Ingenuity Pathway Analysis

User Setup Guide

30th November 2018

Getting Started

Sydney University has a single Ingenuity Pathway Analysis license and is available free of charge to Sydney University students, staff and affiliates. To access Ingenuity, you will need:

1. An account with Sydney Informatics Hub's PPMS. Follow this link to request an account: https://au.ppms.info/sydney/login/?pf=6
   - Fill out the account creation request form and answer all of the questions including: University ID #/ Security card # (staff of student number, if external your institution name); access expiry date (planned thesis submission date, end of contract or end of project date). Nationality is optional.
2. An e-mail address registered with QIAGEN so that you can check out the IPA license – contact Tracy Chew (tracy.chew@sydney.edu.au) to register.
3. Either: a computer with a web browser and a current version of Java

Or download the IPA App installer from: https://analysis.ingenuity.com/pa/installer/select

Logging on

1. Make sure you have an account with SIH's PPMS and your email is registered with QIAGEN
2. Book your session on PPMS: https://au.ppms.info/sydney/login/?pf=6

3. Login to IPA at: http://www.ingenuity.com/products/login or open the IPA app
4. Follow the IPA prompts to run IPA as either a web version or an applet version (i.e. via IpaApplication.jnlp).
5. If you log out and have trouble logging back in try closing your browser then logging back in.
6. If you get the error message "The IPA institutional license you are attempting to access is currently being used by the maximum permitted number of simultaneous individual users. Please try logging into IPA later" check that you have booked IPA via PPMS, if so, use the Incident button on the PPMS booking calendar page to log an incident. Please include the time(s) of day when you were unable to log in.

Resources

The Qiagen Bioinformatics website has a set of training resources. The most popular **webinars** are:

- IPA Introduction
- Data Formatting and uploading
- Interpreting the results

Tips and tricks

- Use excel files
- One column should consist of one or more identifiers for molecules such as genes, RNAs, proteins, or chemicals.
- the other column(s) are for numerical data or 'observations' for example: log2Ratio of fold change and the corresponding p-values.
- a maximum of 20 observations and allows and Expression values per observations can be uploaded, any more will be excluded during the upload process.
- There are also tutorials on [formatting of data](#) and [uploading into IPA](#).
- [Qiagen bioinformatics TV](#) hosts dozens of video including more [introductions](#) and [tutorials](#).

Contact Us

If you need assistance, please contact:

QIAGEN Bioinformatics Technical and Application Support
Email: ts-bioinformatics@qiagen.com
Phone (U.S.): +1 866 464 3684
- Phone support is only available between 0.00 – 17.00 PST time

Sydney University's Bioinformatics Technical Support Officer
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