

approximator, Bayesian prediction of complex computer codes. base.rms, regression transformation between base function and package 'rms'. bio.bio, a function that processes bio.bio data: bio.bio.accept(n) (The function accepts n elements from ndarray and maps them into a list of elements in the order they were defined in the file. This list must have same order as ndarray.If the order of elements is not the same, rms.translate(n, rms.normalize()) will convert it accordingly.

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