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Yanthe E Pearson* (yanthe.pearson@gmail.com), 38 Maryland Ave, Rockville, MD 20850, and **William Fagan, Elise Larsen, Emma Goldberg, Heather Lynch, Hillary Staver** and **Jessica Turner**. *Estimating population growth rates for mammalian species*.

The per capita rate of population growth, r , is a central measure of population biology that is crucial for understanding the dynamics and extinction risks of real species. However, researchers can only calculate this metric for the small subset of species for which adequate time series, life tables, and similar datasets are available. Here we introduce a phylogenetic approach for predicting r for poorly known species by viewing r as a synthetic life history trait that varies among species within a clade. Combining stochastic macroevolutionary models, molecular phylogenies, and life history trait data, we predict the potential for population growth for mammals of the Caniformia and Cervidae. Cross-validation analyses demonstrate that, even with sparse life history data across species, these phylogenetic methods are capable of estimating r to within a factor of 2 routinely, and often do much better. (Received August 16, 2011)