

Package ‘BeastJar’

October 13, 2020

Type Package

Title JAR Dependency for MCMC Using 'BEAST'

Version 1.10.5

Description Provides JAR to perform Markov chain Monte Carlo (MCMC) inference using the popular Bayesian Evolutionary Analysis by Sampling Trees 'BEAST' software library of Suchard et al (2018) <doi:10.1093/ve/vey016>. 'BEAST' supports auto-tuning Metropolis-Hastings, slice, Hamiltonian Monte Carlo and Sequential Monte Carlo sampling for a large variety of composable standard and phylogenetic statistical models using high performance computing. By placing the 'BEAST' JAR in this package, we offer an efficient distribution system for 'BEAST' use by other R packages using CRAN.

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Encoding UTF-8

LazyData true

Imports rJava

URL <https://github.com/beast-dev/BeastJar>

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RoxygenNote 7.1.1

Suggests testthat

NeedsCompilation no

Author Marc A. Suchard [aut, cre, cph],
Andrew Rambaut [cph],
Alexei J. Drummond [cph]

Maintainer Marc A. Suchard <msuchard@ucla.edu>

Repository CRAN

Date/Publication 2020-10-13 13:50:08 UTC

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BeastJar

*BeastJar***Description**

Convenient packaging of the Bayesian Evolutionary Analysis Sampling Trees (BEAST) software package to facilitate Markov chain Monte Carlo sampling techniques including Hamiltonian Monte Carlo, bouncy particle sampling and zig-zag sampling.

Examples

```
# Example MCMC simulation using BEAST
#
# This function generates a Markov chain to sample from a simple normal distribution.
# It uses a random walk Metropolis kernel that is auto-tuning.

# Set seed
seed <- 123
rJava::J("dr.math.MathUtils")$setSeed(rJava::.jlong(seed));

# Set up simple model - Normal(mean = 1, sd = 2)
mean <- 1; sd = 2
distribution <- rJava::.jnew("dr.math.distributions.NormalDistribution",
                             as.numeric(mean), as.numeric(sd))
model <- rJava::.jnew("dr.inference.distribution.DistributionLikelihood",
                      rJava::.jcast(distribution, "dr.math.distributions.Distribution"))
parameter <- rJava::.jnew("dr.inference.model.Parameter$Default", "p", 1.0,
                           as.numeric(-1.0 / 0.0), as.numeric(1.0 / 0.0))
model$addData(parameter)

# Construct posterior
dummy <- rJava::.jnew("dr.inference.model.DefaultModel",
                      rJava::.jcast(parameter, "dr.inference.model.Parameter"))

joint <- rJava::.jnew("java.util.ArrayList")
joint$add(rJava::.jcast(model, "dr.inference.model.Likelihood"))
joint$add(rJava::.jcast(dummy, "dr.inference.model.Likelihood"))

joint <- rJava::new(rJava::J("dr.inference.model.CompoundLikelihood"), joint)

# Specify auto-adapting random-walk Metropolis-Hastings transition kernel
operator <- rJava::.jnew("dr.inference.operators.RandomWalkOperator",
                         rJava::.jcast(parameter, "dr.inference.model.Parameter"),
                         0.75,
                         rJava::J(
                           "dr.inference.operators.RandomWalkOperator"
                         )$BoundaryCondition$reflecting,
                         1.0,
                         rJava::J("dr.inference.operators.AdaptationMode")$DEFAULT
)
```

```

schedule <- rJava::.jnew("dr.inference.operators.SimpleOperatorSchedule",
                        as.integer(1000), as.numeric(0.0))

schedule$addOperator(operator)

# Set up what features of posterior to log
subSampleFrequency <- 100
memoryFormatter <- rJava::.jnew("dr.inference.loggers.ArrayLogFormatter", FALSE)
memoryLogger <-
  rJava::.jnew("dr.inference.loggers.MCLogger",
              rJava::.jcast(memoryFormatter, "dr.inference.loggers.LogFormatter"),
              rJava::.jlong(subSampleFrequency), FALSE)
memoryLogger$add(parameter)

# Execute MCMC
mcmc <- rJava::.jnew("dr.inference.mcmc.MCMC", "mcmc1")
mcmc$setShowOperatorAnalysis(FALSE)

chainLength <- 100000

mcmcOptions <- rJava::.jnew("dr.inference.mcmc.MCMCOptions",
                          rJava::.jlong(chainLength),
                          rJava::.jlong(10),
                          as.integer(1),
                          as.numeric(0.1),
                          TRUE,
                          rJava::.jlong(chainLength/100),
                          as.numeric(0.234),
                          FALSE,
                          as.numeric(1.0))

mcmc$init(mcmcOptions,
          joint,
          schedule,
          rJava::.jarray(memoryLogger, contents.class = "dr.inference.loggers.Logger"))

mcmc$run()

# Summarize logged posterior quantities
traces <- memoryFormatter$getTraces()
trace <- traces$get(as.integer(1))

obj <- trace$getValue(as.integer(0),
                     as.integer(trace$getValueCount()))

sample <- rJava::J("dr.inference.trace.Trace")$toArray(obj)

outputStream <- rJava::.jnew("java.io.ByteArrayOutputStream")
printStream <- rJava::.jnew("java.io.PrintStream",
                          rJava::.jcast(outputStream, "java.io.OutputStream"))

rJava::J("dr.inference.operators.OperatorAnalysisPrinter")$showOperatorAnalysis(

```

```
    printStream, schedule, TRUE)  
  
operatorAnalysisString <- outputStream$string("UTF8")  
  
# Report auto-optimization information  
cat(operatorAnalysisString)  
  
# Report posterior quantities  
mean(sample)  
sd(sample)
```

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