### Set up the environment

- Change runtime to GPU (in the menu select Runtime -> Change runtime type -> GPU)
- Connect Google Drive to be able to save the analysis output:

# Run this cell to connect to Google Drive. To run this cell click on the Play butt
from google.colab import drive

drive.mount("/content/drive")

Drive already mounted at /content/drive; to attempt to forcibly remount, call

• Note: To view connected Google Drive filesystem click on the Folder icon on the left.

+ Code — + Text

- Run the cell below to install tapqir (takes about a minute; green checkmark means you are done):
- !pip install --quiet tapqir > install.log
  - Restart the runtime after installing Tapqir (in the menu click Runtime -> Restart runtime)

### Download input data

In this notebook you can either analyze the example data from the tutorial or your own data. Do A) or B) below.

#### A) Download tutorial data

These data were acquired with <u>Glimpse</u> and pre-processed with the <u>imscroll</u> program (<u>Friedman</u> <u>et al., 2015</u>). Change directory to MyDrive:

%cd drive/MyDrive/

/content/drive/MyDrive

Download data files using wget and then unzip files:

!wget https://zenodo.org/record/5659927/files/DatasetA\_glimpse.zip !unzip DatasetA\_glimpse.zip && rm DatasetA\_glimpse.zip

The raw input data are:

- garosen00267 folder containing image data in glimpse format and header files
- green\_DNA\_locations.dat aoiinfo file designating target molecule (DNA) locations in the binder channel
- green\_nonDNA\_locations.dat aoiinfo file designating off-target (nonDNA) locations in the binder channel
- green\_driftlist.dat driftlist file recording the stage movement that took place during the experiment

#### B) Upload your own data to Google Drive

You will need:

- folder containing image data in glimpse format and header files
- aoiinfo file designating target molecule (DNA) locations in the binder channel
- aoiinfo file designating off-target (nonDNA) locations in the binder channel
- driftlist file recording the stage movement that took place during the experiment

### Create a new analysis folder

To start the analysis create an empty folder (here named tutorial) which will be the working directory:

%mkdir /content/drive/MyDrive/tutorial

# Start the program

To start the program run:

#### from tapqir import gui

#### gui.run()

[

	/content/drive/MyDrive/tu	Itorial		
Extract AOIs	Fit the data	View results	Tensorboard	Post analysis
Tapqir model	cosmos			
🔽 Run comp	utations on GPU?			
AOI batch size	10			
Frame batch siz	ze 512	٢		
Learning rate	0.005	٢		
Number of itera	tions 0	٢		
🗸 Save para	meters in matlab format?			
Priors				
	[			
background	_mean_std 1000	٢		
background	_std_std 100	٢		
lamda_rate	1	٢		
height_std	10000	٢		
width_min	0.75	٢		
width_max	2.25	٢		
	te 1	٢		
proximity_ra				

Fitting the data ... INFO:tapqir:Fitting the data ... DEBUG:tapqir.models.model:Loaded data from /content/drive/MyDrive/tutorial/dat Iteration #74200. Loaded a model checkpoint from /content/drive/MyDrive/tutorial/.tapgir/cosmos model.tpgr INFO:tapgir.models.model:Iteration #74200. Loaded a model checkpoint from /content/drive/MyDrive/tutorial/.tapgir/cosmos model.tpgr DEBUG:tapqir.models.model:Tapqir version - v1.1.12 DEBUG:tapqir.models.model:Model - cosmos DEBUG:tapgir.models.model:Device - cuda DEBUG:tappir.models.model:Floating precision - torch.float64 DEBUG:tapqir.models.model:Optimizer - Adam DEBUG:tapgir.models.model:Learning rate - 0.005 DEBUG:tapqir.models.model:AOI batch size - 10 DEBUG:tapqir.models.model:Frame batch size - 512 1% 1000/100000 [08:05<12:44:29, 2.16it/s] DEBUG:tapgir.models.model:Iteration #74200: Successful. DEBUG:tapgir.models.model:Iteration #74400: Successful. DEBUG:tapqir.models.model:Iteration #74600: Successful. DEBUG:tapqir.models.model:Iteration #74800: Successful. DEBUG:tapgir.models.model:Iteration #75000: Successful. DEBUG:tapqir.models.model:Iteration #75200: Successful. Iteration #75200 model converged. INFO:tapqir.models.model:Iteration #75200 model converged. Fitting the data: Done INFO:tapgir:Fitting the data: Done Computing stats ... INFO:tapqir:Computing stats ... - credible intervals INFO:tapgir.utils.stats:- credible intervals - spot probabilities INFO:tapqir.utils.stats:- spot probabilities ImportError Traceback (most recent call last) /usr/local/lib/python3.7/dist-packages/tapqir/gui.py in fitCmd(b, layout, out, 532 pykeops=True, no input=True, progress bar=tqdm notebook, -> 534 ) 6 frames /usr/local/lib/python3.7/dist-packages/matplotlib/backends/backend agg.py in ] filename or obj, metadata, pil kwargs, \*args, \*\*kwargs) Metadata in the PNG file as key-value pairs of bytes or la 504 encodable strings. According to the PNG specification, keys must be shorter 1 chars. ImportError: cannot import name '\_png' from 'matplotlib' (/usr/local/lib/pythe packages/matplotlib/ init .py)

SEARCH STACK OVERFLOW

ImportError	Traceback (most recent call last)
<u>/usr/local/lib/py</u>	<u>/thon3.7/dist-packages/IPython/core/formatters.py</u> in
call(self, ob	oj)
339	pass
340	else:
> 341	return printer(obj)
342	<pre># Finally look for special method names</pre>
343	<pre>method = get_real_method(obj, self.print_method)</pre>
	2 4 frames
/usr/local/lib/py	thon3.7/dist-packages/matplotlib/backends/backend agg.py in
print png(self, f	Eilename or obj, metadata, pil kwargs, *args, **kwargs)
503	Metadata in the PNG file as key-value pairs of bytes or
latin-1	
504	encodable strings.
> 505	According to the PNG specification, keys must be shorter
than 79	
506	chars.
507	
ImportError: cann	not import name '_png' from 'matplotlib'

#### which will display the Tapqir GUI:

Select working	g directory		
Select	No selection		

# Select working directory

Click the Select button to set the working directory to <a href="https://www.content/drive/MyDrive/tutorial">/content/drive/MyDrive/tutorial</a>:

Working directory: /	/conte	nt/drive/MyDrive/tutorial				
Extract AOIs		Fit the data	View results	Tensorboard	View logs	
Dataset name						
AOI image size	14					
Offset region top	o-left c	corner (x-axis) 10				
Offset region top	o-left c	corner (y-axis) 10				
Offset region siz	e 3	0				
Offset histogram	ı bin s	ize (odd number) 1				
Specify fram	ie ranę	ge?				
🗌 Use off-targe	et AOI	locations?				
Number of color	chan	nels 1				
Channel #0						
Channel nam	ne					
Header/glimp	ose fol	lder				
Select	No	selection				
Driftlist file						
Select	No	selection				
Target molect	ule lo	cations file				
Select	No	) selection				
Extract AC	Ols					
[nitialized Ta	apqi	r at /content/dri	ve/MyDrive/tutoria	al/.tapqir.		
· Checkout the · Get help on	e doo our	cumentation: < <u>htt</u> forum: < <u>https://</u>	<u>ps://tapqir.readt</u> github.com/gelles	<u>hedocs.io/</u> > <u>-brandeis/tapqir/</u>	<u>discussions</u> >	
Configuration	opt: gura	ions are read fro tion data	m /content/drive/N	MyDrive/tutorial/	.tapqir/config.yar	nl.
oading contic	gura	tion data: Done				

Setting working directory creates a .tapqir sub-folder that will store internal files such as config.yaml configuration file, loginfo logging file, and model checkpoints.

### Extract AOIs

To extract AOIs specify the following options in the Extract AOIs tab:

- A dataset name: Rpb1SNAP549 (an arbitrary name)
- Size of AOI images: we recommend to use 14 pixels
- Starting and ending frame numbers to be included in the analysis (1 and 790). If starting and ending frames are not specified then the full range of frames from the driftlist file will be analyzed.
- The number of color channels 1 (this data set has only one color channel available)
- Use off-target AOI locations?: True (we recommended including off-target AOI locations in the analysis).

And specify the locations of input files for each color channel (only one color channel in this example):

- Channel name: SNAP549 (an arbitrary name)
- Header/glimpse folder: /content/drive/MyDrive/tutorial/DatasetA\_glimpse/garosen00267
- Driftlist file: /content/drive/MyDrive/tutorial/DatasetA\_glimpse/green\_driftlist.dat
- Target molecule locations file: /content/drive/MyDrive/tutorial/DatasetA\_glimpse/green\_DNA\_locations.dat
- Off-target control locations file: /content/drive/MyDrive/tutorial/DatasetA\_glimpse/green\_nonDNA\_locations.dat

See Advanced settings below for details on adjusting prior parameters.

**About indexing**. In Python indexing starts with 0. We stick to this convention and index AOIs, frames, color channels, and pixels starting with 0. Note, however, that for starting and ending frame numbers we used 1 and 790 which are according to Matlab indexing convention (in Matlab indexing starts with 1) since driftlist file was produced using a Matlab script.

Next, click Extract AOIs button:

Working directory: /cont	ent/drive/MyDrive/tutorial				
Extract AOIs	Fit the data	View results	Tensorboard	View logs	]
Dataset name Rot	1SNAP549				
AOI image size 14					
Offset region top-left	corner (x-axis) 10				
Offset region top-left	corner (v-axis) 10				
Offset region size	30				
Offset histogram bin	size (odd number) 1				
Specify frame rar	nge?				
Starting frame 1					
Ending frame 790					
✓ Use off-target AC	)I locations?				
Number of color cha	nnels 1				
Channel #0					
Channel name	SNAP549				
Header/glimpse fe	older				
Change /c	content/drive/MyDrive/Dat	asetA_glimpse/garosen0	0267/		
Driftlist file					
Change /c	content/drive/MyDrive/Dat	asetA_glimpse/green_dr	iftlist.dat		
Target molecule lo	ocations file				
Change /c	content/drive/MyDrive/Dat	asetA_glimpse/green_Dl	NA_locations.dat		
Off-target control	locations file				
Change /c	content/drive/MyDrive/Data	asetA_glimpse/green_nc	onDNA_locations.da		
4			•		
Extract AOIs					
Extracting AOIs					
Channel #0 (SNAPS	549)	700/700/0000			
Processing extra	cted AOIs	790/790 [02:04	4<00:00, 5.40lt/sj		
Dataset: N=331 or Data is saved in	<pre>1-target AOIs, Nc= /content/drive/My</pre>	526 off-target AC Drive/tutorial/da	)Is, F=790 frames,	C=1 channels, Px	=14 pixels, Py=1
- saving images	Dono	211707 (00011017 00			
AUIS:	DOILE				•

Great! The program has outputted a data.tpqr file containing extracted AOI images (N=331 target and Nc=526 off-target control locations):

```
%ls /content/drive/MyDrive/tutorial/
```

data.tpqr offset-distribution.png offtarget-channel0.png
offset-channel0.png offset-medians.png ontarget-channel0.png

#### Additionally, the program has saved

• Image files (ontarget-channel0.png and offtarget-channel0.png) displaying locations of on-target and off-target AOIs in the first frame. You should inspect these images to make sure that AOIs are inside the field of view:





• You should also look at offset-channel0.png to check that offset data is taken from a region outside the field of view:



 The other two files show the intensity histograms (offset-distribution.png) and the offset median time record (offset-medians.png) (offset distribution shouldn't drift over time):





# Fit the data

Now the data is ready for fitting. Options that we will select:

- Model the default single-color time-independent cosmos model (Ordabayev et al., 2022).
- Color channel number first chanel (0) (there is only one color channel in this data)
- Run computations on GPU: yes (True).
- AOI batch size use default (10).
- Frame batch size use default (512).
- Learning rate use default ( 0.005 ).
- Number of iterations use default (0)

See Advanced settings below for details on adjusting prior parameters.

**About batch size**. Batch sizes should impact *training time* and *memory consumption*. Ideally, it should not affect the final result. Batch sizes can be optimized for a particular GPU hardware by trying different batch size values and comparing training time/memory usage (nvidia-smi shell command shows Memory-Usage and GPU-Util values).

Next, press Fit the data button:

Vorking directory: /content/drive/MyDrive/tutor	ial			
Extract AOIs Fit the data	View results	Tensorboard	View logs	
Tapgir model cosmos	~			
Channel numbers 0	~			
Run computations on GPU?				
AOI batch size 10				
Frame batch size 512				
Learning rate 0.005				
Number of iterations 0				
Save parameters in matlab format?				
Priors				
background_mean_std 1000				
background_std_std 100				
lamda_rate 1				
height_std 10000				
width_min 0.75				
width_max 2.25				
proximity_rate 1				
gain_std 50				
Fit the data				
itting the data				
teration #6800. Loaded a model	checkpoint from	/content/drive/My	/Drive/tutorial/.tap	qir/cosmos-cha
*** teration #87800 model converged		JU [6.27:09<52:20, 3.82IL	/5]	
itting the data: Done				
credible intervals				
SNR and Chi2-test				
arameters were saved in /conten ummary statistics were saved in	t/drive/MyDrive/t /content/drive/M	utorial/cosmos-ch NDrive/tutorial/d	hannel0-params.tpqr cosmos-channel0-summ	narv.csv
omputing stats: Done		.,	Julii	

The program will automatically save a checkpoint every 200 iterations (checkpoint is saved at .tapqir/cosmos\_model.tpqr). The program can be stopped at any time by clicking in the terminal window and pressing Ctrl-C. To restart the program again re-run tapqir-gui command and the program will resume from the last saved checkpoint.

After fitting is finished, the program computes 95% credible intervals (CI) of model parameters and saves the parameters and CIs in cosmos\_params.tpqr, cosmos\_params.mat (if Matlab format is selected), and cosmos\_summary.csv files.

If you get an error message saying that there is a memory overflow you can decrease either frame batch size (e.g., to 128 or 256) or AOI batch size (e.g., to 5).

### Tensorboard

At every checkpoint the values of global variational parameters (-ELB0, gain\_loc, proximity\_loc, pi\_mean, lamda\_loc) are recorded. Fitting progress can be inspected while fitting is taking place or afterwards with the <u>tensorboard program</u> which shows the parameters values as a function of iteration number:

%load\_ext tensorboard

%tensorboard --logdir /content/drive/MyDrive/tutorial/



Set smoothing to 0 (in the left panel) and use refresh button at the top right to refresh plots.

Plateaued plots signify convergence.

**About number of iterations**. Fitting the data requires many iterations (about 50,000-100,000) until parameters converge. Setting the number of iterations to 0 will run the program till Tapqir's custom convergence criteria is satisfied. We recommend to set it to 0 (default) and then run for additional number of iterations if required.

# View results

This is not supported in the Colab version of Tapqir yet.

## Advanced settings

Tapqir settings can be directly accessed and modified through the configuration file config.yaml under .tapqir sub-folder of the working directory. It also contains additional options that are not available through the GUI.

### Offset

Offset data region (square) can be edited using three variables:

- offset\_x: left corner of the square (default is 10 pixels)
- offset\_y: top corner of the square (default is 10 pixels)
- offset\_P: size of the square (default is 30 pixels)

Bin size for the offset intensity histogram by default is 1. The bin size can be increased (try 3 or 5; odd number) to make the histogram sparser which will speed up fitting.

• bin\_size: offset intensity histogram bin size (default is 1)

### Prior distributions

Parameters of prior distirbutions (Eqs. 6a, 6b, 11, 12, 13, 15, and 16 in Ordabayev et al., 2022):

- background\_mean\_std (default 1000): standard deviation of the HalfNormal distribution in Eq. 6a
- background\_std\_std (default 100): standard deviation of the HalfNormal distribution in Eq. 6b
- lamda\_rate (default 1): rate parameter of the Exponential distribution in Eq. 11
- heiht\_std (default 10,000): standard deviation of the HalfNormal distribution in Eq. 12
- width\_min (default 0.75): minimum value of Uniform distribution in Eq. 13
- width\_max (default 2.25): maximum value of Uniform distribution in Eq. 13
- proximity\_rate (default 1): rate parameter of the Exponential distribution in Eq. 15
- gain\_std (default 50): standard deviation of the HalfNormal distribution in Eq. 16

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