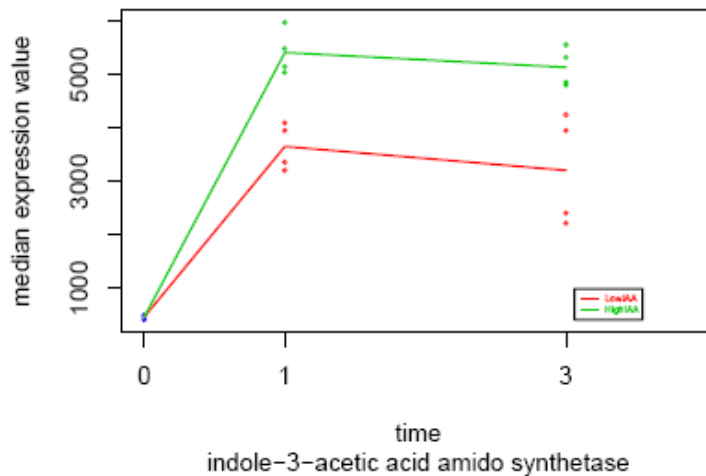
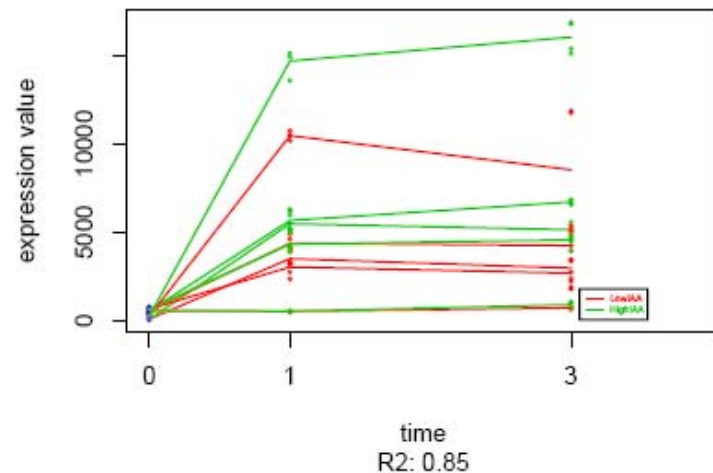


maSigFun analysis of Arabidopsis indole-acetic acid dataset. *Indole-3-acetic acid amido synthetase* class

Profiles 4: 1 functional classes



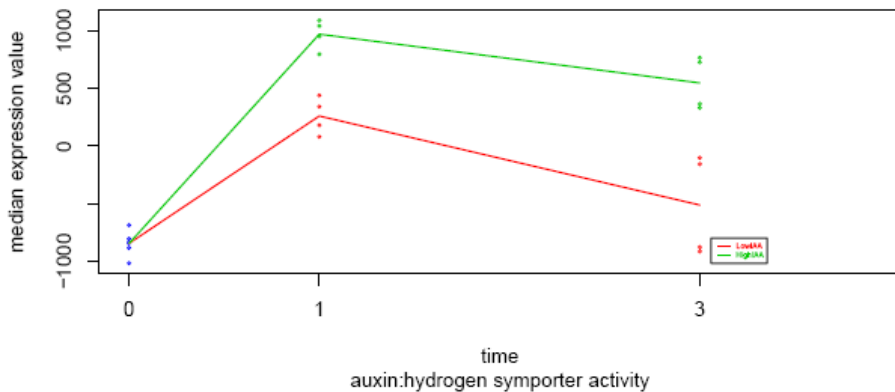
Profiles 4: 5 genes



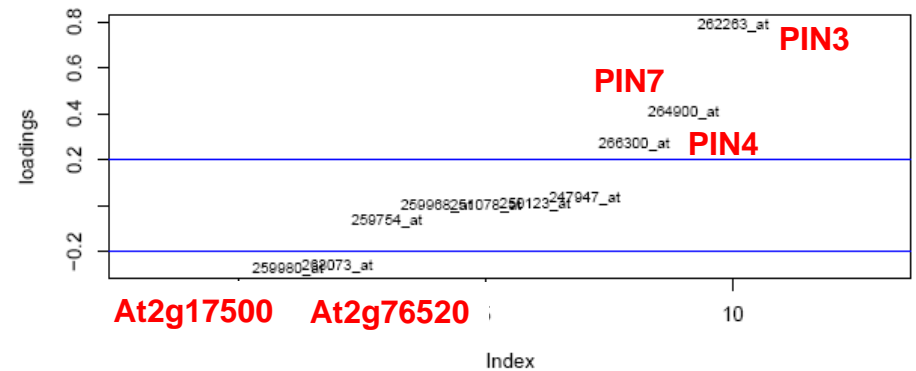
Left panel panel shows the median profile of the class, corresponding to the upregulation of gene expression at time points 1 hour and 3 hours, which is more pronounced at the high IAA dose. The right panel shows the individual expression profiles of the 5 genes annotated to this class. The mean pair-wise correlation of these 5 genes is 0.85.

PCA-maSigFun analysis of Arabidopsis indole-acetic acid dataset. *auxin:hydrogen symporter activity class*

Profile of GO:0009672_1: 1 functional classes

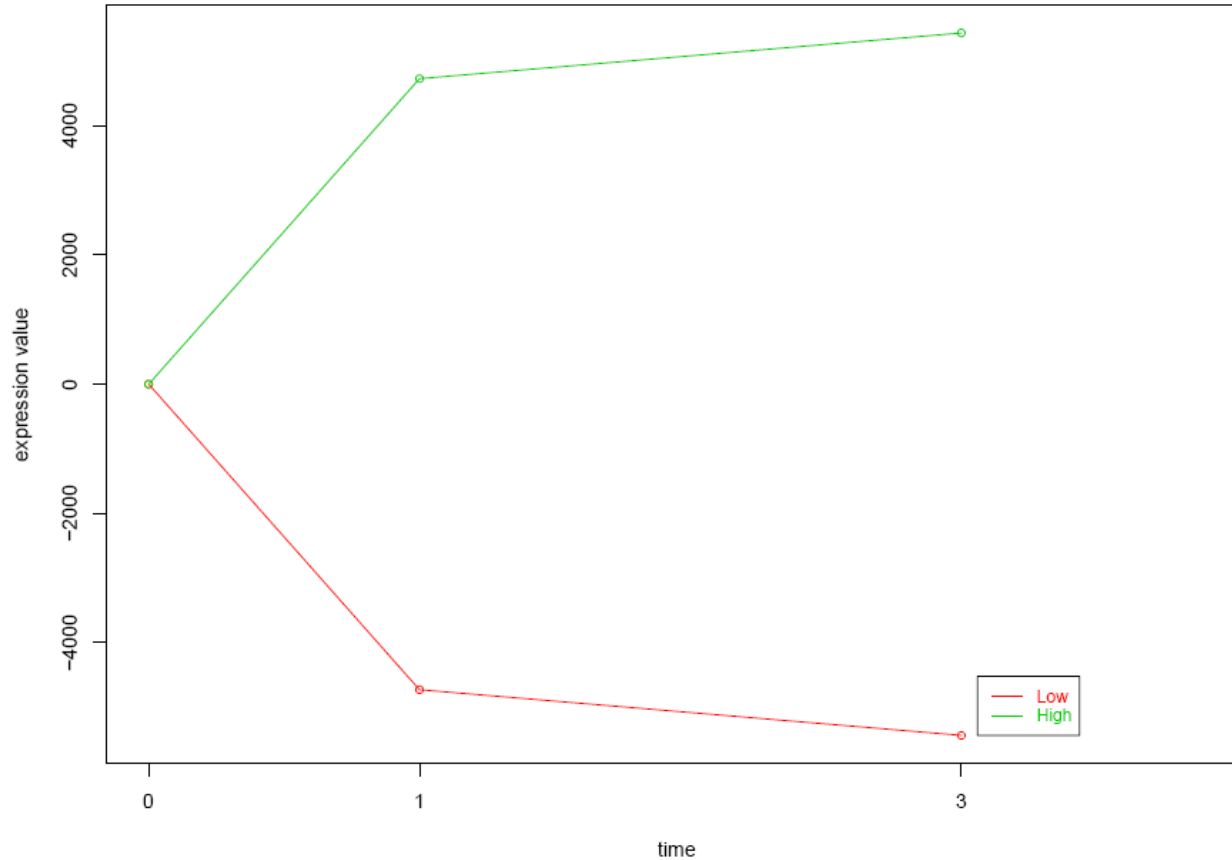


auxin:hydrogen symporter activity_1



The *auxin:hydrogen symporter activity* class is bi-modal. Genes of the PIN class (PIN3, PIN4 and PIN7) are positively correlated (positive loadings, right panel) with the extracted class pattern, i.e. dose-dependent induction at time point 1 hours (left panel). Two other genes (the auxin efflux carrier proteins At2g17500 and At2g76520) show negative correlation (negative loadings) with the class pattern, i.e., are repressed at time point 1 hour.

ASCA functional analysis of Arabidopsis indole-acetic acid dataset. Score plot of Principal Component 1 of time \times treatment submodel



The first principal component (77% explained variability of the time \times treatment interaction) describes the different expression level at time point 1 hours and 3 hours between low and high IAA doses