**ExP Heatmap: visualization of high-dimensional pairwise genomic data**

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**Abstract:**

The Cross-Population Heatmap (ExP heatmap) is a novel method developed by our team to display highly dimensional cross-population data. It is suitable to display several thousands of data-points, each with hundreds of dimensions. We are aiming this tool to cross-population (or pair-wise) data, primarily on 1000 Genomes Project, phase 3, genomic data, but the method can be easily extended or adapted for usage on essentially any type of data that are in form of similarities/distances between groups. The most profound advantage of our method is the ability to display several millions of results (i.e. p-values, distances) in one picture, while allowing the user to clearly identify significant patterns or important genome areas by his or her own sight. All this with fast and user-friendly implementation.

Availability and Implementation: The ExP method was implemented in Python 3.8+ and is ready to be used as Python package or stand-alone command-line tool. It is available from official Python Package Index (PyPI, <https://pypi.org/project/exp-selection/1.0.0/>) or GitHub (<https://github.com/ondra-m/exp-selection>). We are looking forward to several updates of ExP heatmap software coming up in our pipeline.