Subject: Re: CRAN submission P2C2M 0.6
From: Prof Brian Ripley <ripley@stats.ox.ac.uk>
Date: 01/30/2015 02:28 AM
To: Michael Gruenstaeudl <gruenstaeudl.1@osu.edu>, CRAN <cran@r-project.org>

On CRAN now.

On 29/01/2015 20:23, Michael Gruenstaeudl wrote:
> [This was generated from CRAN.R-project.org/submit.html]
>
> The following package was uploaded to CRAN:
> ==
>
> 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>
> 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

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Brian D. Ripley,   ripley@stats.ox.ac.uk
Emeritus Professor of Applied Statistics, University of Oxford
1 South Parks Road, Oxford OX1 3TG, UK