Analysis of iCLIP data with the iCount python module

A short tutorial

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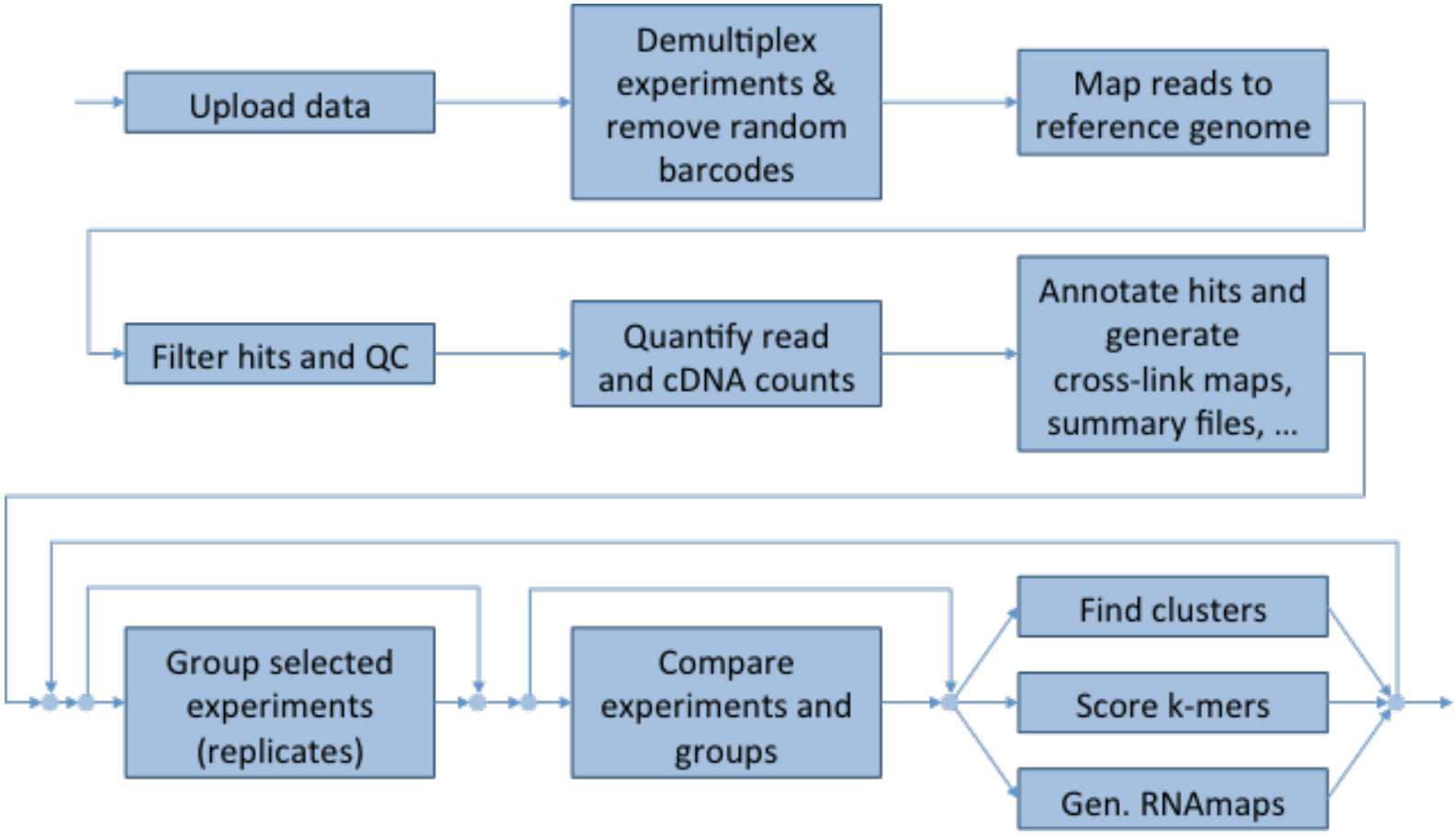
History and acknowledgements for iCount

From its start in late 2008, a great number of people contributed to the development of iCount.
In mid-2016, Jure Zmrzlikar from Genialis helped to improve the code, which is now available on github.

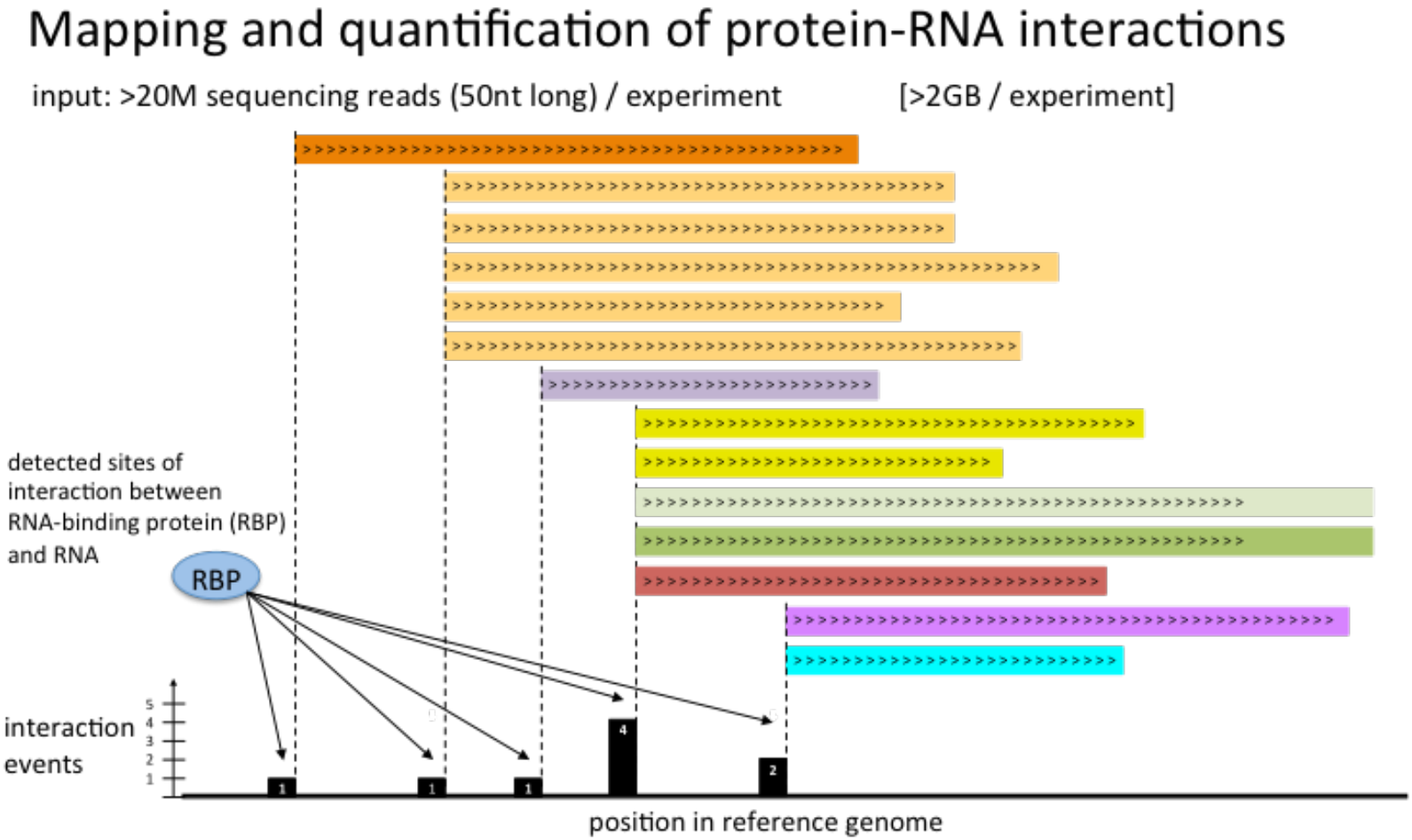
- Tomaž Curk
- Gregor Rot
- Črtomir Gorup
- Julian Konig
- Yoichiro Sugimoto
- Nejc Haberman
- Goran Bobojević
- Jure Zmrzlikar
- Christian Hauer
- Matthias Hentze
- Blaž Zupan
- Jernej Ule

Pipeline



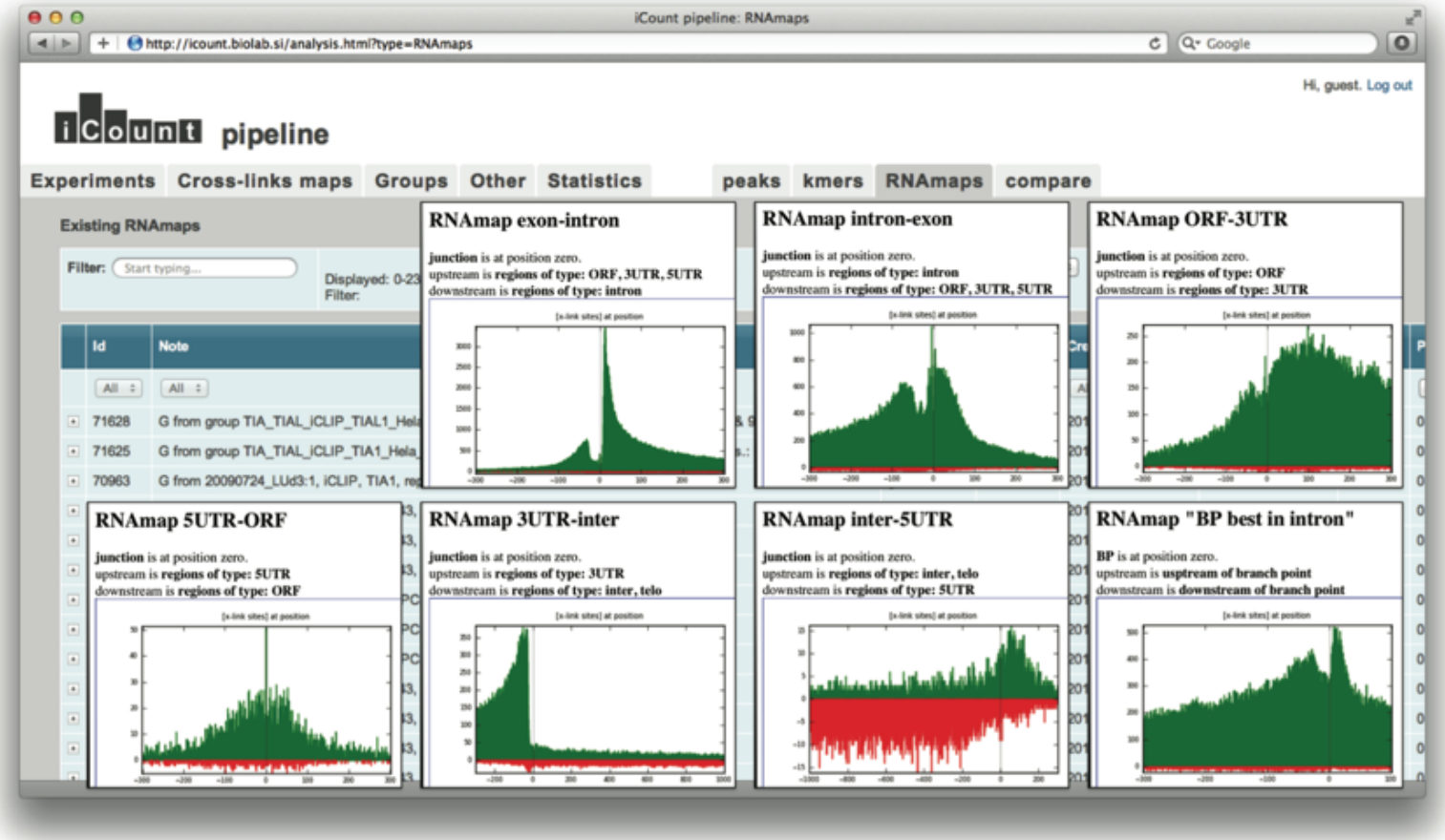
Main steps in the cross-link mapping and annotation pipeline.

Finding cross-linked sites



The most crucial step is site indetification and quantification.

The old web interface

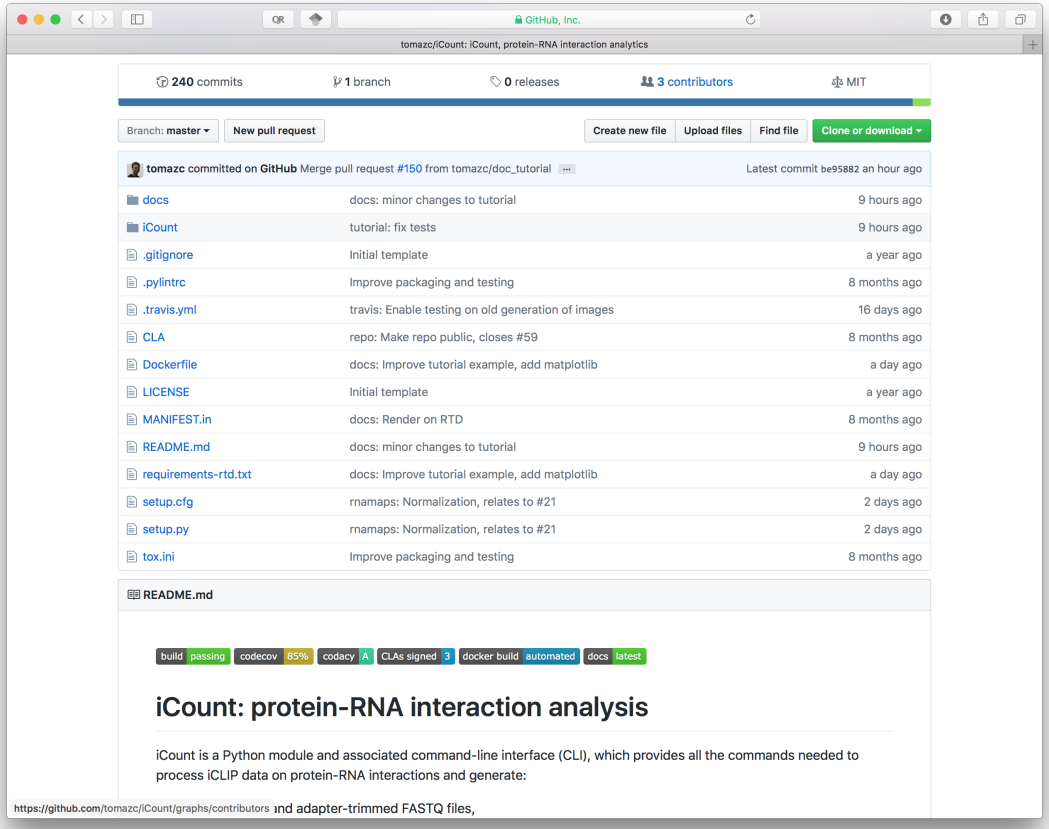


This interface is still in use.
It will be replaced soon by an implementation by Genialis.

The old iCount - impact

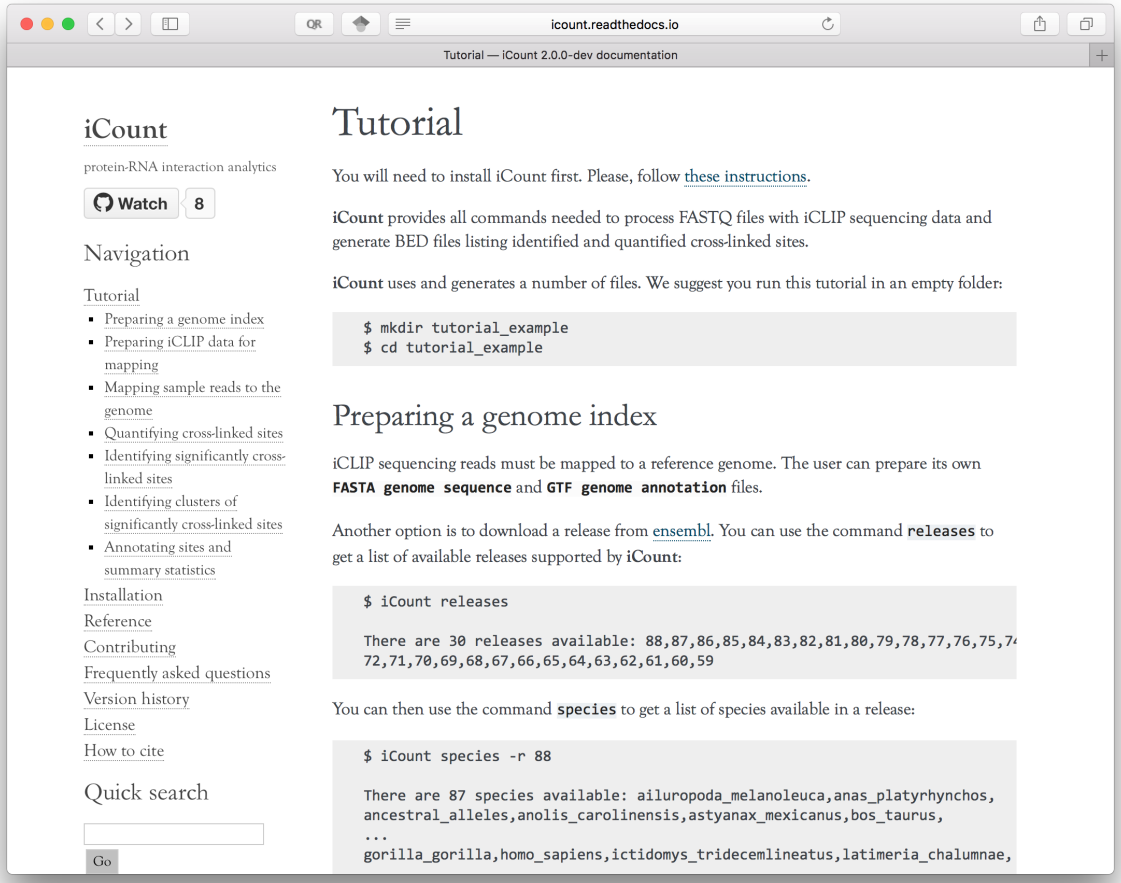
- 100+ users
- 40+ institutions: UCL, MRC LMB, EMBL, mpi-cbg.de, ...
- 2M+ EUR cost of sequencing alone
- 80+ proteins (8% of known human RBPs)
- 5000+ experiments (iCLIP, CLIP, pA-Seq, mRNA-seq,...)
- 800+ user-defined groupings of experiments
- 10 species
- 33000 analyses
- (Co)authors of over 25 publications using results from iCount.

iCount is available on github!



http://github.com/tomazc/iCount
Comments and PR are welcome!

Tutorial



http://icount.readthedocs.io/en/latest/tutorial.html

Use and contribute to iCount

In case of problems, post an issue on github or contact:
tomaz.curk@fri.uni-lj.si
Welcome to contribute to http://github.com/tomazc/iCount

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