



- Clustering and Alignment of ChIP profiles

User Manual

Revised June 20, 2011
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What is it?

CATCH is a cool new tool for clustering of
ChIP profile patterns

Why would I use it?

To unravel the mysteries of epigenetics, you
first have to identify the epigenetic patterns!



How do I use it?

1. Collect or generate **ChIP profiling data**

You probably already did this...

2. Identify your **genomic positions of interest**

Which sites do you want to analyse?

3. **CATCH** your ChIP profiles!

And let CATCH do alignment and clustering for you



The CATCH program

- **Unsupervised clustering** of ChIP profiles
- Input
 - A dataset of profiles, i.e. specific genome regions from your ChIP profiling experiment
 - ChIP signal (wiggle format)
 - Selected positions (bed format)
- Output
 - A clustering+alignment of all profiles from the dataset



The CATCH workflow

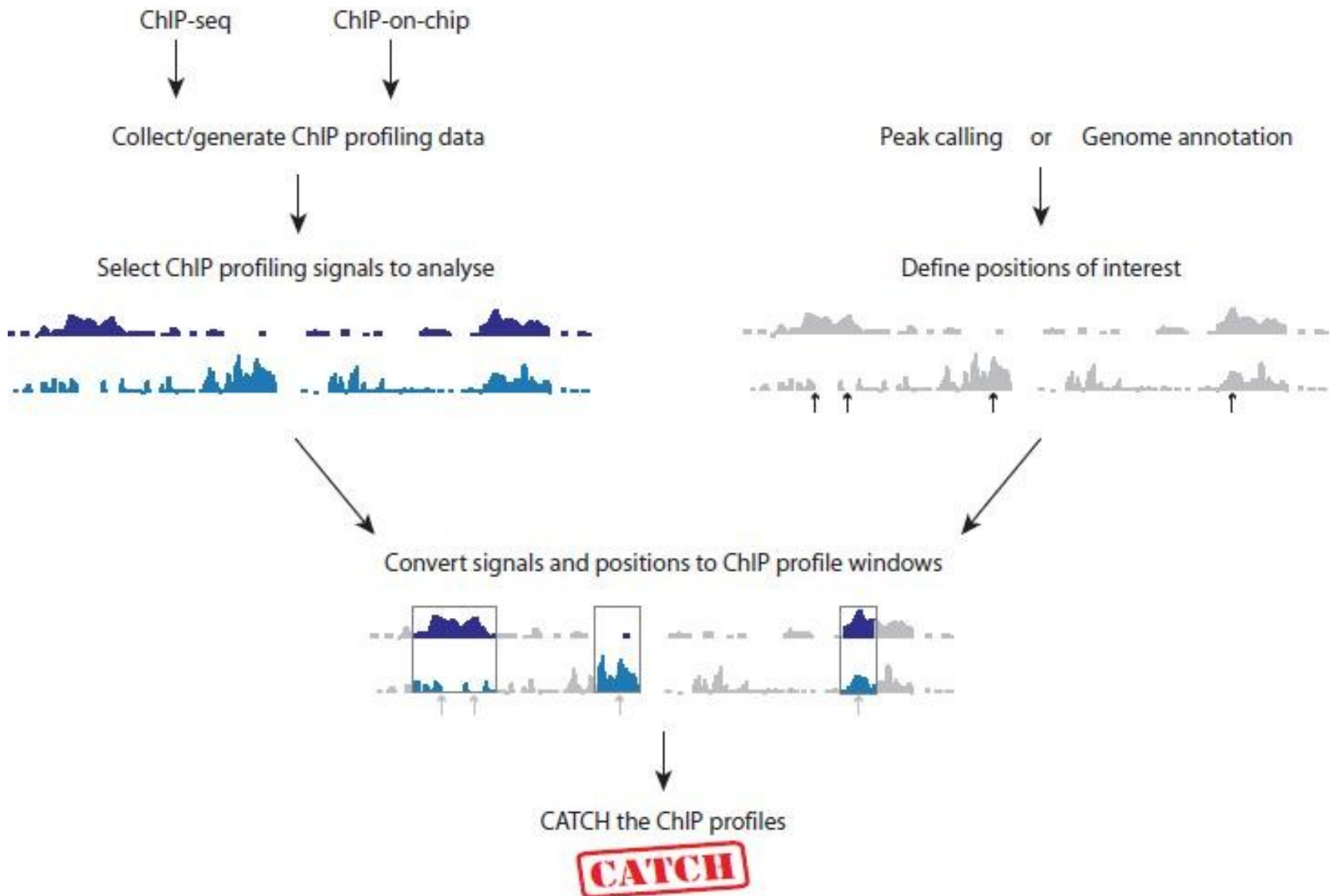
(small datasets)

- 1) Import profiles
- 2) View profiles
- 3) Start CATCH algorithm
- 4) Browse patterns in clustering tree
- 5) Export interesting profiles for further analysis

The import procedure has more steps when working with large datasets (1000+ profile regions) ... →



The CATCH workflow





The CATCH workflow

(large datasets)

- 1) Generate profile wiggle files (pwig)
 - Load and view dataset in CATCHprofiles
- 2) Make json input file from pwig files
- 3) Start CATCH algorithm from commandline
 - Generating json output file
- 4) Load json result in CATCHprofiles

Example workflow

1. make a bed file of your regions of interest

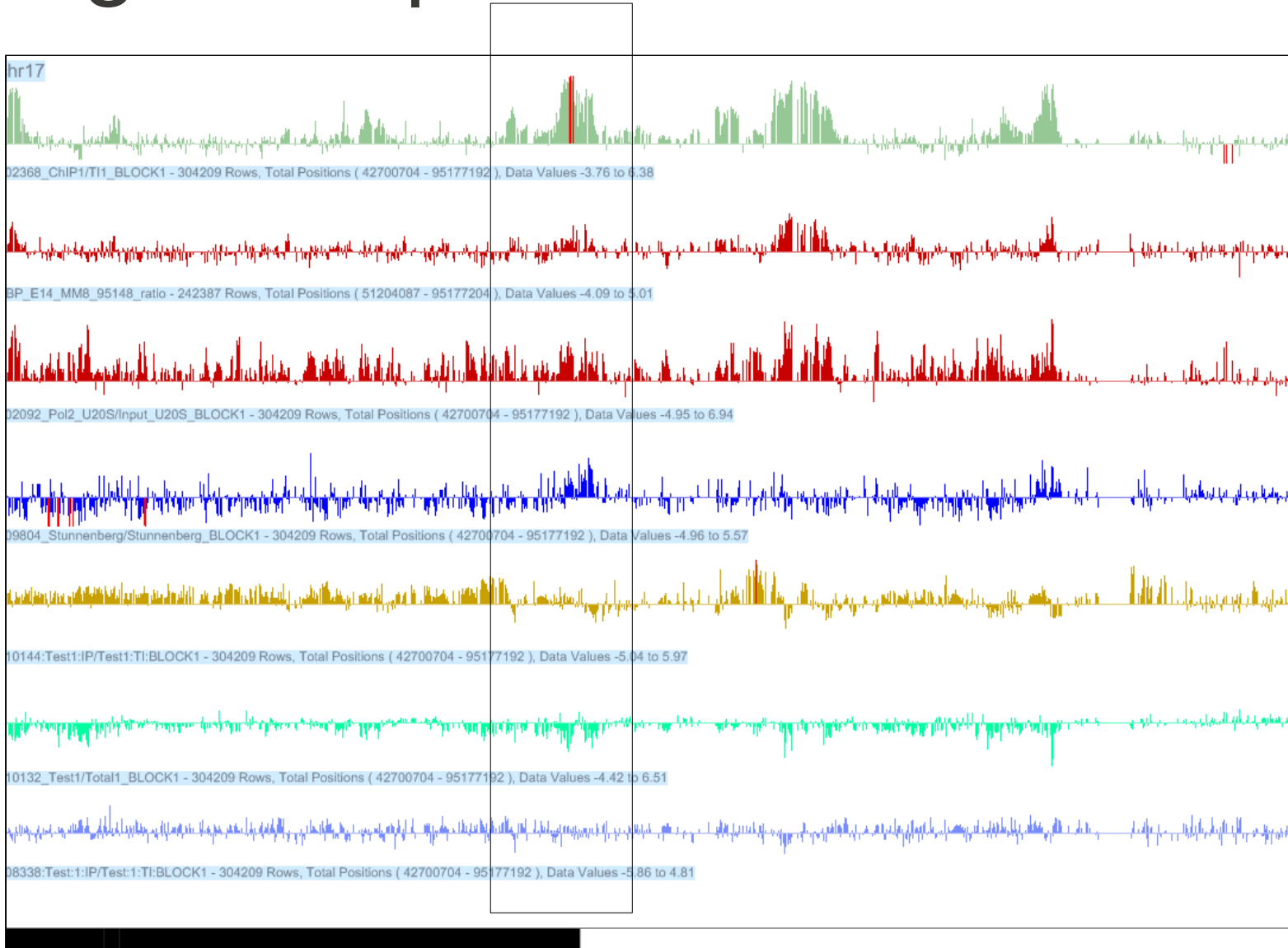
Profile regions

- You decide which areas are interesting to you:
 - Regions of annotation (TSS, CPG islands etc)
 - Peak regions
 - Other

Example workflow

1. make a bed file of your regions of interest

e.g. TSS profiles in ChIP-on-chip



TSS

Import to CATCH

2. import your wiggle files and bed file using File → 'Import Profiles'

The screenshot shows the 'Import Profiles' dialog box in the CATCH software. It is divided into three main sections: file selection, configuration, and action buttons.

- Signal Files (.wig):** A list of 10 files with paths starting with `/home/fiona/Desktop/CATCHlivedemo/Heintzm`. A preview of a signal profile is shown above the list.
- Position Files (.bed):** A list with one file: `/home/fiona/Desktop/CATCHlivedemo/RefSeq..`. A preview of a position profile with four vertical markers is shown above the list.
- Configuration:** On the right side, there are several options:
 - A 'Convert and add in CATCH' button.
 - A radio button selected for 'Width of profile window (BP)' with a value of 2000.
 - An unselected radio button for 'Profile window specified in ...'.
 - An unselected checkbox for 'Use merge position (BP)' with a value of 1000.
 - A 'Ref point interval' field with a value of 38.
 - A 'Cancel' button.
- Action Buttons:** At the bottom, there are four buttons: 'Add Signal Files', 'Add Position Files', 'Remove selected Signal Files', and 'Remove selected Position Files'.

View profiles

3. Examine your data

File Operations Export Options Help

Unaligned Datasets ENCODE regions(RefSe...
Aligned Datasets none
Active set Rename regions_hg17_H3.30.gff.pwig

Add tracks
CATCH selected tracks
Add to Job Manager
Delete currently active set

Rename	Track n...	Vi...	CA...	Color
Rename	H3.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H3K4Me1.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H3K4Me2.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H3K4Me3.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H3ac.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H4ac.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	RNAP.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	TAF.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	p300.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color

Graphs Cluster view (tree) Branch view (tree)

Start CATCH

4. Click 'CATCH selected tracks' and wait..

The screenshot displays the CATCH software interface. On the left, a menu bar includes 'File', 'Operations', 'Export', 'Options', and 'Help'. Below it, there are dropdown menus for 'Unaligned Datasets' (ENCODE regions\RefSe...) and 'Aligned Datasets' (none). The 'Active set' is 'regions_hg17_H3.30.gff.pwig'. A list of tracks is shown with columns for 'Rename', 'Track n...', 'Vi...', 'CA...', and 'Color'. The 'CATCH selected tracks' button is highlighted with a green box. On the right, a 'Graphs' panel shows a multi-panel plot with 'Cluster view (tree)' and 'Branch view (tree)' tabs. A large red stamp with the word 'CATCH' is overlaid on the graph area.

Rename	Track n...	Vi...	CA...	Color
Rename	H3.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H3K4Me1.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H3K4Me2.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H3K4Me3.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H3ac.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	H4ac.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	RNAP.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	TAF.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color
Rename	p300.30.gff	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Color

Examine profile clusters 4. Browse results interactively

File Operations Export Options Help

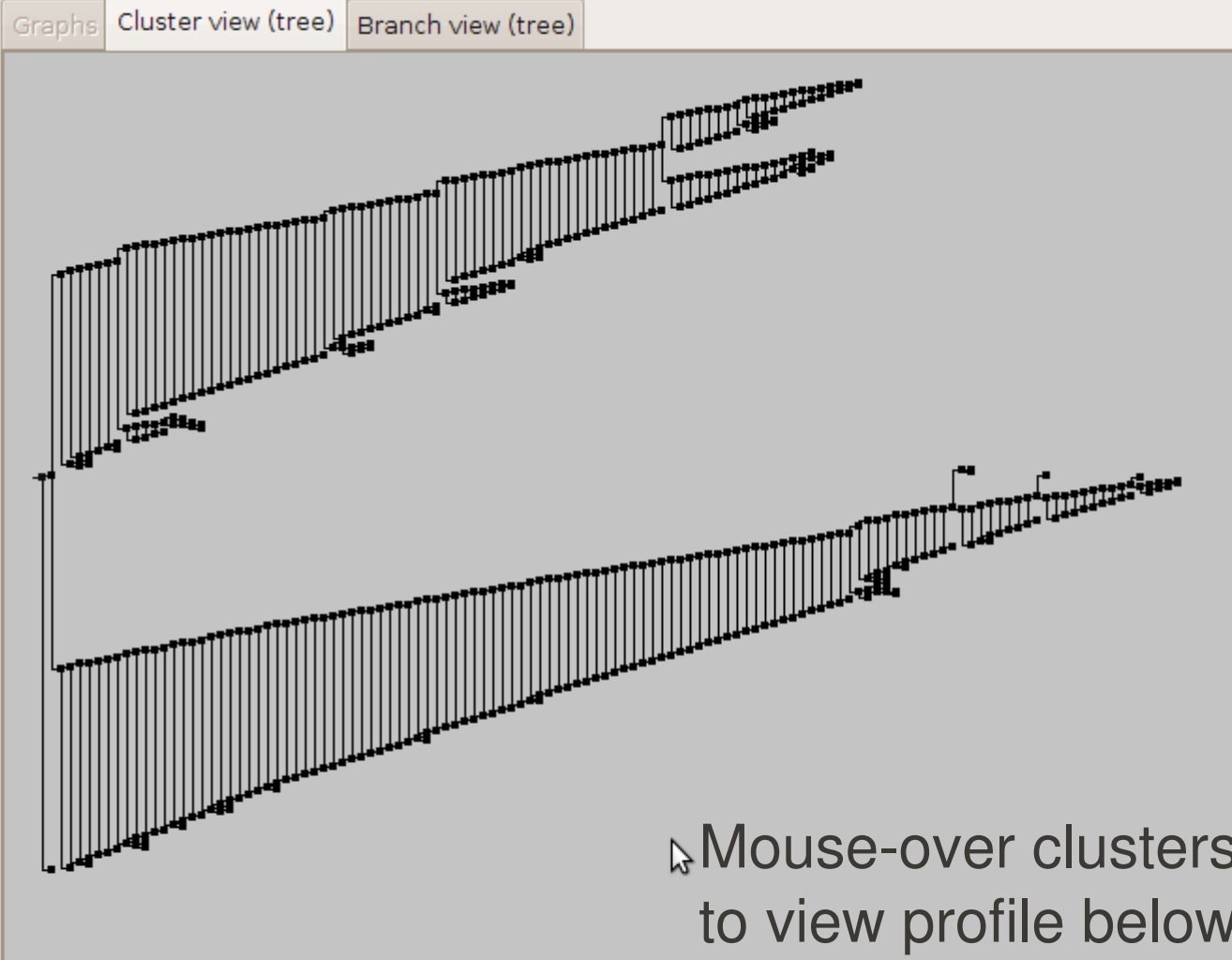
Unaligned Datasets

Aligned Datasets

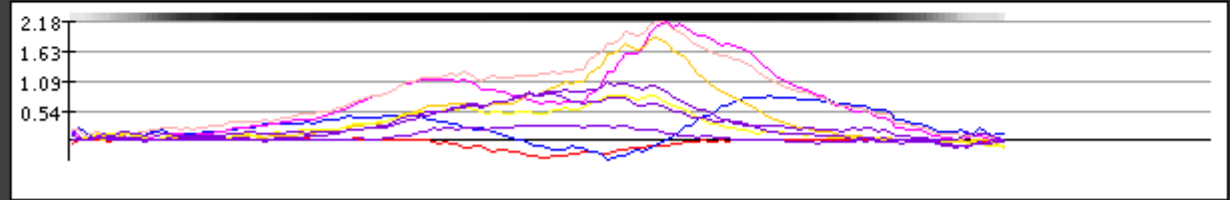
Active set

Rename	Track n...	Vi...	CA...	Color
<input type="button" value="Rename"/>	<input type="text" value="H3.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>
<input type="button" value="Rename"/>	<input type="text" value="H3K4Me1.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>
<input type="button" value="Rename"/>	<input type="text" value="H3K4Me2.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>
<input type="button" value="Rename"/>	<input type="text" value="H3K4Me3.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>
<input type="button" value="Rename"/>	<input type="text" value="H3ac.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>
<input type="button" value="Rename"/>	<input type="text" value="H4ac.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>
<input type="button" value="Rename"/>	<input type="text" value="RNAP.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>
<input type="button" value="Rename"/>	<input type="text" value="TAF.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>
<input type="button" value="Rename"/>	<input type="text" value="p300.30.qff"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="button" value="Color"/>

Graphs Cluster view (tree) Branch view (tree)



Mouse-over clusters to view profile below





interactive browsing

- Browse clustering tree:
 - Zoom: + and –
 - Collapse subtree: ctrl + leftclick
 - Highlight: leftclick

- Right-click to:
 - Open subtree
 - Export results



Save & Export

- CATCH clustering result (.catch)
 - To browse later or share results
- Use the export menu or right click to export:
 - Profile patterns (.csv)
 - Positions (.bed)
 - Cluster tree (.newick)



Quick Start Guide

1. Ensure JAVA 1.6 is installed
(follow link from <http://catch.cmbi.ru.nl>)
2. Prepare your data
 - ChIP profiling tracks in wiggle format
 - Your chosen peaks/positions in .bed format
3. Start CATCH
4. Import files or load dataset
5. CATCH your ChIP profiles!



Java memory issues

- Run CATCH from the commandline:
 - `Java -Xmx1000m -Xss2000k -jar CATCH3v513.jar`
- If you get errors of insufficient Java memory:
 - Heapsize: increase -Xmx value
 - Stacksize: increase -Xss value
- If 'Import files' fails on big files:
 - Use script to generate datasets (.pwig)
 - Use script to generate CATCH input file (.json)



Big datasets?

- Use scripts to generate input files in JSON format
- Execute CATCH from the commandline
 - `./execute.sh catch jobin.json jobout.json`
 - Where second argument is the name of the executable
 - win: `catch`
 - linux: `catch-linux-static-x86`
 - mac: `catch-macOSX`
- Load json result in CATCHprofiles



More information

- Go to the CATCH homepage:
<http://catch.cmbi.ru.nl>
 - User manual, examples and links
- Updates?
 - Subscribe to: CATCH-updates@bioinformatics.org
- Questions?
 - Send them to: CATCH-users@bioinformatics.org

CATCH

Load files

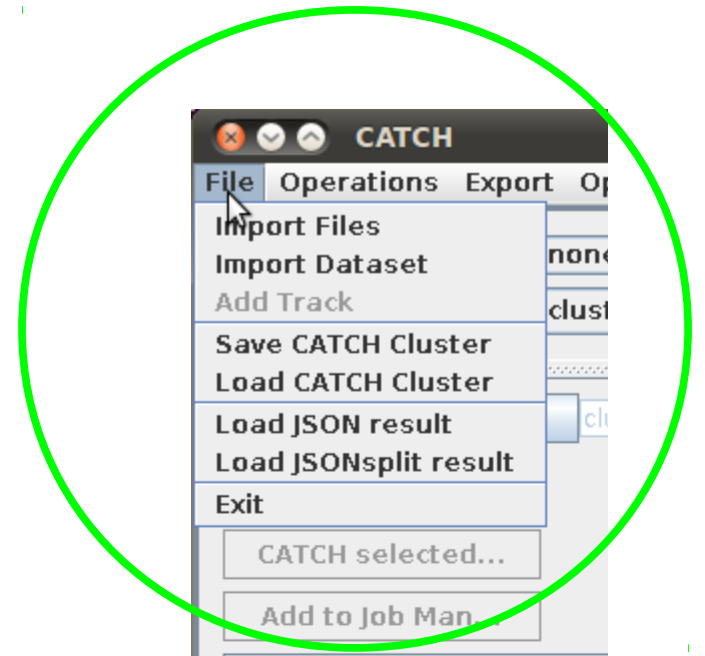
The screenshot shows the CATCH software interface. The 'File' menu is open, and the 'Load JSON result' option is highlighted. A green circle highlights the File menu area. The interface includes a menu bar with 'File', 'Operations', 'Export', 'Options', and 'Help'. The 'File' menu contains options: 'Import Files', 'Import Dataset', 'Add Track', 'Save CATCH Cluster', 'Load CATCH Cluster', 'Load JSON result', 'Load JSONsplit result', and 'Exit'. Below the menu are buttons for 'CATCH selected...', 'Add to Job Man.', and 'Delete currently active set'. At the bottom, there is a table with columns 'Rename', 'Track ...', 'V...', 'CA...', and 'Color'. The 'Track ...' column contains 'H3K4me3', and the 'Color' column shows a red square.

Rename	Track ...	V...	CA...	Color
Re...	H3K4me3	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	



File formats

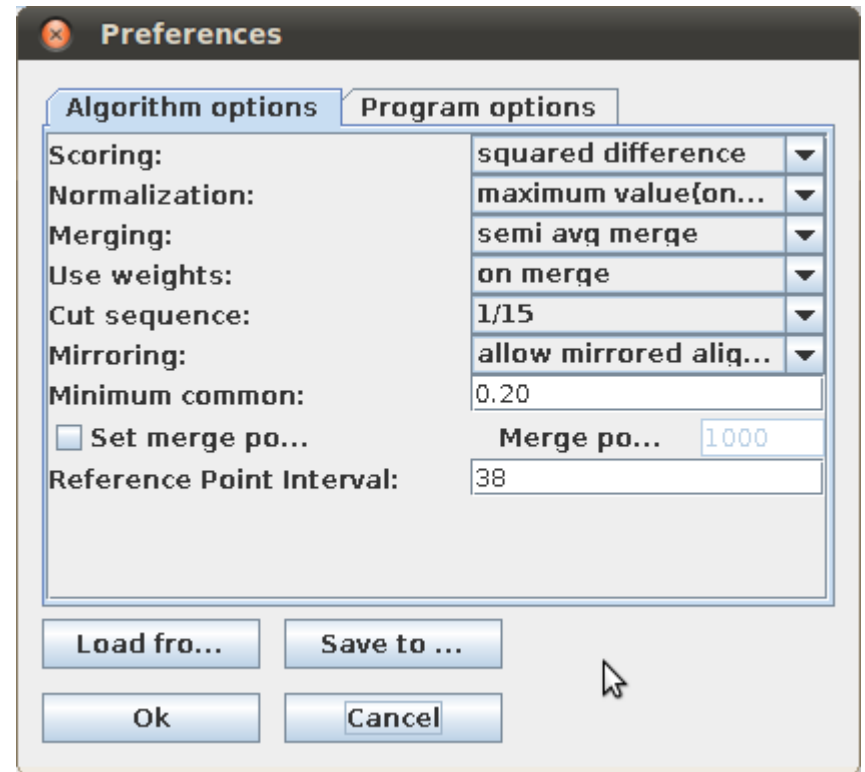
- Import files: **wiggle** and **bed**
- Import dataset: **pwig**
- CATCH cluster: **catch**
- JSON result: **json**





Change settings

- Check and save your default settings before starting the CATCH clustering
- Settings are written to the json-formatted input file before executing the CATCH core algorithm





Source code repository

- The CATCH source code is maintained in an SVN repository (<http://subversion.tigris.org/>) hosted by bioinformatics.org
- To browse the repository and the code, you can use the SVN web interface by pointing your browser to:

<http://www.bioinformatics.org/websvn/listing.php?repname=catch>

- To download the source code from the CATCH svn, you can use anonymous checkout (after installing SVN on your system):

```
svn checkout svn://bioinformatics.org/svnroot/catch/branches/CATCH\
3/trunk/CATCH\ 3/
```



Compile executables

- The catch core algorithm (catch-engine) and the CATCHprofiles user interface are compiled separately
- To compile the catch core algorithm, download the “catch-engine” branch from svn and compile use the accompanying makefile:

```
catch:~/catch-engine> make
```

```
gcc-4.3 -static catch.o JSON_parser.o ConvertUTF.o -lm -lgomp  
-lpthread -o catch-linux-static-x86
```

- The CATCHprofiles Java GUI can be compiled using a development tool like Eclipse (<http://www.eclipse.org/>):
 - Import the “CATCH 3” directory from the “CATCH 3/trunk” branch from CATCH svn
 - Export the main program `programControllers.CATCH.java` as a “runnable jar file”
- For any further questions concerning CATCH development, please send your question to the CATCH mailinglist: CATCH-dev@bioinformatics.org

Acknowledgements

IMADA, Odense:

- **Kasper Markus**
first implementation
of CATCH
- **Lene Favrholt**

Nijmegen:

- **Moniek Riemersma**
- **GiPCATCH** team
- **Maarten Kooyman**
The PinkThing

Supervisors:

Henk Stunnenberg

Molecular Biology

Martijn Huynen

CMBI

Acknowledgements

CATCH users:

Hendrik Marks
Rasa Jurgelenaite

Copenhagen:

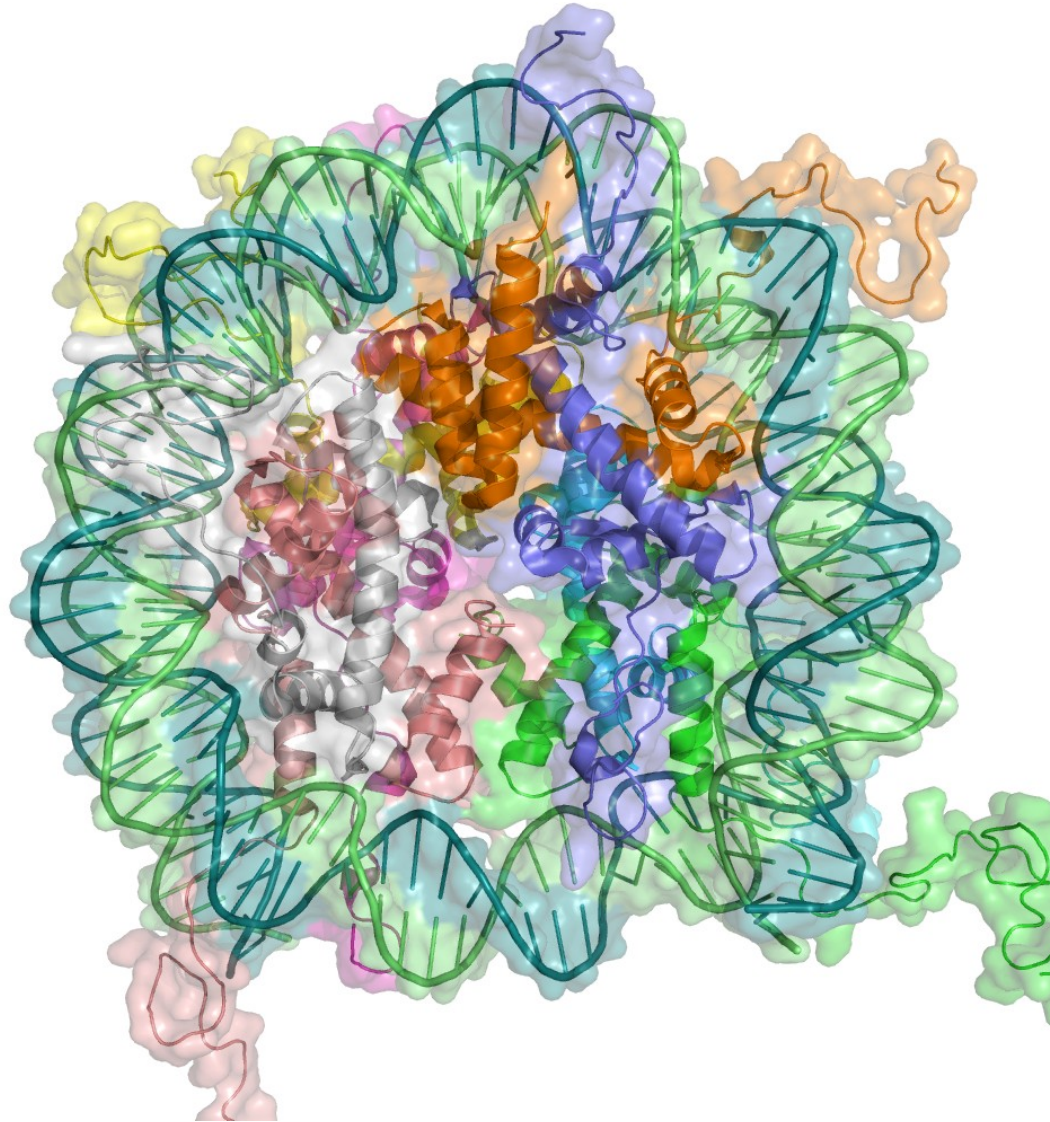
Rune Friborg



Funding:

HEROIC – mouse epigenetics

Thank you for using CATCHprofiles



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