

EXAMPLE in afflmGUI

Using zombie on homo_sapiens as a model xspecies experiment.

Please substitute the word zombie for your species throughout
(- and homo_sapiens for your recipient species chip)

Using a synthesised CDF file called zombie_100.cdf to make an species CDF directory called zombiecdf:

You will need to install makecdfenv into R as normal (**packages>select repositories then install package(s)>makecdfenv**)

Set the home directory to the one containing the zombie_100.cdf using **File> change Dir**:

Then:

```
> library(makecdfenv)
> make.cdf.package("zombie_100.cdf",packagename="zombiecdf", species="homo_sapiens")
```

This is what it will roughly respond with (the specifics will be different for you):

[Reading CDF file.](#)

[Creating CDF environment](#)

[Wait for about 472](#)

[dots.....](#)

.....
Creating package in /Users/seanatwork/Desktop/xspecies/zombiecdf

README PLEASE:

A source package has now been produced in

/Users/seanatwork/Desktop/xspecies/zombiecdf.

Before using this package it must be installed via 'R CMD INSTALL'
at a terminal prompt (or DOS command shell).

If you are using Windows, you will need to get set up to install packages.

See the 'R Installation and Administration' manual, specifically

Section 6 'Add-on Packages' as well as 'Appendix E: The Windows Toolset'

for more information.

Alternatively, you could use make.cdf.env(), which will not require you to install a package.

However, this environment will only persist for the current R session

unless you save() it.

This creates a directory called zombiecdf

Because you might want to use various modified cdfs, it is better to install the CDF packages as and when you need them within the session that you are using them (INSTEAD of the advice in the blue text above).

Make sure you are still in the directory where the zombiecdf directory is stored (don't descend into it).

```
install.packages("zombiecdf",repos=NULL,type="source")
```

This makes the CDF package available to you.

When you want to use it instead of the standard CDF:

From **within afflmGUI** click on Evaluate

type:

```
RawAffyData@cdfName <- "zombiecdf"
```

and click on run (it won't work if you haven't already loaded your targets file)

THAT'S IT.

For synthesising the new CDF files, you can read our xspecies papers and instructions at <http://affy.arabidopsis.info/xspecies/>