

**Supplemental Text 1.** We provide detailed instructions and screenshots for how to launch ILC regulatory network visualization tools. Note that networks can also be downloaded to your computer by following installation instructions on the page below.

1. Use a web browser to navigate to <https://github.com/flatironinstitute/ILCnetworks>.
2. Press the “launch binder” button to launch the binder of ILC networks:

The screenshot shows the GitHub repository page for `flatironinstitute/ILCnetworks`. At the top, there's a navigation bar with links for Features, Business, Explore, Marketplace, Pricing, and Sign in or Sign up. Below the header, there's a search bar and some repository statistics: 4 watches, 0 stars, and 0 forks. The repository name is `flatironinstitute / ILCnetworks`. Under the repository name, there are links for Code, Issues (0), Pull requests (0), Projects (0), and Insights. A prominent "Join GitHub today" banner is displayed, followed by a "Sign up" button. The main content area shows the repository details: 10 commits, 1 branch, 0 releases, and 2 contributors. A dropdown menu shows the current branch is "master". There are buttons for "Find file" and "Clone or download". Below this, a list of commits is shown, all made by user `emiraldi`. The commits include removing encryption materials, updating notebooks, and fixing build scripts. The most recent commit was 3 days ago. At the bottom of the page, there's a section titled "ILC regulatory network explorer" with a "Launch binder" button highlighted by a red box and arrow. Below this, there's a brief description of the repository and its purpose, mentioning the use of Jupyter notebooks and the `jp_gene_viz` tool. It also describes the repository's design for running in the cloud using Binder or locally using repo2docker.

Inc. [US] | <https://github.com/flatironinstitute/ILCnetworks>

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ILC regulatory networks

10 commits 1 branch 0 releases 2 contributors

Branch: master ▾ New pull request Find file Clone or download ▾

emiraldi removed encryption materials Latest commit 553c5eb 3 days ago

ILC\_TRN\_Notebooks removed encryption instructions from README.md 3 days ago

.gitignore Initial commit 4 months ago

README.md removed encryption instructions from README.md 3 days ago

postBuild fix postBuild for binder 4 months ago

requirements.txt initial checkin with encrypted data 4 months ago

runtime.txt initial checkin with encrypted data 4 months ago

README.md

## ILC regulatory network explorer

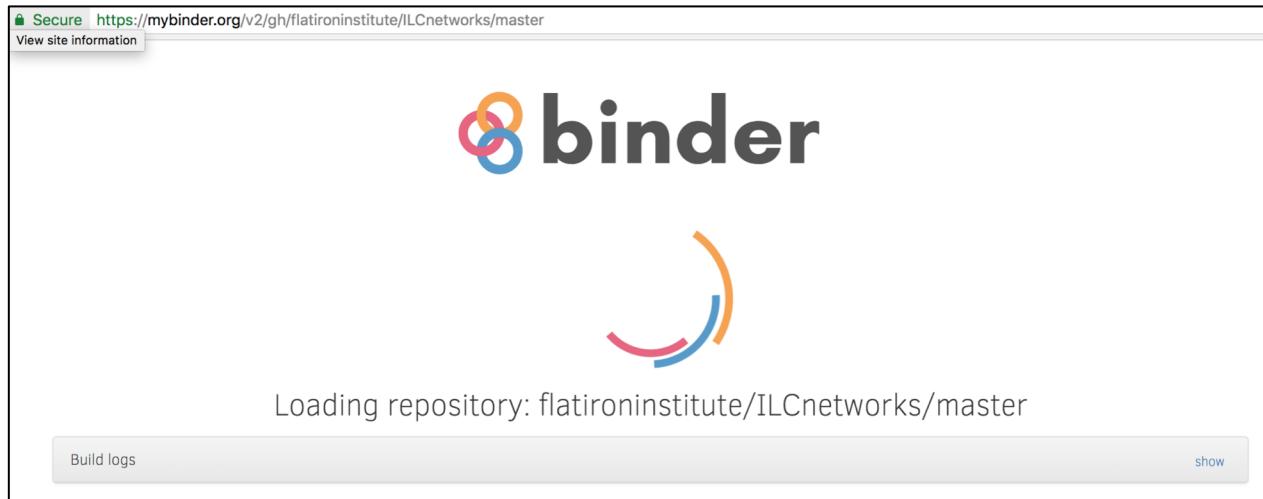
[Launch binder](#) ← Launch binder button

Interactive visualization of transcriptional regulatory networks (TRNs) and gene expression heatmaps from Miraldi\*, Pokrovskii\* et al. (2018) "Characterization of transcriptional regulatory networks that drive the identities and functions of intestinal innate lymphoid cells"

This repository uses Jupyter notebooks to interactively visualize TRNs with `jp_gene_viz`

This repository is designed to either run in the cloud using [Binder](#) or locally in an encapsulated container using [repo2docker](#) to build and run a `docker` container which includes the code for running the analysis and all needed dependencies. The `repo2docker` tool requires the `docker` infrastructure and Python 3 to run. See the [Installation instructions](#).

3. Wait for the binder to load (~30 seconds). You'll see this temporarily:



4. A directory will load. Click on blue text “ILC\_TRN\_Notebooks” to open the directory containing .ipynb notebook interactive network visualizations:

Secure | <https://hub.mybinder.org/user/flatironinstitute-ilcnetworks-s8jqmv39/tree>

jupyter

Files Running Clusters

Select items to perform actions on them.

	Name	Last Modified	File size
<input type="checkbox"/>	0		
<input type="checkbox"/>	conda-bld	a day ago	
<input checked="" type="checkbox"/>	ILC_TRN_Notebooks	32 minutes ago	587 B
<input type="checkbox"/>	src	27 minutes ago	
<input type="checkbox"/>	postBuild	32 minutes ago	587 B
<input type="checkbox"/>	README.md	32 minutes ago	1.24 kB
<input type="checkbox"/>	requirements.txt	32 minutes ago	17 B
<input type="checkbox"/>	runtime.txt	32 minutes ago	10 B

Upload New ↗

Quit Logout

5. You will now see several notebooks (files ending with .ipynb). Click on any notebook to see a particular network view, and it will open in a new tab. Below we describe which networks pertain to figures in the manuscript:

	Name	Last Modified	File size
<input type="checkbox"/> 0	..	seconds ago	
<input type="checkbox"/> Bcl6KO_TRNs		39 minutes ago	
<input type="checkbox"/> GeneExpression		39 minutes ago	
<input type="checkbox"/> GeneSets		39 minutes ago	
<input type="checkbox"/> qATAC_10_1_bias25_maxComb	Bc6 KO RNA-seq heatmaps (Fig. 7, S7)	39 minutes ago	
<input type="checkbox"/> Bcl6_KO_geneExpressionStudy_heatmaps.ipynb	ILC subset “core” TRNs (Fig. 3)	39 minutes ago	3.78 kB
<input type="checkbox"/> core_ILC_TRNs_FDR1E-5_TopN.ipynb	Full ILC TRN (all 63,382 TF-gene interactions)	39 minutes ago	44.4 kB
<input type="checkbox"/> full_ILC_TRN.ipynb	Multi-study ILC gene expression heatmaps	39 minutes ago	31.7 kB
<input type="checkbox"/> ILC_heatmaps.ipynb	TF-TF Modules (Fig. 4)	39 minutes ago	3.95 kB
<input type="checkbox"/> TfTfModules-Positive-c57.ipynb		39 minutes ago	41.7 kB

6. For example, click on the “core\_ILC\_TRNs\_FDR1E-5\_TopN.ipynb”. It will open in a new tab.

```

In [1]: # Visualization of core TRNs unique to or shared by specific ILC subsets (ILC1, NK, ILC2, CCR6+ILC3, CCR6-ILC3)
# Miraldo*, Pokrovskii* et al. (2018) "Characterization of transcriptional regulatory networks that drive the identities
# and functions of intestinal innate lymphoid cells"

# TO START: In the menu above, choose "Cell" --> "Run All", and network + heatmap will load
# NOTE: Default limits networks to TF-TF edges in top 1 TF / gene model (.93 quantile), to see the full
# network hit "restore" (in the drop-down menu in cell below) and set threshold to 0 and hit "threshold"
# You can search for gene names in the search box below the network (hit "Match"), and find regulators ("targeted by")
# Change "canvas" to "SVG" (drop-down menu in cell below) to enable drag interactions with nodes & labels
# Change "SVG" to "canvas" to speed up layout operations
# More info about jp_gene_viz and user interface instructions are available on Github:
# https://github.com/simonsfoundation/jp_gene_viz/blob/master/doc/dNetwork%20widget%20overview.ipynb

# Edge key:
# Solid lines -- supported by ATAC-seq data and gene expression modeling
# Dotted lines -- supported by gene expression modeling only

In [2]: # Please choose how many TFs you'd like per network.
# Options are limited to Top: "5", "10", "15", or "Inf" (Inf == no limit) that were significantly enriched per TF
topN = "10"

# directory containing gene expression data and network folder
directory = "."
# folder containing networks
netPath = "qATAC_10_1_bias25_maxComb/ILCupDownSetsSI_2fdrlp0E-05_top" + topN

```

7. Select “Cell” → “Run All” to load interactive network visualizations and heatmaps:

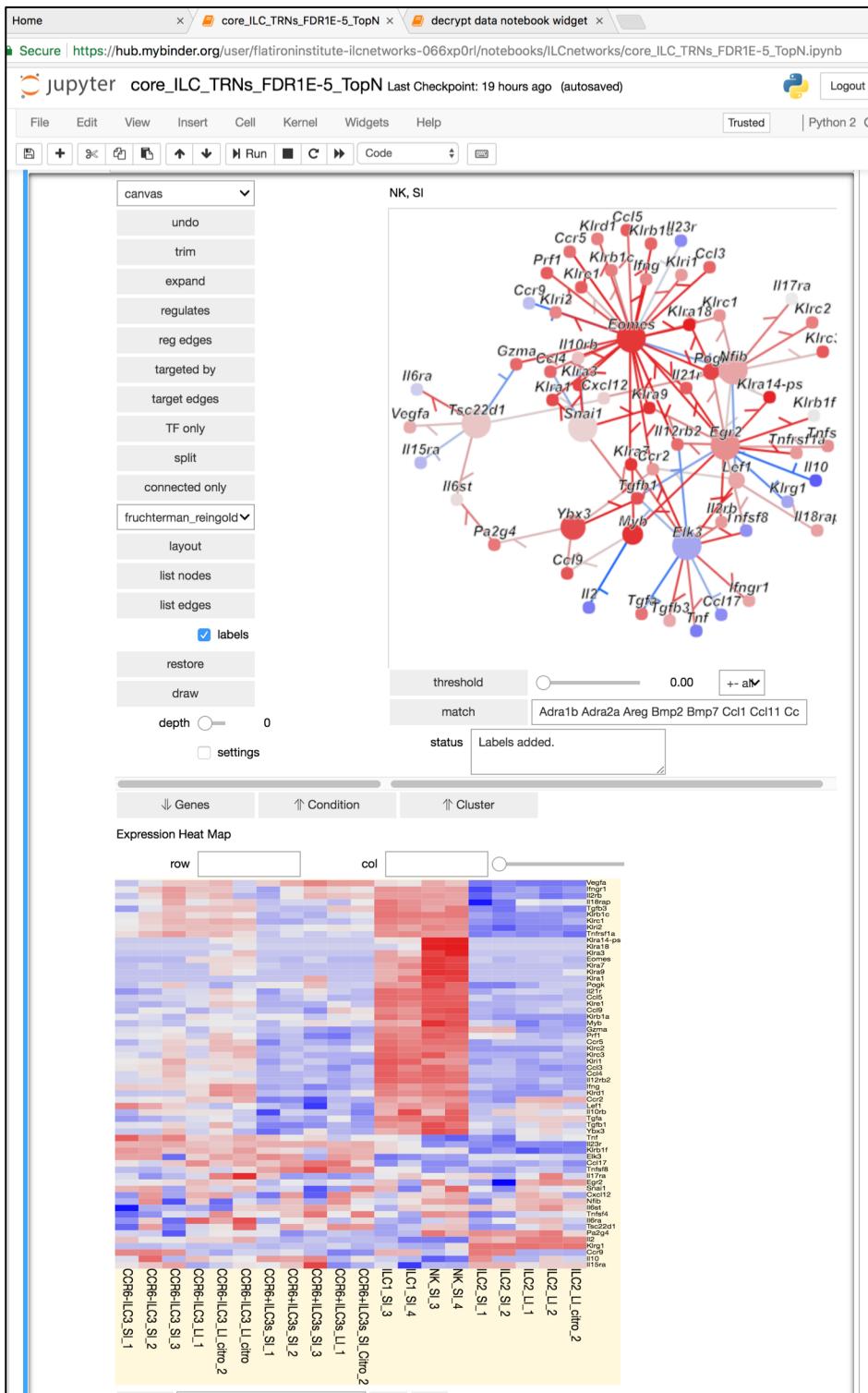
The screenshot shows a Jupyter Notebook interface. The top bar includes tabs for 'Home', 'core\_ILC\_TRNs\_FDR1E-5\_TopN', and 'decrypt data notebook widget'. Below the tabs, the title 'jupyter core\_ILC\_TRNs\_FDR1E-5\_TopN' and 'Last Checkpoint: 19 hours ago (unsaved changes)' are displayed. On the right, there are 'Logout' and 'Python 2' buttons. The main area shows two code cells. Cell [6] contains several lines of Python code related to gene expression and regulatory networks. Cell [7] contains code for setting up a network analysis. A red arrow points to the 'Run All' option in the 'Cell' menu, which is highlighted in red. The tooltip for 'Run All' says: "Select ‘Run All’ to run all cells in the current notebook, or shared by specific ILC subsets (ILC1, NK, ILC2, CCR6+).".

8. Wait for interactive network viewers to load before attempting interactions. Wait for the hourglass symbol (~30 seconds) to return to the book symbol, and then scroll down to view the core subtype TRNs (Step 11)

The screenshot shows two consecutive screenshots of a browser window. The top screenshot shows the URL 'https://hub.mybinder.org/user/flatironinstitute-ilcnetworks-066xp0rl/notebooks/ILCnetworks/core\_ILC...' and the bottom screenshot shows the same URL. A red arrow points from the top screenshot down to the bottom one. A red box highlights the text 'Wait for hourglass symbol to return to book symbol'.

9. Scroll down to find interactive networks and interface. Please refer to notes at the top of the notebook as well as detailed interaction instructions about the interface here:

[https://github.com/simonsfoundation/jp\\_gene\\_viz/blob/master/doc/dNetwork%20widget%20overview.ipynb](https://github.com/simonsfoundation/jp_gene_viz/blob/master/doc/dNetwork%20widget%20overview.ipynb)



10. Please send comments and suggestions to BOTH:

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