## Adding new code to Rtoolbox:

* Fetch/Clone latest repository
* Copy the additional R files to the R folder of the local GITHUB repository folder (e.g., M:\Github\AGOtools\R)
  + Make sure that the R files contain Roxygen2 notes (see below). In particular **@export** needs to be included for it to be added to the NAMESPACE document.
  + Note that multiple R functions can be included in a single document as long as they all have an export function (see for example common\_plotting\_functions.R)
* Do not make manual changes to any document aside from the Rfiles that you are adding. All other changes will be generated automatically in the next steps.
* Load AGOtools.Rproj (this will set environment to be the AGOtools folder)
* Enter roxygen2::roxygenise() (this will build the new NAMESPACE document)
* Commit

## **Roxgen2**

To make use of **roxygen2** comments in R, you write structured comments above your function definitions using #'.

### Example:

#' @param input\_variable\_1 description

#' @return A list of vectors:

#' \* `returned\_variable1` : description (the \* should make it a bulletpoint list)

#' \* `returned\_variable2` : description

#' @importFrom dplyr ungroup (imports specific function from package

#' @import dplyr (imports entire package)

#' @export (exports to NAMESPACE)

**Common Roxygen Tags:**

| **Tag** | **Description** |
| --- | --- |
| @param | Describes a function argument |
| @return | Explains what the function returns |
| @export | Makes the function available to users of the package |
| @examples | Shows how to use the function |
| @details | Optional, for longer explanation |
| @seealso | Link to related functions |
| @import | Import another package |