GENSTATES
 - Queues run using GenStates.config.
- VERIFY
 - Queues run using VerificationScenarios.config.

Options 3

- GENDATA
 - Saves out XML files for substances, environments, patients, and compounds.
 - These values are stored in CSV files (Substances.csv, Environments.csv, Patients.csv, Compounds.csv) editing any of these files then running GENDATA ensures that all changes are reflected in the respective XML files.

Keywords

- **THREADS – J**
 - Must be followed by a valid integer, specifies thread count for current run of cmd_bio.
 - Giving ‘-1’ as the value results in the use of the maximum number of threads, minus one.
 - If no input is given, the thread count is set to the maximum number of threads, given by `std::thread::hardware_concurrency()`.

MultiWords

- **TEST**
 - Runs circuit tests, valid inputs are {cdm,bge}.
 - In order for this option to produce any results, BioGears must be built with CMake option 'BUILD_CIRCUIT_TESTS' enabled.
- **VALIDATE**
 - Valid inputs are {patient,drug,system,all} queues runs of ValidationPatients.config, ValidationDrugs.config, ValidationSystems.config, or all of the aforementioned files and VerificationScenarios.config.
 - Note that VALIDATE all is equivalent to 'VALIDATE patient drug system VERIFY'.
- **CONFIG**
 - Takes list of config files to queue.
- **SCENARIO**
 - Takes list of scenario files to queue.
- **GENTABLES**
 - Valid inputs are {html,md,xml,web,all} this sets the format of the validation tables produced by cmd_bio.

Examples 1

- ‘VALIDATE patient’
 - Executes run with ValidationPatients.config.
- ‘VALIDATE all’
 - Executes runs of ValidationSystems.config, ValidationPatients.config, ValidationDrugs.config, and VerificationScenarios.config.
- ‘HELP VERSION GENSEPSIS –J 4’
 - Prints help dialog, the inputs will be accepted, however execution will stop after printing.

Examples 2

- ‘SCENARIO Patient\AcuteStress.xml Patient\BrainInjury.xml’
 - Executes runs of the xml files. The MultiWord SCENARIO automatically prepends ‘Scenario\’ to inputs. So These xml files are housed in ‘Scenario\Patient\’.
- ‘CONFIG VerificationScenarios.config ValidationPatients.config’
 - Executes runs using config files.

.config Files

- In order to provide greater flexibility, cmd_bio has the ability to parse config files.
- These are essentially lists of different scenario tests with specifications for running.
- These are tools to facilitate batching a large number of BioGears runs together.

.config File Elements

- Driver

```
Driver ScenarioTest : ScenarioTestDriver {  
    Option Computed="Scenarios/"  
    Option Scenario="Patient/BasicStandard.xml"  
}
```

- Test

```
ScenarioTest( BasicStandard )
```

Driver

- Specifies driver for individual scenario runs.
- Driver types are:
 - ScenarioTestDriver
 - BGEUnitTestDriver
 - CDMUnitTestDriver
- For almost all runs a BioGears user should select ScenarioTestDriver.
- In order to run scenarios using the BGEUnitTestDriver or CDMUnitTestDriver, BioGears must be built with the CMake option “BUILD_CIRCUIT_TESTS” enabled.

Driver Options

- Computed
 - Specifies a location to write out results from the run. With the specifications on the right, results would be written to the directory “Scenarios/Patient” housed in the runtime directory.
- Scenario
 - Specifies a default scenario file to be run by this driver.

```
Driver ScenarioTest : ScenarioTestDriver {
    Option Computed=“Scenarios/”
    Option Scenario=“Patient/BasicStandard.xml”
}
```

Test

- ‘Driver(Name, Parameters)’
- Driver
 - Specifies driver for test
- Name of individual test.
- Parameters
 - Specifies driver options, this overrides the specifications inside of the Driver declaration itself.

`ScenarioTest(BrainInjury, Scenario=Patient/BrainInjury.xml)`

Example

```
Driver ScenarioTest : ScenarioTestDriver {
    Option Computed="Scenarios/"
    Option Scenario="Patient/BasicStandard.xml"
}
```

```
Driver BurnWoundTest : ScenarioTestDriver {
    Option Computed="Scenarios/"
    Option Scenario="Patient/BurnWound.xml"
}
```

```
ScenarioTest( BasicStandard )
```

```
BurnWoundTest( BurnWound )
```

```
ScenarioTest( BrainInjury, Computed ="Results/" Scenario=Patient/BrainInjury.xml )
```

Additional Driver Options

- Baselines
- Results
- NoCompare
- FastPlot
- FullPlot
- FastPlotErrors
- FullPlotErrors
- MemoryFastPlot

These options will not cause an error if they are included, but any data given will not be used.

.config file additional settings

- ExecuteTests - True/False
- PlotResults - True/False
- PercentDifference - Float
- Threads - Integer
- Subject - String
- Recipients - String
- Sender - String
- Smtplib - String
- Smtplib_Password - String
- Smtplib_Username - String
- Sendemail - True/False
- Group - String

These are currently unused, but are fields for a potential future update which would allow cmd_bio to email out results of completed runs.

Scenario Files

- XML Files describing a scenario for BioGears to simulate.
- Earlier versions of cmd_bio did not support certain scenario file features, for example the use of engine state files or inline patient data specification. As of the 7.3.0 release this is no longer an issue.