

The Edinburgh Pathway Editor – a graphical editor for biological pathways.

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The explosion in biological data resulting from high-throughput experiments threatens to overwhelm an individual's ability to comprehend the information available for a given biological process or entity. Furthermore, the increased numerical data relating to biological pathways has also rendered feasible the ability to mathematically model these pathways.

This new information requires new software tools to manipulate and display it in a way that can make knowledge accessible, to summarise the information, and to integrate disparate sources of information.

The Edinburgh Pathway Editor (EPE) aims to provide a solution to these requirements. EPE is a graphical editor for biological pathways. Maps can be drawn in two major ways. Firstly, they can be imported from external sources and laid out using automated layout algorithms. Secondly, they may be created *de novo* using a sophisticated drawing palette. EPE is distributed with several common visual notations (e.g., Kegg, STKE) but also allows the user to define their own notations. Users can annotate map elements with biological information, or link them to external databases. EPE also supports the SBML initiative, which facilitates compatibility between systems biology software applications, and allows maps generated in the editor to be used in mathematical modelling tools.

EPE stores its maps in an internal relational database, which enables searching of maps. Maps can also be hyperlinked to one another, which allows a hierarchy of maps to be developed.

EPE is available for MacOSX, Windows and Linux GTK platforms and is available for download at <http://www.bioinformatics.ed.ac.uk/epe/>.