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# ColeOR: R package for automating more effective and efficient processing of OR gene models. Developed with beetle genomes in mind :)

NOTE See the file <https://github.com/radamsRHA/ColeOR/ColeOR.pdf> for detailed instructions

## Installing R package ColeOR from github

The R package ColeOR is freely available to download and distribute from github <https://github.com/radamsRHA/ColeOR/>. To install and load ColeOR, you must first install the R package `devtools`,

```
install.packages("devtools")
```

Now using devtools we can install ColeOR from github:

```
library(devtools)
install_github("radamsRHA/ColeOR")
library(ColeOR) # Load package
```

ColeOR also requires the following dependencies to be installed:

```
install.packages('seqinr')
```

ColeOR also requires the following dependencies to be installed and available on your path `$PATH`:

- DeepTMHMM: <https://biolib.com/DTU/DeepTMHMM/> (`biolib` must be in your path)
- Brief instructions for installing DeepTMHMM (from <https://biolib.com/DTU/DeepTMHMM/>)

```
# you can install DeepTMHMM directly from the terminal
pip3 install pybiolib
biolib run DTU/DeepTMHMM --fasta input.fasta
```

To begin using ColeOR try using the examples associated with each function.

## Example: Run `Function.RunDeepTMHMM_Pipeline` on a large fasta file

We can use `Function.RunDeepTMHMM_Pipeline` with option specified for the working directory (in this case: the Desktop) and a input file (in this case: `ExampleModelsORs.fasta` that is included with the ColeOR install)

```
#####
# Load depends #
#####
library(ColeOR)
```

```

library(seqinr)

#####
# get path to fasta file.
# This fasta file represents amino acid sequences for predicted OR gene models.
# This file can be located on your Desktop, and we include an example fasta file with the install of Co
#####

#####
# Read example chromosome alignment #
#####
String.Path_ExampleModels <- system.file("extdata", "ExampleModelsORs.fasta", package="ColeOR") # path

#####
# run TMD predictions #
#####
handle.RESULTS <- Function.RunDeepTMHMM_Pipeline(string.PathDir = '~/Desktop/',
                                                  string.FastaFile = String.Path_ExampleModels)

```

Function.RunDeepTMHMM\_Pipeline will run DeepTMHMM for each of the amino acid sequences provided in the given file (in this case, we used the example fasta file provided with the install) The results will be logged in a TempFile in the working directory that Function.RunDeepTMHMM\_Pipeline creates (on the Desktop, in this case) Also, the results will be logged in the handle.RESULTS object created by Function.RunDeepTMHMM\_Pipeline.