The reviewer (Xia Shen) suggested improvements to the RepeatABEL package. The main points being:

1. Correct warnings from R CMD check --as-cran.
2. Make sure that I follow the GenABEL coding style (by using <- instead of =,  and by adding blank spaces around operators).
3. Add the tutorial as a vignette to the package.
4. Use roxygen2 to generate documentation.
5. Motivate why this should be a separate package and not just a function.

**RESPONSE**

1. Version 1.0 of the RepeatABEL package gives one note from R CMD check --as-cran, because one of the examples takes more than 5 s to run (~15 s on my mac). No other notes or warnings were generated (output below on next page).
2. Coding style corrected
3. Tutorial added as a vignette to the package
4. Roxygen2 was used to generate the documentation from the source files. This will definitely help in the future to make any required package updates.
5. I guess that simply this question being raised shows that the package is well-integrated with the GenABEL style, but there are several major reasons why this should be a separate package. Here, I point out three of the most important ones:

1. The package combines a GenABEL object with an R data frame including repeated measurements. Although the code is well integrated with the GenABEL style it allows modelling on a new more advanced level, which requires some GenABEL experience. Therefore it is not suitable to add the functions as part of the GenABEL package and tutorial is included as a vignette to the RepeatABEL package. Perhaps most importantly, having it as a separate package will guarantee that it will be updated regularly by the maintainer.

2. Having repeated measurements means that more advanced modelling is possible, e.g. spatial modelling. The preFitModel function give these possibilities and extends the GenABEL::polygenic\_hglm function (which only allows one VC, the genotypic variance). The modelling possibilities are actually increased rather dramatically compared to GenABEL::polygenic\_hglm. Some of these possibilities are described in the package vignette.

3. We have evaluated the package in a manuscript (pending minor revision in MEE) and a number of research groups in wildlife ecology have already shown interest in our work on this package. Hence, we expect a number of citations to it, which will give an even wider group of users for the GenABEL suite of packages. In the CITATION file we have included both references to the MEE manuscript and GenABEL.

\* using log directory ‘/Users/lars/Dropbox/flycatcher\_projects/RotateLMM\_package/RepeatABEL/RepeatABEL\_0\_2\_Nov2015/TEMP\_working/RepeatABEL.Rcheck’

\* using R version 3.1.1 (2014-07-10)

\* using platform: x86\_64-apple-darwin13.1.0 (64-bit)

\* using session charset: UTF-8

\* checking for file ‘RepeatABEL/DESCRIPTION’ ... OK

\* checking extension type ... Package

\* this is package ‘RepeatABEL’ version ‘1.0’

\* checking CRAN incoming feasibility ... NOTE

Maintainer: ‘Lars Ronnegard <lrn@du.se>’

New submission

\* checking package namespace information ... OK

\* checking package dependencies ... OK

\* checking if this is a source package ... OK

\* checking if there is a namespace ... OK

\* checking for executable files ... OK

\* checking for hidden files and directories ... OK

\* checking for portable file names ... OK

\* checking for sufficient/correct file permissions ... OK

\* checking whether package ‘RepeatABEL’ can be installed ... OK

\* checking installed package size ... OK

\* checking package directory ... OK

\* checking DESCRIPTION meta-information ... OK

\* checking top-level files ... OK

\* checking for left-over files ... OK

\* checking index information ... OK

\* checking package subdirectories ... OK

\* checking R files for non-ASCII characters ... OK

\* checking R files for syntax errors ... OK

\* checking whether the package can be loaded ... OK

\* checking whether the package can be loaded with stated dependencies ... OK

\* checking whether the package can be unloaded cleanly ... OK

\* checking whether the namespace can be loaded with stated dependencies ... OK

\* checking whether the namespace can be unloaded cleanly ... OK

\* checking dependencies in R code ... OK

\* checking S3 generic/method consistency ... OK

\* checking replacement functions ... OK

\* checking foreign function calls ... OK

\* checking R code for possible problems ... OK

\* checking Rd files ... OK

\* checking Rd metadata ... OK

\* checking Rd line widths ... OK

\* checking Rd cross-references ... OK

\* checking for missing documentation entries ... OK

\* checking for code/documentation mismatches ... OK

\* checking Rd \usage sections ... OK

\* checking Rd contents ... OK

\* checking for unstated dependencies in examples ... OK

\* checking contents of ‘data’ directory ... OK

\* checking data for non-ASCII characters ... OK

\* checking data for ASCII and uncompressed saves ... OK

\* checking sizes of PDF files under ‘inst/doc’ ... OK

\* checking installed files from ‘inst/doc’ ... OK

\* checking files in ‘vignettes’ ... OK

\* checking examples ... OK

Examples with CPU or elapsed time > 5s

              user system elapsed

preFitModel 15.159  0.837  16.167

\* checking for unstated dependencies in vignettes ... OK

\* checking package vignettes in ‘inst/doc’ ... OK

\* checking running R code from vignettes ... OK

\* checking re-building of vignette outputs ... OK

\* checking PDF version of manual ... OK

NOTE: There was 1 note.​