# *Simplified from* [*https://github.com/PathwayAndDataAnalysis/causalpath/blob/master/wiki/OutputFiles.md*](https://github.com/PathwayAndDataAnalysis/causalpath/blob/master/wiki/OutputFiles.md)

# Possible output files from a CausalPath run and their description

CausalPath program argument = name of a directory that should contain the parameters.txt file; CausalPath output generated into the same directory; output files that as CasalPath results are all tab-delimited (except the two json files)

results.txt: Each row = the prior **binary relation and the matching experiment data**; for correlation-based analysis: **correlation value and its p-value**; for comparison-based analysis: **change amount and p-values** for both source and target data changes

causative.sif: SIF result file for identified causal relations (**gene-centric**); (**for vizualitation with ChiBE** - causative.format file should be in the same directory)

causative.format: Complements causative.sif **for ChiBE** by providing visual features of the result network

causative.json: **For vizulation of the result causal network with web-service** (alternative to ChiBE)

causative-data-cetric.sif: SIF network that uses nodes for the data IDs(**data-centric**); **for visualization with ChiBE**; only generated if generate-data-centric-graph = true.

causative-data-cetric.format: Complements causative-data-centric.sif **for ChiBE** by providing visual features

conflicting.sif: **network showing the causal priors with contradicting experiment data** (contradicting = the data change is significant within the thresholds, but the change direction is opposite to what we expect by the causal priors); **for vizualisation with ChiBE**

conflicting.format: Complements conflicting.sif by providing visual features of the network for **vizualisation with ChiBE**

conflicting.json: For **web-service vizualisation of the result conflicting network**

unknown-site-effects.txt: Provides the list of **sites with unknown effect**, and also there are changes at the downstream that could be explained by the upstream changes only if we knew these site effects. CausalPath does not know functional effects of every measured site; users can manually curate these effects from the literature and add them into the proteomic data file; if users manually curate the effect of a site in this file, it can produce an additional edge in the final network with 50% chance

pval-uniformity.txt: Generated whenever FDR controlled within CausalPath as a **graphical guide showing the intensity of the signal in the data**. Users can plot this table in to see the deviation of the ranked p-values from the x=y line (the more deviation toward x-axis = signal with higher intensity).

significance-pvals.txt: Generated only if network significance is calculated. 1st row = overall **network significance**; following table provides p-value(s) for each gene downstream; correlation-based analysis: 1 p-value per gene; comparison-based analysis: 3 p-values for each gene (downstream overall size, activation-suggesting downstream, inhibition suggesting downstream); CausalPath uses these values after correcting for multiple hypothesis testing.

**value-changes.txt:** **Value changes for each loaded data in a comparison-based analysis**; if original data used by applying a t-test on the data, will show the t-value and p-value coming from the test, per data row.