**Software requirement specification**

**V.1.1**

**for: MPA – metabolic pathway analysis**

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1. **Introduction**

**A tool to identify significantly perturbed metabolic pathways from Reactome for a condition under study when comparing to control/healthy**

[**https://reactome.org/PathwayBrowser/**](https://reactome.org/PathwayBrowser/)**­**

1. **Overall description**

**Input: High-throughput metabolite levels for condition and control samples**

**Output: Ranked list of Reactome pathways that perturbed in the condition under study – the rank is based on a score or p-value that results from evaluating the pathway disruption given the data and the pathway information from the Reactome database**

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1. **Requirements**

**Input data format for gene expression: text file with metabolites on the rows and samples (condition or control) on the columns**