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Poster presentation

Microarrays expression measurement Richard Pearson*

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Microarrays can measure the expression levels of all genes within a species. This can give insight into the molecular basis of stress responses in plants. Recent microarray analysis methods can give probability distributions of expression levels as well as point estimates, which can be propagating through subsequent analyses yielding improved results. Such methods are currently slow, applicable only to certain types of arrays, and cannot be applied to multi-factorial experiments. There are also no methods available for analyzing multi-species experiments. Our work aims to address all these shortcomings of current analysis methods, and create a Propagating Uncertainty in MicroArrays (puma) package for biologists.

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