HASH License

January 12, 2013

HASH is an automated program for predicting H^{α} chemical shifts using the chemical shifts of nearby backbone atoms (i.e., adjacent atoms in the sequence). HASH combines a new fragment-based chemical shift search approach with a non-parametric regression model, called the generalized additive model, to effectively solve the prediction problem. HASH is developed in the lab of Prof. Bruce Donald at Duke University.

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<signature of Bruce Donald>, 01 May, 2012

Bruce R. Donald, Professor of Computer Science and Biochemistry

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[a] Jianyang Zeng, Pei Zhou, and Bruce Randall Donald. HASH: a program to accurately predict protein Ha shifts from neighboring backbone shifts. *Journal of Biomolecular NMR*, Dec 16, 2012. [Epub ahead of print]

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The "Minimal Corresponding Source" for a Combined Work means the Corresponding Source for the Combined Work, excluding any source code for portions of the Combined Work that, considered in isolation, are based on the Application, and not on the Linked Version.

The "Corresponding Application Code" for a Combined Work means the object code and/or source code for the Application, including any data and utility programs needed for reproducing the Combined Work from the Application, but excluding the System Libraries of the Combined Work.

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If you modify a copy of the Library, and, in your modifications, a facility refers to a function or data to be supplied by an Application that uses the facility (other than as an argument passed when the facility is invoked), then you may convey a copy of the modified version:

- a) under this License, provided that you make a good faith effort to ensure that, in the event an Application does not supply the function or data, the facility still operates, and performs whatever part of its purpose remains meaningful, or
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