

**Subject:** CRAN submission P2C2M 0.6  
**From:** Michael Gruenstaeudl <gruenstaeudl.1@osu.edu>  
**Date:** 01/29/2015 03:23 PM  
**To:** CRAN <cran@r-project.org>

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The following package was uploaded to CRAN:

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Package Information:  
Package: P2C2M  
Version: 0.6  
Title: Posterior Predictive Checks of Coalescent Models  
Author(s): Michael Gruenstaeudl, Noah Reid  
Maintainer: Michael Gruenstaeudl <[gruenstaeudl.1@osu.edu](mailto:gruenstaeudl.1@osu.edu)>  
Depends: R (>= 3.0.0)  
Suggests: genealogicalSorting (>= 0.92), phybase (>= 1.3.1), Rmpi (>= 0.6-5), xtermStyle (>= 2.2-4)  
Description: P2C2M is an R package to conduct posterior predictive checks of coalescent models using gene and species trees generated by BEAST or \*BEAST. The functionality of P2C2M can be extended via two third-party R packages that are available from the author websites only: genealogicalSorting (<http://www.genealogicalsorting.org>) and phybase (<http://odyssey.bioinformatics.uga.edu/~lliu/phybase/>). To use these optional packages, the installation of the Python libraries NumPy (>= 1.9.0) and DendroPy (= 3.12.0) is required.  
License: GPL (>= 2)  
Imports: ape (>= 3.1-4), apTreeshape (>= 1.4-5), ggplot2 (>= 1.0.0), rPython (>= 0.0-5), stringr (>= 0.6.2)

The maintainer confirms that he or she has read and agrees to the CRAN policies.

Submitter's comment: Issues of previous submission have been addressed

R-devel version used for checking:  
latest r-devel build of R version 3.1.2  
(2014-10-31)

Purpose of submission: Update package to version 0.6