

Random Jungle, version 1.0.359

A powerful Random Forests (TM) implementation
Edition 1.0.359, 8 April 2010

by Daniel F. Schwarz
(bug@randomjungle.com)

This manual (8 April 2010) is for Random Jungle (RJ) version 1.0.359, a package containing an implementation of the Random Forests (TM) method.

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`Random Jungle` is an implementation of Random Forests (TM). It is mostly compatible to the original fortran code. `Random Jungle` also has additional builtin functions.

`Random Jungle` is written by Daniel F. Schwarz and few volunteers. All names and email addresses can be found in the files '`randomjungle-1.0.359/AUTHORS`' and '`randomjungle-1.0.359/THANKS`' from the Random Jungle distribution.

This is release 1.0.359. It is considered unstable: future releases are meant to add new features, fix bugs, increase speed, or improve documentation. However...

1 Introduction and preliminaries

This first chapter explains what **Random Jungle** is, where **Random Jungle** comes from, how to read and use this documentation, how to call the **Random Jungle** program, and how to report bugs about it. It concludes by giving tips for reading the remainder of the manual.

The following chapters then detail all the features of the **Random Jungle** .

1.1 Introduction to Random Jungle

Random Jungle is an implementation of Random Forests (TM). It is supposed to analyse high dimensional data. In genetics, it can be used for analysing big Genome Wide Association (GWA) data. Random Forests (TM) is a powerful machine learning method. Most interesting features are variable selection, missing value imputation, classifier creation, generalization error estimation and sample proximities between pairs of cases.

Random Jungle is mostly compatible with the Linux and Windows (TM). Also, there exists compatibilities with Solaris.

1.2 Historical references

First ideas were seeded in 2006 during GAW15 workshop in Florida. In the beginning of 2008, Daniel F. Schwarz released 0.5.0 and 0.5.1 which was a "way pre-release" and fast, but lagged of features and documentation. However, the williams award was won at the International Genetic Epidemiology Society (IGES) conference 2008 in St. Louis with release 0.5.2. In late 2008 and 2009, intensive work improved the platform compatibility, added documentation and raised the number of features of **Random Jungle**.

1.3 Problems and bugs

If you have problems with **Random Jungle** or think you've found a bug, please report it. Before reporting a bug, make sure you've actually found a real bug. Carefully reread the documentation and see if it really says you can do what you're trying to do. If it's not clear whether you should be able to do something or not, report that too; it's a bug in the documentation!

Before reporting a bug or trying to fix it yourself, try to isolate it to the smallest possible input file that reproduces the problem. Then send us the input file and the exact results **Random Jungle** gave you. Also say what you expected to occur; this will help us decide whether the problem was really in the documentation.

Once you've got a precise problem, send e-mail to bug@randomjungle.com. Please include the version number of **Random Jungle** you are using. You can get this information with the command `rjungle --version` or `rjungle -Z`.

Non-bug suggestions are always welcome as well. If you have questions about things that are unclear in the documentation or are just obscure features, please report them too.

1.4 Using this manual

This manual contains a number of examples of **Random Jungle** input and output, and a simple notation is used to distinguish input, output and error messages from **Random Jungle**. Examples are set out from the normal text, and shown in a fixed width font, like this

This is an example of an example!

To distinguish input from output, all output from `Random Jungle` is prefixed by the string ‘`⇒`’, and all error messages by the string ‘`[error]`’. When showing how command line options affect matters, the command line is shown with a prompt ‘`$ like this`’, otherwise, you can assume that a simple `rjungle` invocation will work. Thus:

```
$ command line to invoke rjungle
```

```
Example of input line
```

```
⇒Output line from rjungle
```

```
[error] and an error message
```

The sequence ‘`^D`’ in an example indicates the end of the input file. The sequence ‘`␣`’ refers to the newline character. The majority of these examples are self-contained, and you can run them with similar results by invoking `rjungle -d`. In fact, the testsuite that is bundled in the `Random Jungle` package consists of the examples in this document! Some of the examples assume that your current directory is located where you unpacked the installation, so if you plan on following along, you may find it helpful to do this now:

```
$ cd randomjungle-1.0.359
```

2 Compiling and installing

2.1 Compiling and installing Random Jungle

There are pre-compiled versions on the internet site <http://www.randomjungle.com/>. Maybe, there exists a pre-compiled version for your platform (computer) and you do not need to compile it.

Random Jungle uses some GNU tools, libraries and other free open source code. The installation routine (`./configure`) prompt you to install packages which are missing on your machine. It is also recommended to compile the sources with an openMP supporting compiler (i.e. GNU gcc > 4.2). Invoke the following commands to compile `randomjungle`:

```
./configure
make
make check
make install
```

For compiling **Random Jungle** with MPI (message passing interface) support, configure RJ using option `--enable-mpi`. The program is optimized for Open MPI (<http://www.open-mpi.org/>). The MPI mode should be used by experienced users only.

```
./configure --enable-mpi
```


3 Invoking Random Jungle

The format of the `Random Jungle` command is:

```
rjungle [option...]
```

or

```
rjunglesparse [option...]
```

All options begin with ‘-’, or if long option names are used, with ‘--’. On some platforms long options might not work. A long option name need not be written completely, any unambiguous prefix is sufficient. POSIX requires `Random Jungle` to recognize arguments intermixed with files, even when `POSIXLY_CORRECT` is set in the environment. Most options take effect at startup regardless of their position, but some are documented below as taking effect after any files that occurred earlier in the command line. The argument ‘--’ is a marker to denote the end of options.

With short options, options that do not take arguments may be combined into a single command line argument with subsequent options, options with mandatory arguments may be provided either as a single command line argument or as two arguments, and options with optional arguments must be provided as a single argument. In other words, `rjungle -QPDfoo -d a -df` is equivalent to `rjungle -Q -P -D foo -d -df -- ./a`, although the latter form is considered canonical.

With long options, options with mandatory arguments may be provided with an equal sign (=) in a single argument, or as two arguments, and options with optional arguments must be provided as a single argument. In other words, `rjungle --def foo --debug a` is equivalent to `rjungle --define=foo --debug= -- ./a`, although the latter form is considered canonical (not to mention more robust, in case a future version of `Random Jungle` introduces an option named ‘--default’).

`Random Jungle` understands the following options, grouped by functionality.

3.1 Command line options for operation modes

Several options control the overall operation of `rjungle`:

-h

--help Print a help summary on standard output, then immediately exit `rjungle` without reading any input files or performing any other actions.

-Z

--version

Print the version number of the program on standard output, then immediately exit `rjungle` without reading any input files or performing any other actions.

-f *FILENAME*

--file=*FILENAME*

FILENAME of input file with data. Input data has to be numerical. The default *FILENAME* is `input.dat(.gz)`. In R (<http://www.r-project.org>), save data to file using `write.table` as follows:

```
> make.your.data.in.R
> write.table(yourData, file = "input.dat", row.names = FALSE, quote = FALSE)
> quit()
$ rjungle -f input.dat [...]
```

In plink (pngu.mgh.harvard.edu/~purcell/plink/), save data to raw file using the `recodeA` option, set the ped file option and char memory mode option in `rjungle` as follows:

```
$ plink --file yourDataFile --recodeA
$ rjungle -f yourDataFile.raw -p -M 2 [...]
```

Avoid missing values in data. See See [Chapter 4 \[Input data\]](#), page 13, for more details.

`-o FILEPREFIXNAME`

`--outprefix=FILEPREFIXNAME`

`FILEPREFIXNAME` of output files is the first part of output files (i.e. `rjungle.importance`, `rjungle.prediction`, ...). The default `FILEPREFIXNAME` is `rjungle`. Use for example `-o my_analysis_no123`.

`-e CHAR`

`--delimiter=CHAR`

Set the delimiter in your input file to `CHAR`. Default is a space.

`-w2`

Save model (forest) to a file `FILEPREFIXNAME.jungle.xml`.

`-P FILENAME`

Predict data with model (forest) in file `FILENAME` (data is given with option `-f`). Predictions will be written to `FILEPREFIXNAME.prediction`.

`-y ID`

`--treetype=ID`

Choose base classifier by setting `ID` There are several treetypes but only CART is fully supported. Explanatory or exposure variables will be named: input variables. Explained or response variable will be named: output variable. If you want to use CART like Random Forest (TM) does choose one of three possible values as follows:

`= 1 or 5` `[ID]`

CART, y (output variable): nominal, x (input variable(s)): numeric, `ID = 1` is recommended for less different values in the input variables (i.e. GWA SNP data or integer data). `ID = 5` is recommended for more different values in the input variables (i.e. many floating point numbers). Like original Breiman/Cutler/Friedman algorithm.

`= 2` `[ID]`

CART, y (output variable): nominal, x (input variable(s)): nominal,

`= 3` `[ID]`

CART regression trees, y (output variable): numeric, x (input variable(s)): numeric,

= 4 [ID]
 CART regression trees, CART regression trees, y (output variable): numeric, x (input variable(s)): nominal,

Default is a 1.

-t *SIZE*

--ntree=*SIZE*

SIZE is the number of trees in jungle. If *SIZE*=0 then the size will be set automatically depending on mtry and variable size (experimental feature). Default is 500.

-m *SIZE*

--mtry=*SIZE*

SIZE of randomly chosen variable sets. At each node building step, a variable will be selected out of the set, that serves the biggest information gain. The bigger *SIZE* is set, the higher computing time might be. The bigger *SIZE* is set, the more similar trees in jungle will be. High noised data sets should processed with a big *SIZE*. Default is square root of number of input variables.

-x *NUM*

--missingcode=*NUM*

Missings should always coded as NA or *NUM* in your data. The program takes *NUM* as a internal representation of a missing value. Default is -99.

-i *ID*

--impmeasure=*ID*

Variable selection: Choose an method for estimating variable importance as follows:

= 1 [ID]

Intrinsic Importrance (i.e. GINI-Index).

= 2 [ID]

Permutation Importance by Breiman, Cutler (observed in Fortran code).

= 3 [ID]

Permutation Importance by Liaw, Wiener (in R-package RandomForest).

= 4 [ID]

Permutation Importance, raw values, no normalization.

= 5 [ID]

Permutation Importance by Meng et. al

The results will be written to file *FILEPREFIXNAME.importance*. Default is 1 and you can not turn off variable importance output.

-B *ID*

Variable selection/ model optimization: Choose an method for estimating variable importance as follows:

= 0 [ID]

No backward elimination.

= 1 [ID]
 Backward elimination. Discard 50% at each step (slow). Stop if number of variables shrunk to *STOPSIZE*, see option -j.

= 2 [ID]
 Backward elimination. Discard 33% at each step (slow). Stop if number of variables shrunk to *STOPSIZE*, see option -j.

= 3 [ID]
 Backward elimination. Discard only negative values at each step (slow/recommended). (Shown at IGES2007 by Inke R. Konig).

Default is 0.

-j *STOPSIZE*

--nimpvar=*STOPSIZE*

Only necessary if --impmeasure = 2,3,5,6 or 7. How many variable should remain. The lesser *STOPSIZE* is, the reliable the result might be. The smaller *SIZE* is, the higher computing time will be. Default is 100.

-v

--verbose

Print some nice information to screen. Otherwise put information to file *FILEPREFIXNAME.verbose* (default).

-u

--downsampling

Choose randomly samples without replacement. Switched off is default.

-M *ID*

--memmode=*ID*

Usage of the heap memory (RAM) as follows:

= 0 [ID]
 Double precision floating point (BIG).

= 1 [ID]
 Single precision floating point (Normal).

= 2 [ID]
 Char (small). CHAR normally fits in one byte. DATA CELL VALUE HAS TO BE AN INTEGER IN [-127..127].

If you want to use very small data coding, i.e. for SNP analysis, give *rjunglesparse* a try! Default is 0.

-C *FILE*

--colselection=*FILE*

Only use selected columns listed in *FILE*. Example content of *FILE*:

```
var1
var20
var1000
```

`var300`

Default is take all variables.

`-D NAME`

`--depvarname=NAME`

Output variable name in the data SET! If *NAME* is empty then the `randomjungle` switches to unsupervised mode.

`-s`

`--sampleproximities`

It computes proximities between pairs of cases that can be used in clustering, locating outliers, or (by scaling) give interesting views of the data. Can be used as the distance matrix for Multidimensional Scaling (MDS). The results will be written to file *FILEPREFIXNAME.samproximity*. Default: switched off

`-z`

`--seed` Seed of random number generators.

`-U`

`--nthreads=NUM`

Maximally use *NUM* threads (CPUs) for parallel processing. Limit for *NUM* is number of CPUs in computer. Default: Number of CPUs in computer.

`-p`

`--pedfile`

Input file has got ped format (i.e. plink output with recodeA). Default: switched off.

`-I NUM`

`--impute=NUM`

Impute missings in input data using Random Forest(TM)'s imputation algorithm. The number of iterations is given by *NUM*. For imputing continuous data, use option `-A` (`--impcont`) as well. For more information, have a look at http://www.stat.berkeley.edu/~breiman/RandomForests/cc_home.htm.

Do not try to impute untyped SNPs (Schwarz et al. 2009, BMC Proceedings, 3, S65) if case-control-status is missing. Try a different program like: IMPUTE, MACH, PLINK, ... Default: switched off.

`-k NUM`

`--maxtreedepth=NUM`

This is a stop criterium/tunning parameter. Tree growing will stop, when the tree exceeds a depth of *NUM*. Default: switched off.

`-l NUM`

`--targetpartitionsize=NUM`

This is a stop criterium/tunning parameter. Tree growing will stop, when a partition falls below a size of *NUM* samples. Default: switched off.

`-d -g -n -r -c -a -b -w -V -S -P -A -G -E -X`

Those options are experimental. Be cautious about using one of those.

4 Input data

This chapter describes various input file types of `rjungle`.

4.1 Input the whole data

Random Jungle analyses data given in a file, see option `-f`. The file format is matrix like and is as follows:

names [Variable]

The first line of the input file contains the variable names. The variable name must not contain quotes or space characters. The variables are separated by space characters.

cells [Data]

Each following line represents one sample (observation). Every single sample needs to have one numerical value for each variable. The values are separated by space characters and are ordered corresponding to the variable names (of course).

Here, an example of an input file:

```
responseVar inputVar1 inputVar2 inputVar3 inputVar4
0 1.2 3.4 5.6 7.8
0 1.1 3.3 5.5 7.7
0 2.2 4.4 6.6 8.8
1 1.0 3.0 5.0 7.0
1 1.0 3.0 5.0 7.0
1 2.0 4.0 6.0 8.0
```

If you choose the ped file option `-p` then the input file format is ped like. The file must have variables FID, IID, PAT, MAT, SEX, PHENOTYPE and at least three variables (SNPs). Here, an example of an input file:

```
FID IID PAT MAT SEX PHENOTYPE rs1 rs2 rs3 rs4
1000 NA2001 0 0 2 0 0 1 0 1
1000 NA2002 0 0 2 0 0 2 0 1
1001 NA2003 0 0 1 0 1 2 0 1
1001 NA2004 0 0 1 0 1 1 1 1
1002 NA2005 0 0 2 1 1 1 1 1
1004 NA2006 0 0 2 1 1 2 1 1
1005 NA2007 0 0 2 1 2 2 2 2
1006 NA2008 0 0 1 1 2 2 2 2
1007 NA2008 0 0 1 1 2 2 2 2
```

4.2 Restricted analysis

The `rjungle` can be run also with just a subset of all variables which are given in the input file (option `-f`). See description of option `-C`, for more details.

5 Output data

This chapter describes various output file types of `rjungle`.

5.1 The standard output files

If `rjungle` is executed it will always produce three files. See [Section 5.2 \[Log file\]](#), page 15, [Section 5.3 \[Confusion file\]](#), page 15 and [Section 5.5 \[Importance file\]](#), page 15. You can run an example in your `randomjungle-1.0.359` directory and see it.

```
$ cd tests
$ rjungle -f test.ped -p -v -M2
$ ls
rjungle.importance  rjungle.log  rjungle.prediction  test.ped
```

5.2 Log file

The log file contains all options / parameter of the `rjungle` execution. This is useful to reproduce results.

5.3 Confusion file

The `rjungle` always evaluates the classifier. The accuracy on training and test data. Test data is called oob data which is collected during growing process (similar to cross validation's test sets). The results are shown in so-called confusion matrices in file `FILEPREFIXNAME.confusion`. Columns represent the predicted values and rows represent the real values.

When using option `-y1` a file `FILEPREFIXNAME.confusion2` will be created. The file contains class specific error rates.

5.4 Prediction file

The `rjungle` is able to perform new data to a saved classifier (option `-w2` and `-P`). The predicted results will be saved to file `FILEPREFIXNAME.prediction`.

5.5 Importance file

Random Jungle estimates the importance of variables (option `-i`). The results are saved to file `FILEPREFIXNAME.importance` and/or `FILEPREFIXNAME.importance2`. The first file contains four columns but most interesting columns are `varname` (variable name) and `value` (importance value). The higher the `value`, the more important is the variable with name `varname`. This list is sorted ascending. So, look at the tail of file to see the most important variables. The second file contains various permutation importance informations.

5.6 Verbose file

If Random Jungle is invoked from command line without verbose option it is very schtum and do not output anything to screen. It writes all information occurring during a run to file `FILEPREFIXNAME.verbose`. Nevertheless, if you want a takly `rjungle` which puts all process information to screen then use option (`-v`)

```
$ cd tests
$ rjungle -f test.ped -p -v

Start: Thu Nov 27 12:19:26 2008
+-----+-----+-----+
| RandomJungle | ..... | 2008 |
+-----+-----+-----+
| (C) 2008 Daniel Frederik Schwarz et al., GNU GPL, v2 |
| daniel@randomjungle.com |
+-----+-----+-----+

Output to:
rjungle.*
loading data...
Read 9 row(s) and 10 column(s).
Use 9 row(s) and 6 column(s).
dependent variable name: PHENOTYPE
Growing jungle...
Number of variables: 6 mtry = 2
1 thread(s) growing 500 tree(s)
Growing time estimate: ~0 sec.
Generating and collecting output data...
Compiling trees.
Writing accuracy information...
calculating confusion matrix...

Elapsed time: 0 sec
Finished: Thu Nov 27 12:19:26 2008

$
```

6 Error codes

This chapter describes error codes.

6.1 Runtime error codes

Error code description can be found in `randomjungle-1.0.359/src/library/error_codes.txt` or http://www.randomjungle.com/tags/newest/error_codes.txt.

7 Some nice examples

This chapter describes various examples of working with `rjungle`. You can run the examples in your `randomjungle-1.0.359/tests` directory.

7.1 Simple example

We want to grow a simple forest. So, our input data contains 9 input (V1-V9) and 1 output variable(y). 8 output variables are non informative. Only variable V1 is informative.

```
$ rjungle -f test.dat -U1 -z1 -v -D y -o example1
$ ls example1.*
...
```

7.2 Simple example with ped file

Using Plink PED-files:

```
$ rjungle -f test.ped -p -o example2
...
```

7.3 Estimating variable importance

In the first example we used the data in file `test.dat`. As we know, only variable V1 is informative and therefore it is the most important variable. Firstly, lets estimate the fast GINI-Importance with 1000 trees.

```
$ rjungle -f test.dat -U1 -z1 -t1000 -v -D y -o example3.1
$ cat example3.1.importance
...
```

We see that variable V1 is the most important (highest value).

Secondly, we now want to estimate the permutation importance.

```
$ rjungle -f test.dat -U1 -z1 -t1000 -v -D y -i2 -o example3.2
$ cat example3.2.importance2
...
```

Now, we got even a more reliable result. In most cases, only variable V1 is positive. It means that only V1 contributes to a high accurate classification.

7.4 Using R and rjungle

We want to analyse data from R.

```
$ R
...
> mydata = iris
> mydata$Species = as.integer(mydata$Species) # convert factor to integer
> write.table(mydata, file = "data_from_r.dat",
+   row.names = FALSE, quote = FALSE)
> quit("no")
$ rjungle -f data_from_r.dat -U1 -z1 -t500 -v -D Species -o example4
$ cat example4.confusion
```

```
...
$ cat example4.importance
...
```

7.5 Using plink and rjungle

```
$ plink --file gwadata --recodeA
$ rjungle -f plink.raw -p -M2 -v -o example5
...
$ tail example5.importance
```

or

```
$ plink --file gwadata --recodeA
$ rjungleparse -f plink.raw -p -v -o example5
...
$ tail example5.importance
```

The `rjungleparse` uses less memory than `rjungle`. But your data should only use the values 0,1,2 and 3(missing code).

7.6 Prediction

```
$ rjungle -f train.dat -D DependVar -v -w2 -o example6a
...
$ rjungle -f test.dat -D DependVar -v -P example6a.jungle.xml -o example6b
$ cat example6b.confusion
$ cat example6b.prediction
...
```

7.7 Imputation

SNP data (raw/fast imputation):

```
$ rjungleparse -f mypedfile.raw -p -t1 -I1 -o example7_1_1
```

The imputation result was written to `example7_1_1.imputed.dat.gz` and can be used for analysis. E.g.:

```
$ rjungleparse -f example7_1_1.imputed.dat.gz -p ... -o example8_1_2
```

Imputing continuous data:

```
$ rjungle -f continuous.dat -A -D DependVar -I6 -o example7_2
```

or imputing categorical data:

```
$ rjungle -f cate.dat -D DependVar -I6 -o example7_3
```

or imputing data with no groups to classify on (unsupervised learning):

```
$ rjungle -f continuousAndNoGroups.dat -A -I5 -o example7_4
```

7.8 Using plink and rjungleparse

The `rjungleparse` is the same program like `rjungle`, but you can use just a small set of values: 0,1,2 (and 3 as missing coding). You might want to use `rjungleparse` in conjunction with `plink`. The memory consumption of `rjungleparse` is very small.

```
$ plink --file gwadata --recodeA
$ rjunglesparse -f plink.raw -p -v -o example8
...
$ tail example8.importance
```

7.9 Using MPI

For high speed parallel processing, RJ could be used on computer clusters using MPI mode (RJ has to be compiled for MPI!). The program was performed on huge data successfully using 150 processors (300 processes) in parallel on a high performance cluster. However, the MPI mode should be used by experienced users only. In MPI mode, performing permutation importance (option `-i2`, .., `-i5`) is allow exclusivly. Execute RJ as follows:

```
$ plink --file gwadata --recodeA
$ mpirun -np 200 --host hostname1, hostname2, ... rjunglesparse -f plink.raw -
p -v -i4 -o example9
...
$ tail example9.importance
```

Each process writes temp files to working directory (`example9_mpi_id_*.*`). Final results are written to usual files (`example9.*`).

Appendix A How to make copies of the overall Random Jungle package

This appendix covers the license for copying the source code of the overall Random Jungle package. This manual is under a different set of restrictions, covered later (see [Appendix B \[Copying This Manual\]](#), page 35).

A.1 License for copying the Random Jungle package

Version 3, 29 June 2007

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Preamble

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Appendix C Indices of concepts and macros

C.1 Index for all `rjungle` macros

This index covers all `rjungle` builtins, as well as several useful composite macros. References are exclusively to the places where a macro is introduced the first time.

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