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CLIP - A Command-Line Interface to Certara's Phoenix-NLME

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Introduction

Phoenix-NLME[1] is a module of Certara's Phoenix platform that performs population PK/PD modeling and simulation. As a single-threaded graphical platform, however, there are limitations to perform computationally intensive modeling scenarios.

Objective

The main objective of this project is to meet this growing need with a command-line alternative to the graphical interface of Phoenix-NLME so that researchers can fully harness to the computing resources available to them.

Methods

A command-line application was developed as a Python[2] package to provide an easy-to-use and extensible toolkit for novice and advanced users alike to perform routine modeling and simulation tasks. It's input is a single model file comprising a model declaration written in the Phoenix Modeling Language (PML) and its run-time configuration. The PML is used to create Phoenix-NLME's modeling engine, while the run-time configuration specifies its execution.

Results

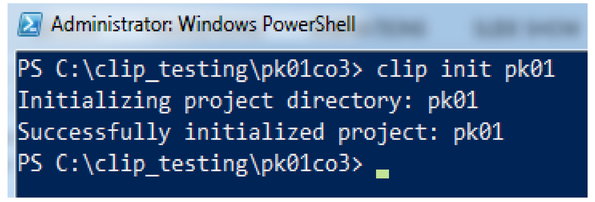
With CLIP, researchers can model anywhere from a single-core system to a cluster of computers in order to take full advantage of one's computing resources. The application has been able to accurately estimate and simulate models faster than its equivalent graphical operations and with equivalent accuracy. The method of stochastic simulation and estimation has also been implemented to indicate that the core of this program is extremely extensible and capable of performing non-trivial tasks with higher performance and greater ease.

Results

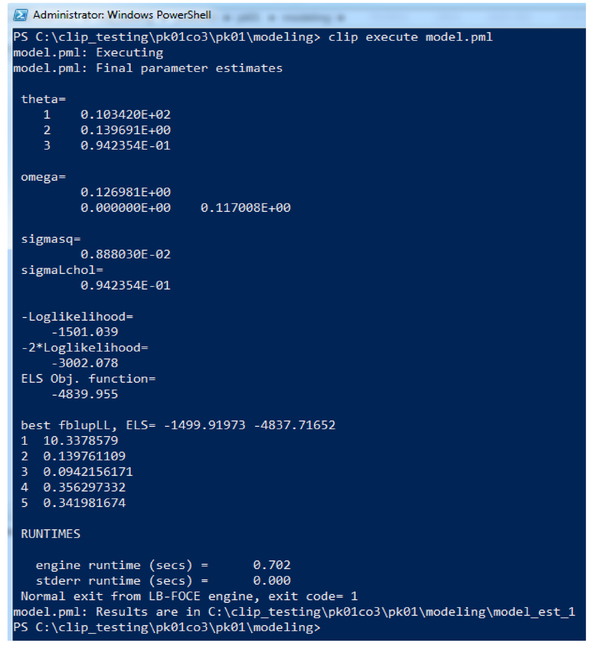
Figure 1: PML Model File

```
coldef: id("id")  time("time")  dose(A1<-"dose")
  covr(sex<-"sex")  covr(wt<-"wt")  covr(age<-"age")
  obs(CObs<-"conc")
data:
  file: data.csv
estimation:
  iterations: 10000
  method: 3
  estimate-covariates: [0,1,2]
tables:
  - file: test1.csv
    times: [0,1,2,5,10,20,30,40,50,60,70,90,130,150]
    obs:  CObs
    dose: A1
    variables: C
    covr: sex,age,wt
---
  test() {
    cfMicro(A1, Cl / V)
    dosepoint(A1)
    C = A1 / V
    error(CEps = 0.0942615)
    observe(CObs = C * (1 + CEps))
    stparm(V = tvV * (wt/75)^dVdwt * exp(dVdsex1*(sex==1)) * exp(nV))
    stparm(Cl = tvCl * (wt/75)^dCldwt * (age/40)^dCldage * exp(nCl))
    covariate(sex())
    covariate(wt)
    covariate(age)
    fixef(tvV = c(, 10.1888, ))
    fixef(tvCl = c(, 0.139397, ))
    fixef(dVdwt(enable=c(0)) = c(, 1.20304, ))
    fixef(dCldwt(enable=c(1)) = c(, 1.16756, ))
    fixef(dCldage(enable=c(2)) = c(, -0.46234, ))
    fixef(dVdsex1(enable=c(3)) = c(, 1, ))
    ranef(diag(nV, nCl) = c(0.10872238, 0.082517582))
  }
---
notes:
  basedon:  model_with_bw.pml
  description:
```

Figure 2: Project Workflow

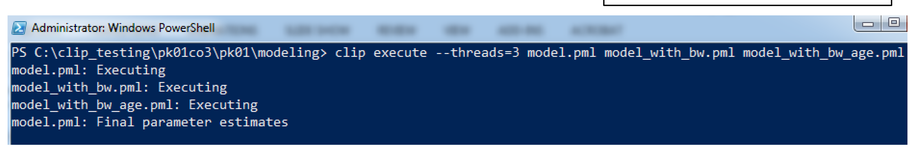


Initiate Project



Execute Model

Run parallel models



Conclusions

CLIP is capable of not only duplicating the functionality of Phoenix-NLME at a faster speed, but it is also capable of more intensive operations not practical to perform in a graphical windows environment. Future development will involve extending this product to the Linux operating system.

References

1. Certara, L.P., 210 North Tucker Boulevard Suite 350, St. Louis, MO 63101 USA
2. https://www.python.org