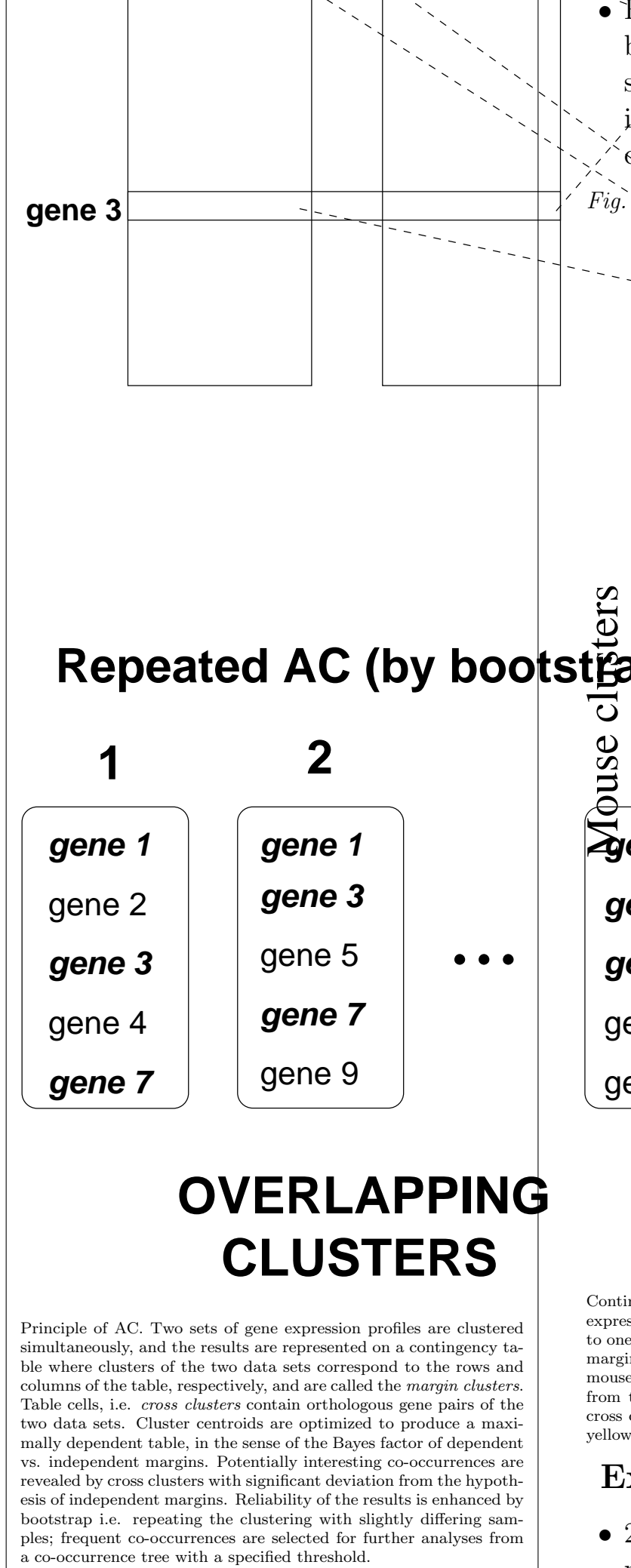


Functions of human genes are often studied indirectly, by model organisms such as the mouse. An underlying assumption is that genes with a common evolutionary origin i.e. orthologous genes, have similar functional roles in both species.

It is critical to know whether the function of orthologues is really similar. Orthologous gene groups with unexpectedly many similarly expressed gene pairs may highlight important physiological similarities between the species. Diverged gene function may refer to significant evolutionary changes.

Here a dependency exploration tool called associative clustering (AC) [2] is used to identify orthologous man-mouse gene pairs with potentially interesting regularity in their expression (Fig. 1).



## Methods

- AC explores dependencies in paired

