Windows and Rtools 4.0

Install error on R-devel-ATC

```
Error: package or namespace load failed for 'PLNmodels' in library.dynam(lib, package,
package.lib):

DLL 'Rhdf5lib' not found: maybe not installed for this architecture?

Error: loading failed
```

https://github.com/grimbough/Rhdf5lib/issues/24

Rtools 4.0

- New experimental toolchain for R on Windows based on **gcc 8** and **msys2**
- https://cran.r-project.org/bin/windows/testing/rtools40.html
- Can be installed alongside **Rtools 3.5** without conflict
- You can use **pacman** for installing system dependencies

Windows is special

- Rhdf5lib has a pre-compiled version of libhdf5.dll which is copied during Windows installation
- I build this manually when I change HDF5 version (using **Rtools 3.5**)
  - Hard to get BioC Windows builder to match my setup
  - Is Rhdf5lib the only package that does this?
- Seemed likely that there was some incompatibility between **Rtools 3.5** & **4.0**

Reported issues with several BioC packages

- zlibbioc, Rhtslib, Rprotobuflib, Rhdf5lib
- https://github.com/r-windows/checks/issues/43
- No comments since August 2019 until yesterday

R-testing.exe

- Super straightforward to experiment with the ATC
- The daily build of R-testing is a modified version of R-devel configured for the new toolchain.
- For now, R-testing automatically sets the PATH in R to use make and gcc from **Rtools 4.0**

Rhdf5lib is fine!

- Package builds and installs for both x86 and x64
- All tests in **rhdf5** pass

“The error message from R *DLL 'Rhdf5lib' not found* means that the package was built in single-arch mode, which is the default if the package has a `configure.win`”

- `R CMD build --merge-multiarch` should fix this issue

rwinlib

- Static libraries for building R packages on Windows
- https://github.com/rwinlib
- I don’t really know how to use these, except:

“These packages [magick, pdftools] automatically download binaries from rwinlib, and I have put the static libs in the corresponding folder names” - @jeroen

- Is this distinct from using **pacman**?

Do we need to do anything?

- Should we experiment with building BioC packages using ATC?
  - I think CRAN may be doing this already: *“However as we are now in the toolchain transition, CRAN is temporarily also building the Bioc packages.”* - @jeroen
- Would of our ‘library’ packages be more flexible if they use the **rwinlib** binaries
  - Maybe some could be retired?