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Fira Fair Data 2024

David Gomez-Cabeza
Postdoctoral Researcher

MIPMED
MOLECULAR IMAGING
for PRECISION MEDICINE

Financiado por la Unión Europea NextGenerationEU
GOBIERNO DE ESPAÑA
MINISTERIO DE CIENCIA E INNOVACIÓN
Plan de Recuperación, Transformación y Resiliencia
Next Generation Catalunya
Generalitat de Catalunya
Departament de Recerca i Universitats

IBEC
Institute for Bioengineering of Catalonia

My Datasets

Computational Simulations and Scripts

Microscopy Images

Nuclear Magnetic Resonance Spectra

Magnetic Resonance Images (MRI)

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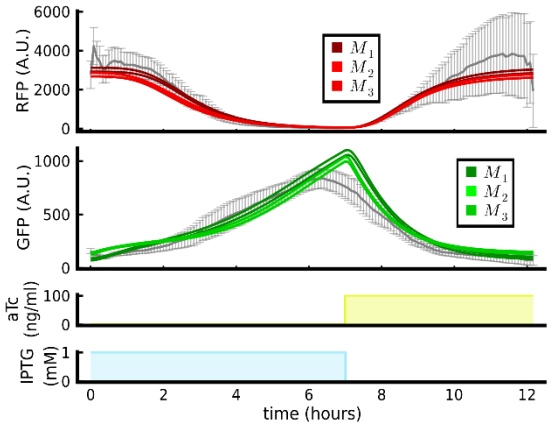
Computational Simulations and Scripts

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function restructDatInf(paths)

    ######################## OBSERVABLES ########################

    m = length(paths);

    DataAll = Array{Any,1}(undef, m)

    for i in 1:m
        DataAll[i] = Matrix(CSV.read(paths[i], DataFrame));
    end
    stslm = maximum([size(DataAll[i])[1] for i in 1:m]);
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    obser = 2;
    obSta = Array{Int,2}(undef, 1, 2)
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    Means = Array{Float64,3}(undef, stslm, m, obser);
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    sts = Array{Int,2}(undef, stslm, m).*0
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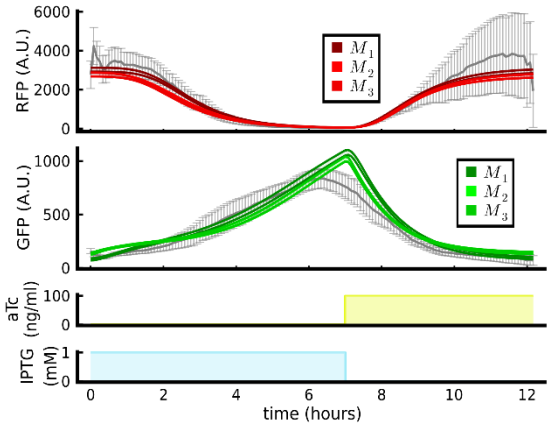


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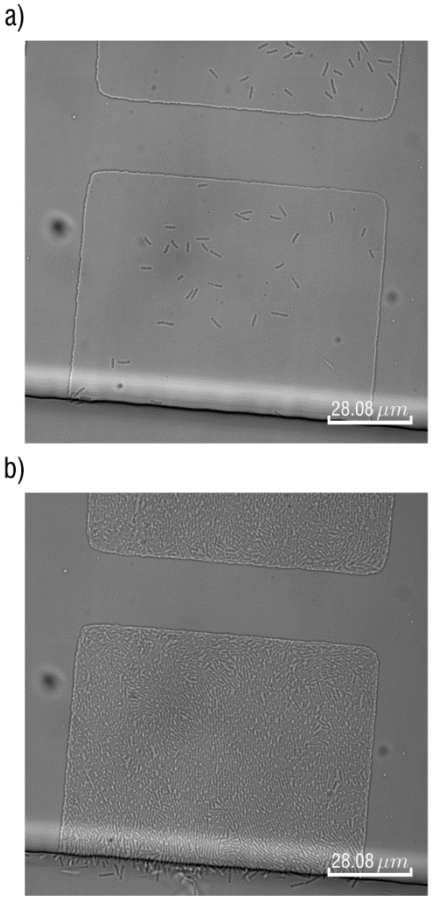

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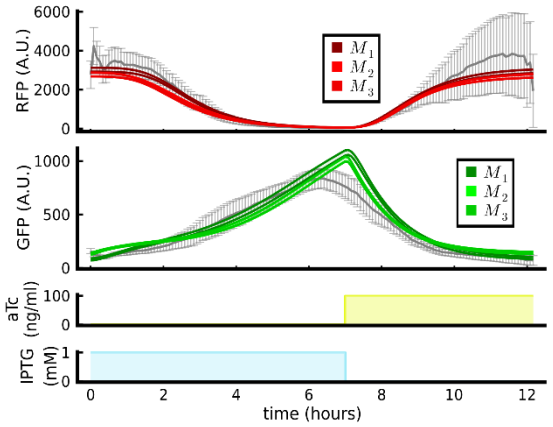


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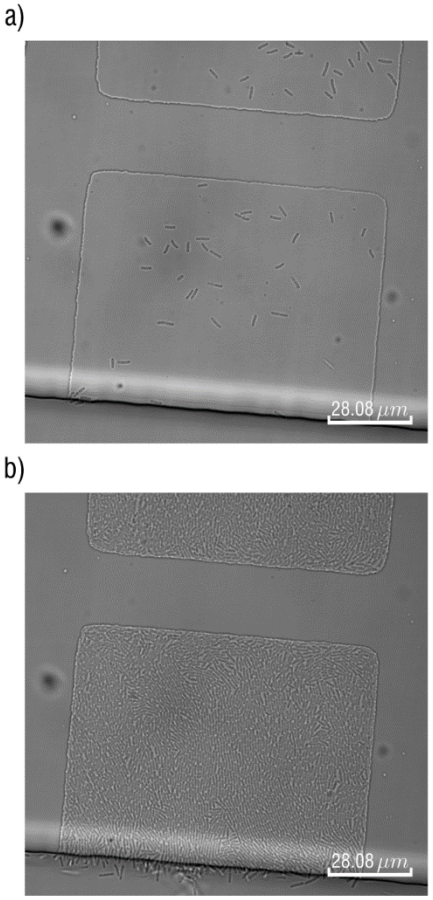

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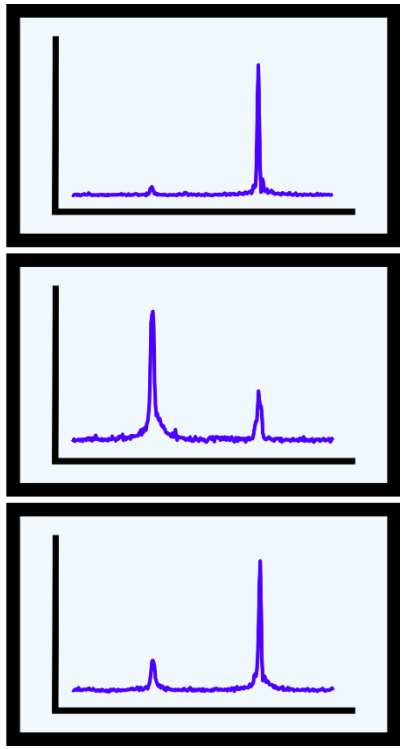

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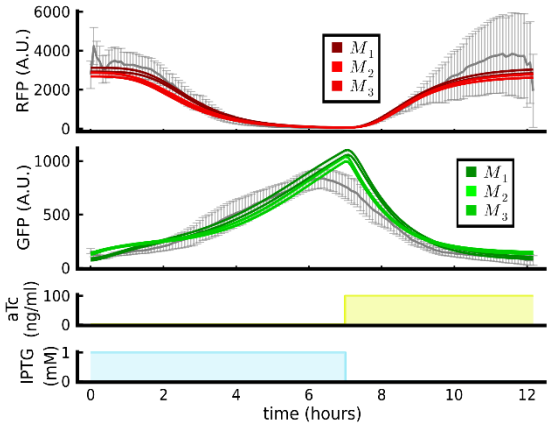

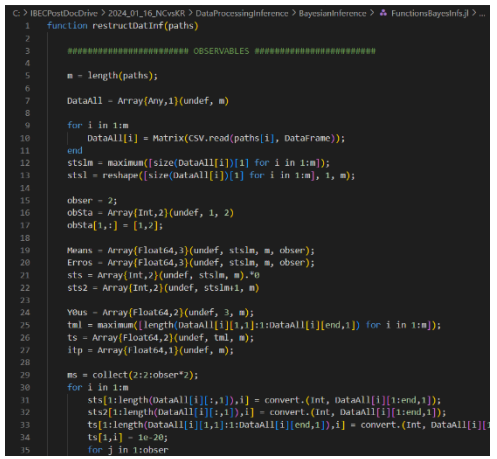

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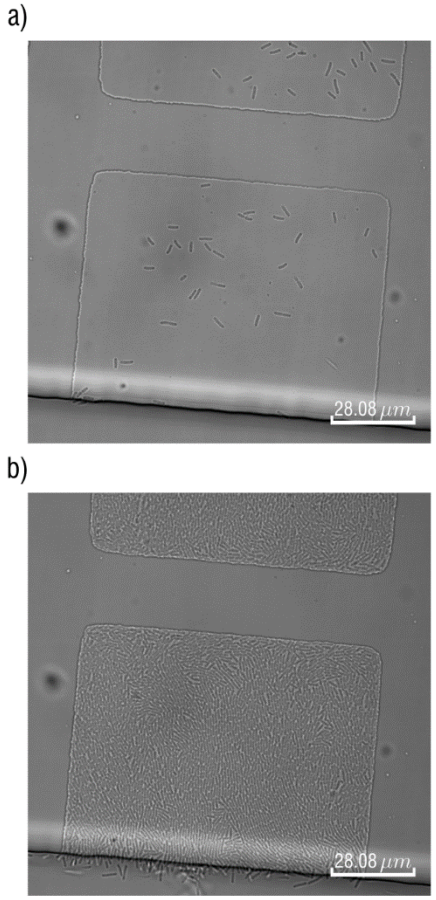
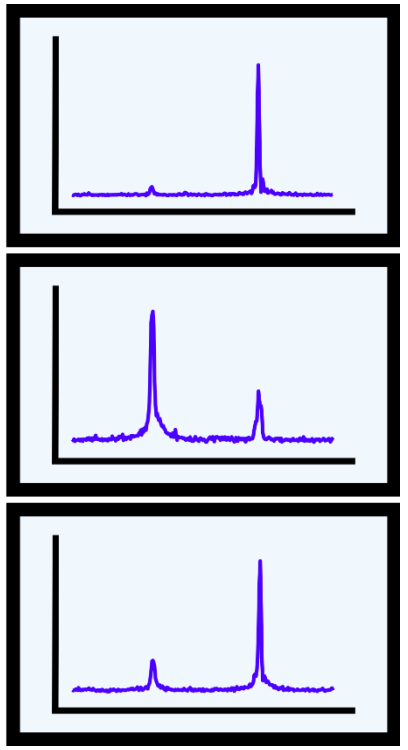
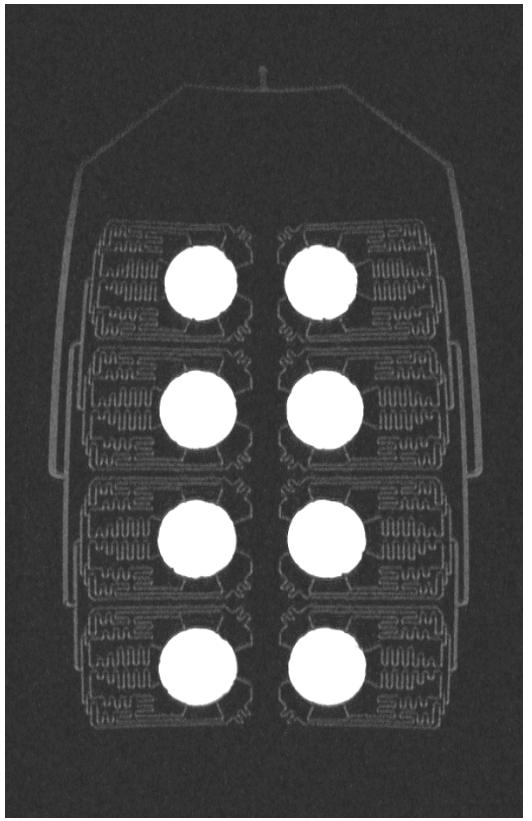


Nuclear Magnetic Resonance Spectra



Magnetic Resonance Images (MRI)



During PhD

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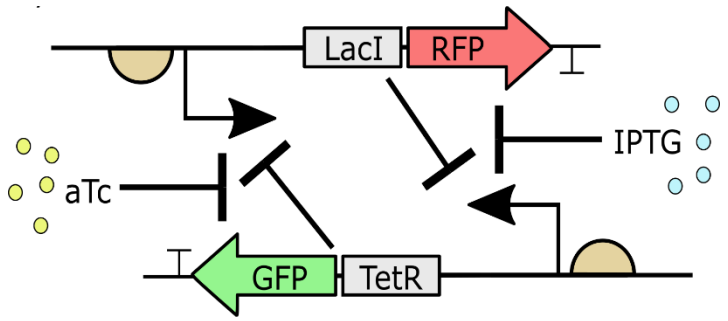

$$\frac{d[aTc]}{dt} = k_{aTc}\left(u_{aTc} - [aTc]\right) - g^P\,[aTc]$$
$$\frac{d[IPTG]}{dt} = k_{IPTG}\left(u_{IPTG} - [IPTG]\right) - g^P\,[IPTG].$$

$$P(\theta|D) = \frac{P(D|\theta)\;P(\theta)}{P(D)}$$

$$\frac{d[LacI]}{dt} = \frac{1}{g_L^m}\left(\kappa_L^{pm0} + \frac{\kappa_L^{pm}}{1+\left(\frac{[TetR]}{\theta_{TetR}}\,\frac{1}{1+\left(\frac{[aTc]}{\theta_{aTc}}\right)^{\eta_{aTc}}}\right)^{\eta_{TetR}}}\right) - g_L^P\,[LacI]$$

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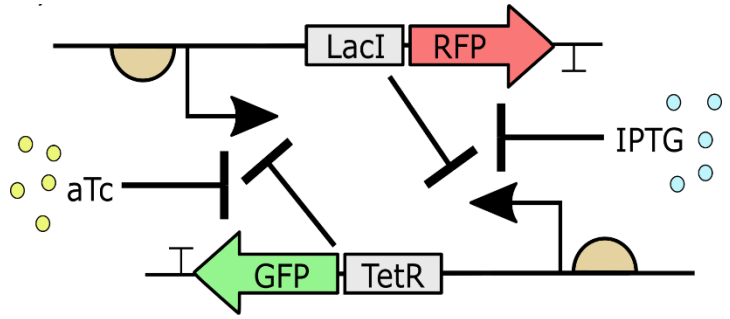

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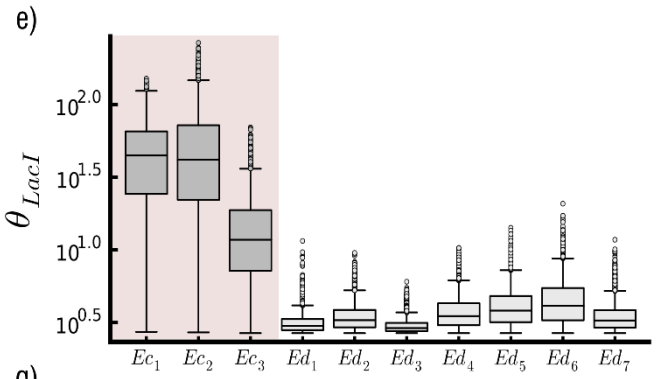

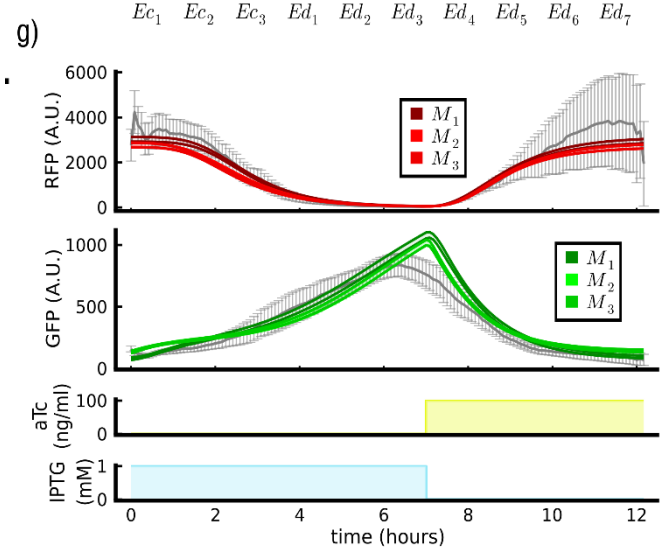

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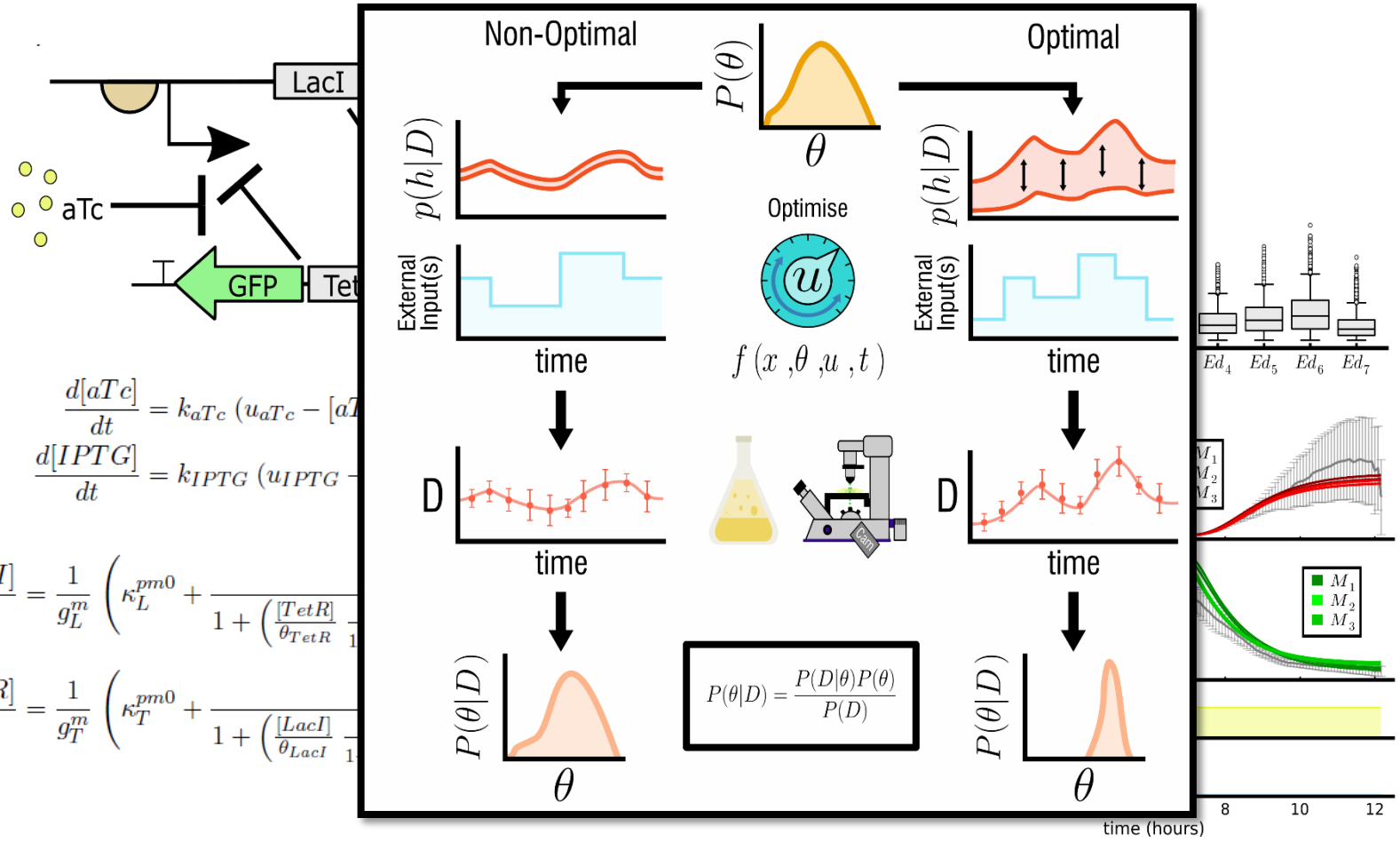

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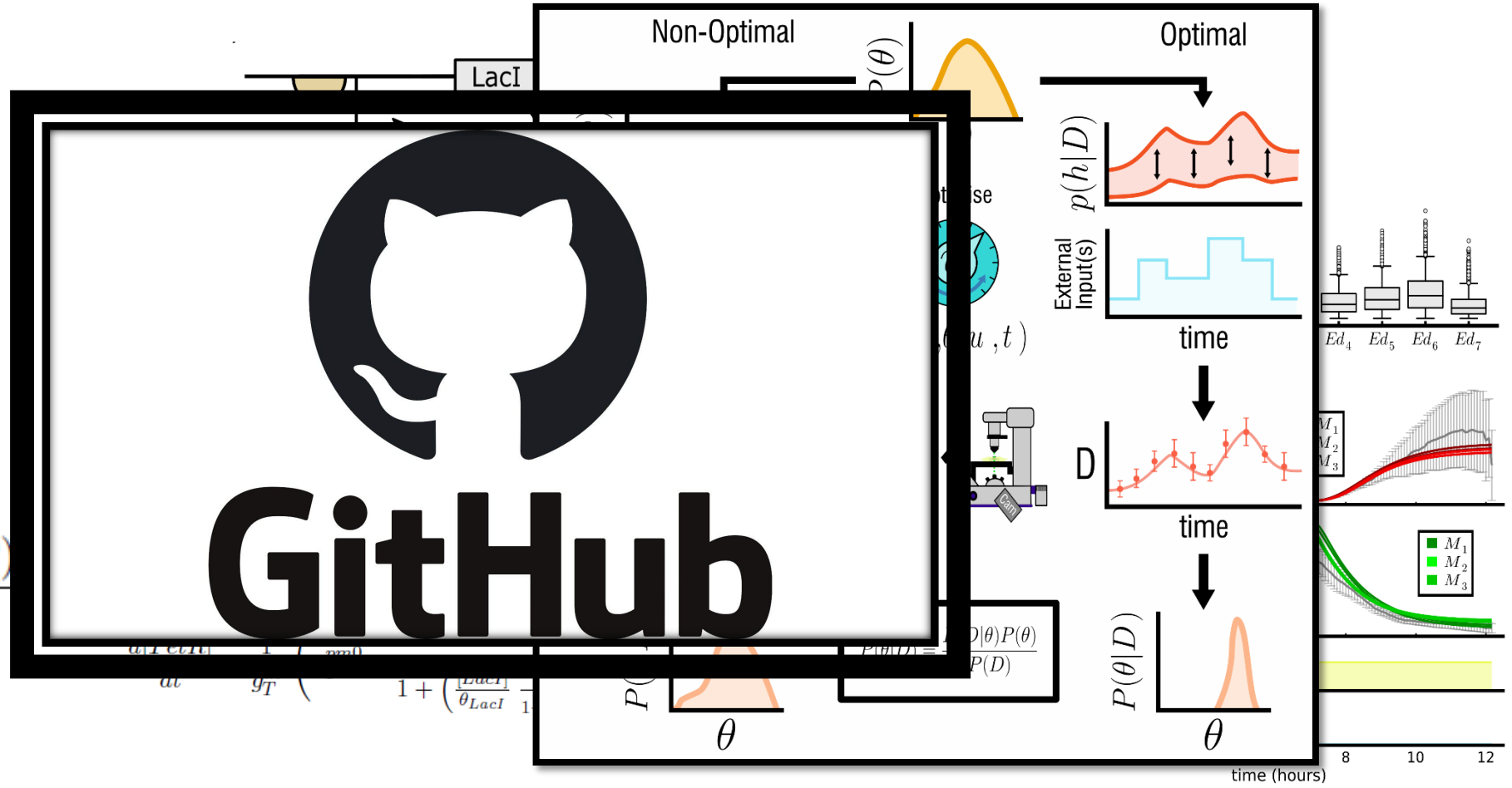

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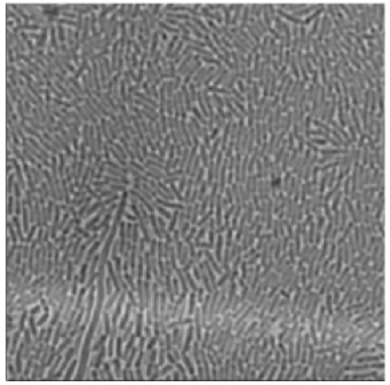
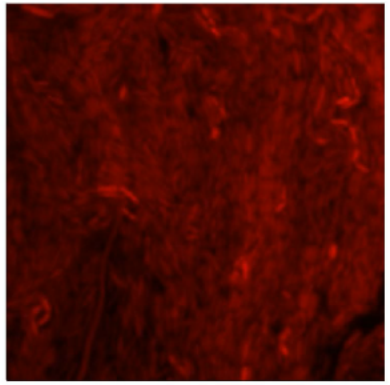
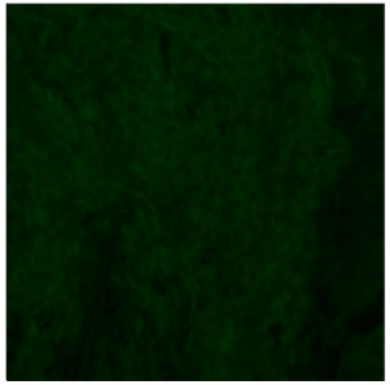
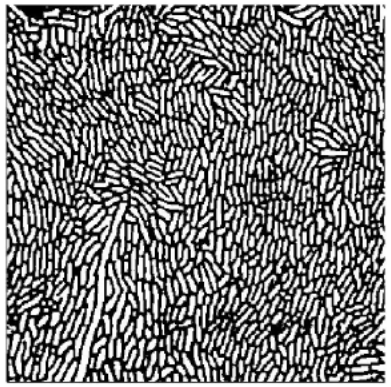
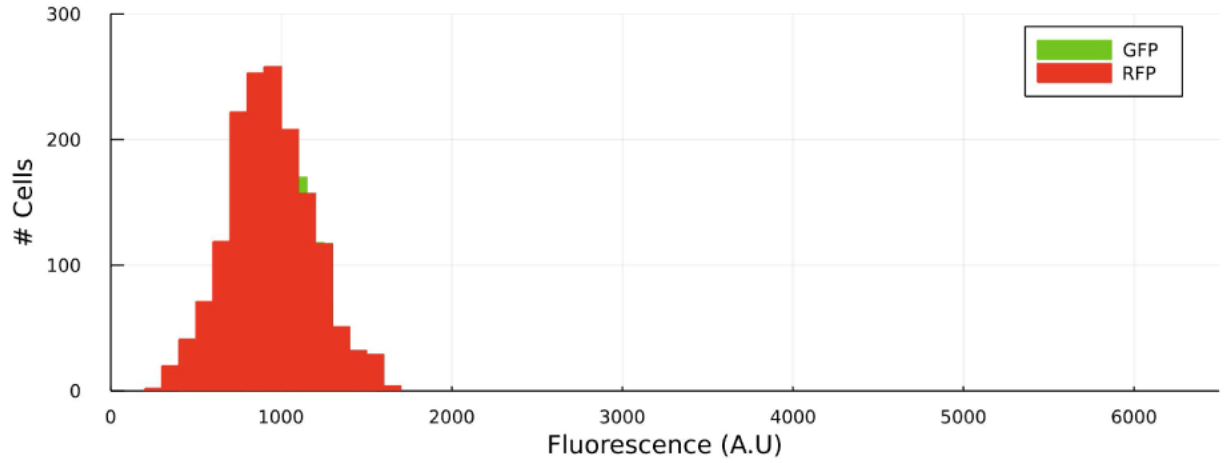




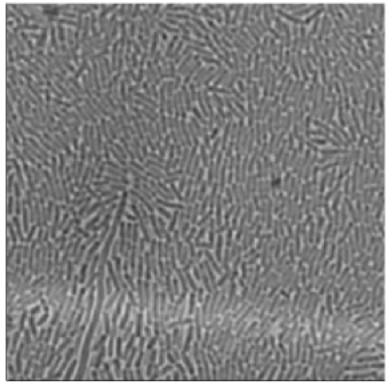


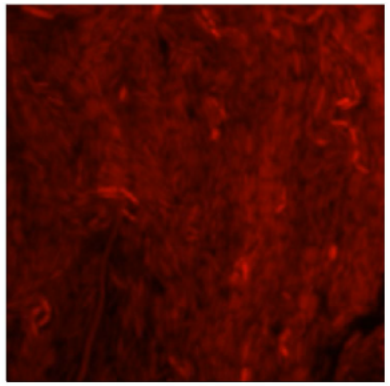


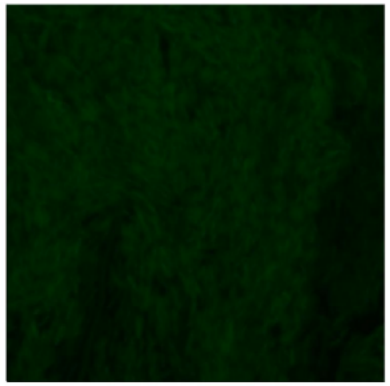

300
200
100
0
Cells
0
1000
2000
3000
4000
5000
6000
Fluorescence (A.U)
GFP
RFP

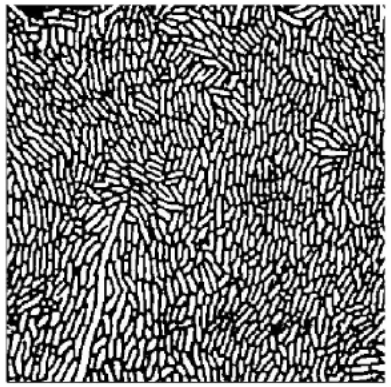
During PhD

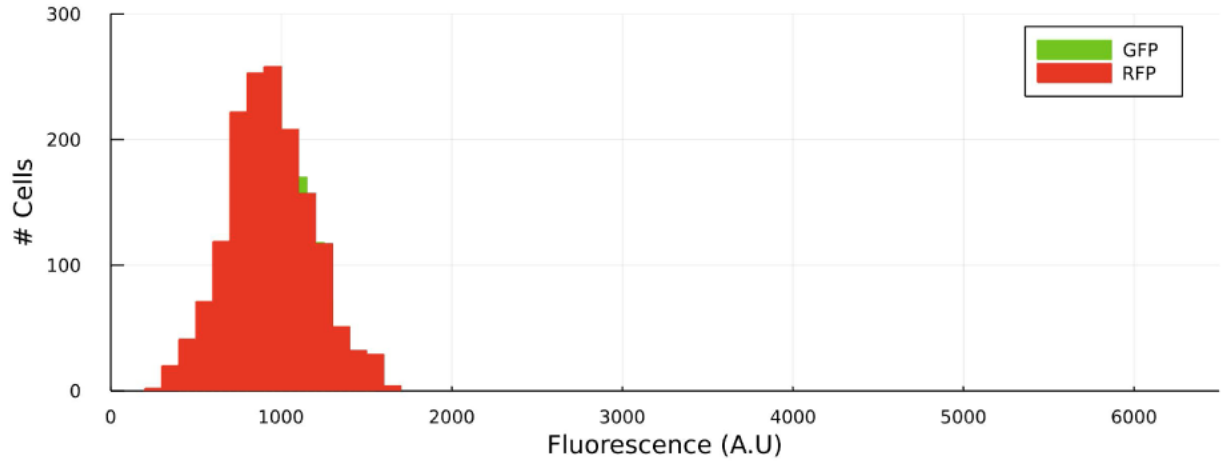
3 channels * 8 Positions * Acquisition Every 5 min for 48 hours = 13824 per experiment











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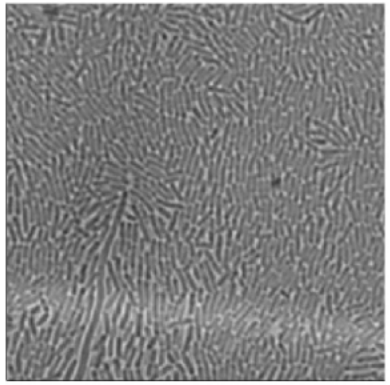

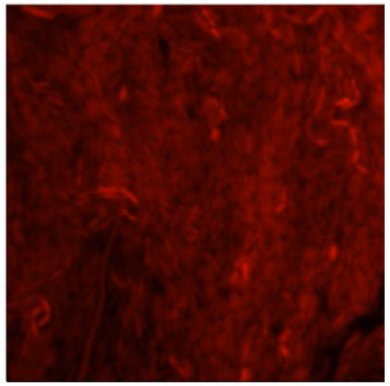

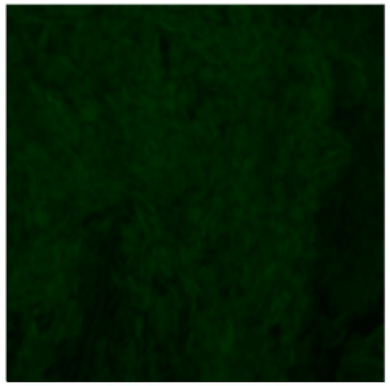

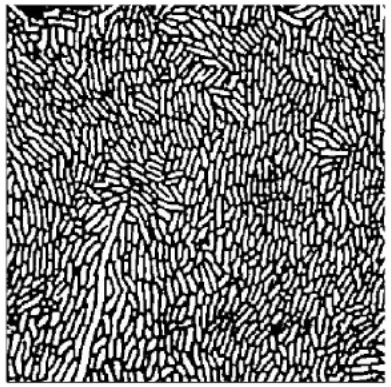

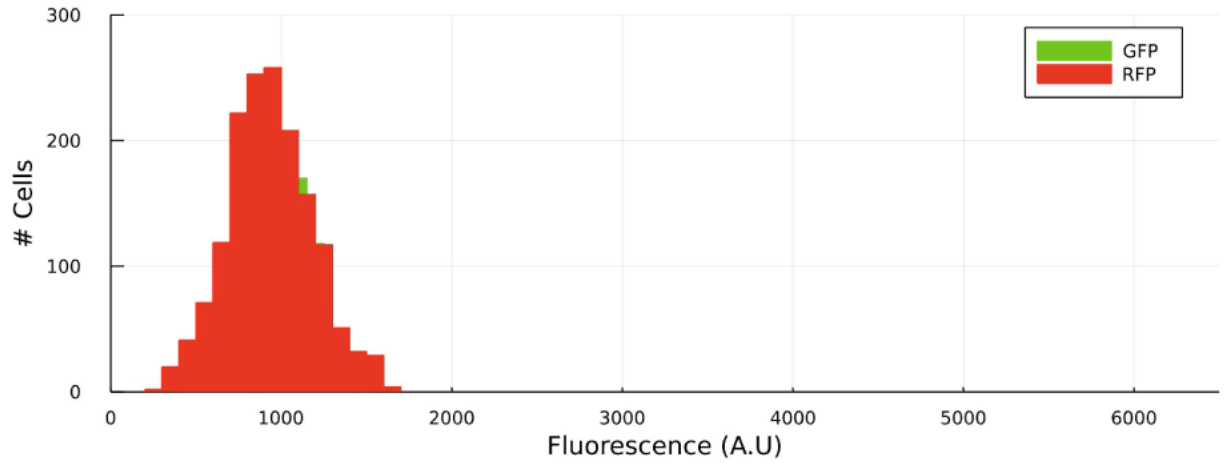

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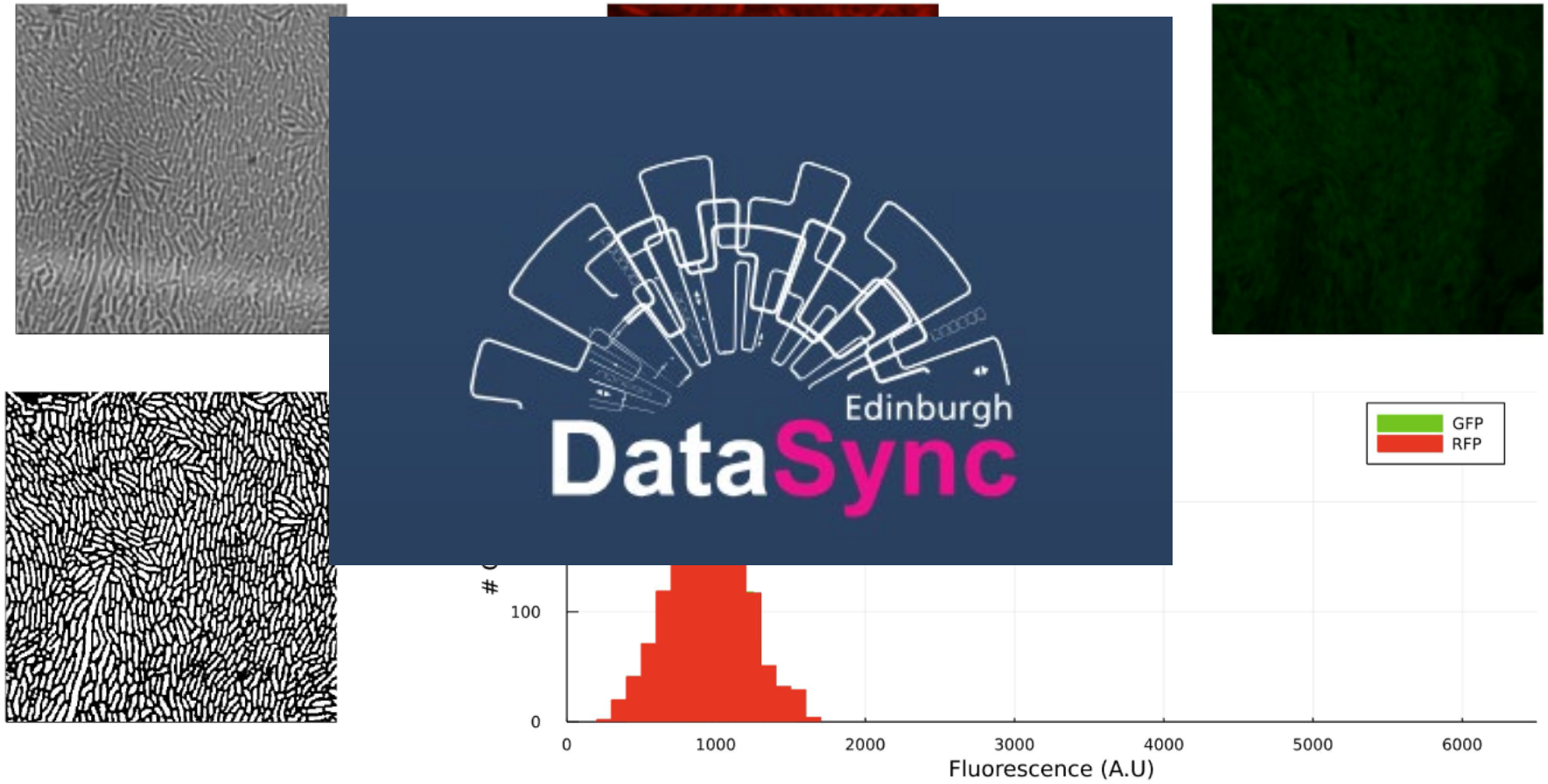

During PhD

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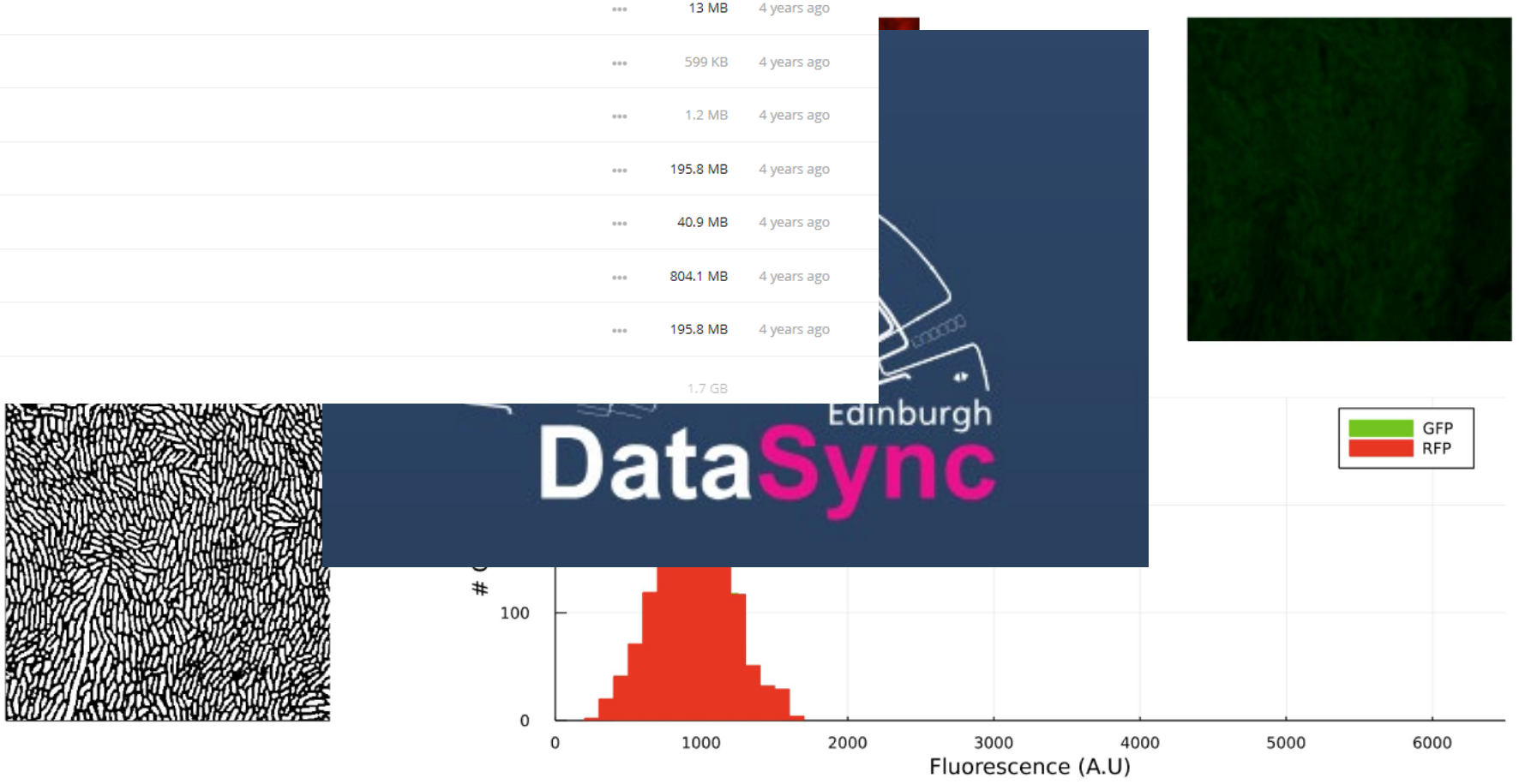
Name	Size	Modified
Bayesian_MS	526.7 MB	4 years ago
Figure2_Data	13 MB	4 years ago
Figure3_Data	599 KB	4 years ago
Figure5_Data	1.2 MB	4 years ago
Figure6_Data	195.8 MB	4 years ago
FigureS1_Data	40.9 MB	4 years ago
Frequentist_MS	804.1 MB	4 years ago
Stability_Analysis	195.8 MB	4 years ago
8 folders	1.7 GB	

or 48 hours = 13824 per experiment

n mask per image!!!



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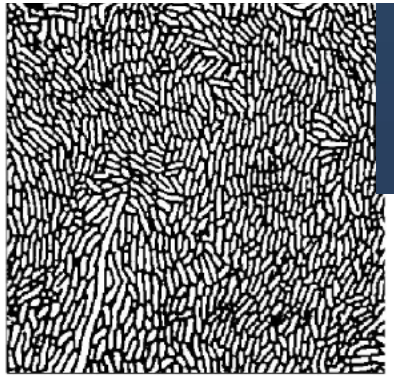
or 48 hours = 13

n mask per imag



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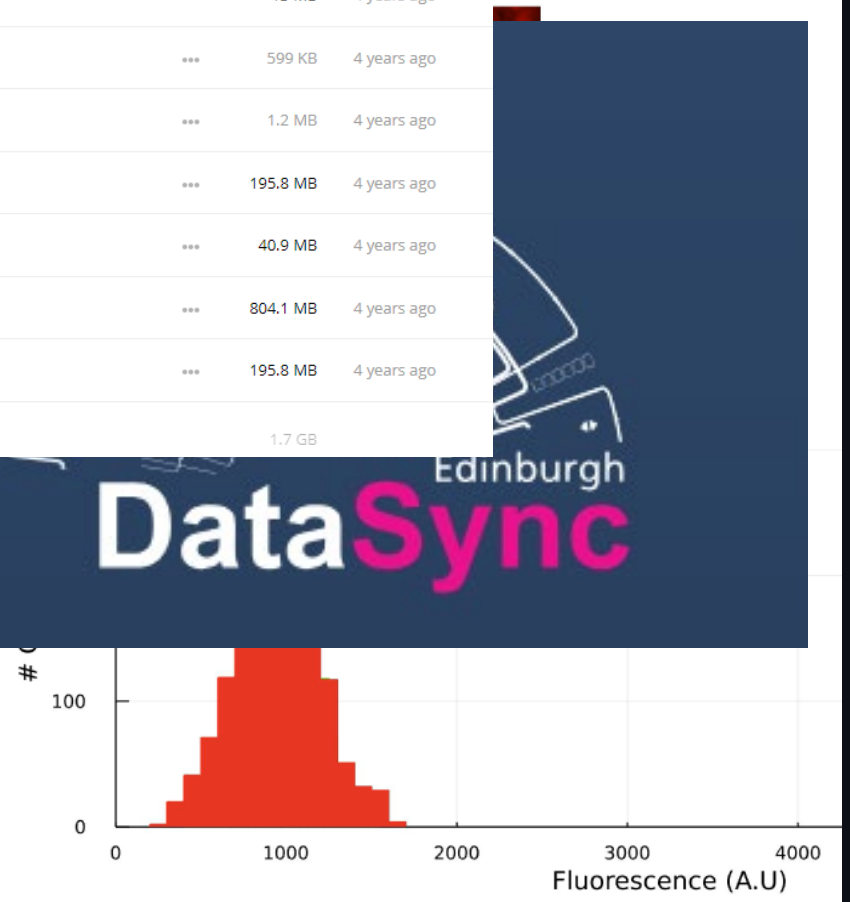

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DavidGomezC aa 5f9353a · 4 years ago | 17 Commits

Bayesian_MS	aa	4 years ago
Frequentist_MS	Change directory name	4 years ago
Images	Update clean image scripts	4 years ago
PriorShapeEffect	InferenceScript	4 years ago
Stability_Analysis	First push all scripts	4 years ago
README.md	Update README.md	4 years ago

README

Optimally Designed Model Selection in Synthetic Biology

Here the scripts used to generate, analyse and visualise the data presented in the paper are made available.

The use of the scripts requires the RStan Package, available at the link:

https://cran.r-project.org/web/packages/rstan/index.html

And the use of the Bayesian Optimisation package available at the link:

https://github.com/fmfn/BayesianOptimization

For the Matlab toolbox AMIGO2, refer to:

https://sites.google.com/site/amigo2toolbox/

The data for the *Bayesian* case is organised in the following subfolders (Bayesian_MS Directory):

- **Inference:**
  - *ODE_Model1.stan*, stan statistical model script with Model 1 (M1) published by Lugagne *et al.*, used to perform Bayesian Inference of the experimental data from [1].
  - *ODE_Model2.stan*, stan statistical model script with Model 2 (M2) used to perform Bayesian Inference of the experimental data from [1].
  - *ODE_Model3.stan*, stan statistical model script with Model 3 (M3) used to perform Bayesian Inference of the experimental data from [1].
  - *MultiExtractExp.R*, script designed to access the experimental data and experimental schemes from [1] to generate an appropriate list of objects to be passed to the stan model prior to the inference. The csv files are generated using the script DataExtraction.m.
  - *DataExtraction.m*, script to extract the desired experimental data and experimental profiles from [1].
  - *masterRun.R*, script to perform inference through RStan using the designed model ODE_Model.stan and the list of data extracted from MultiExtractExp.R. The script allows performing inference on single datasets in series or on the combined set.
  - *masterRunOptim.R*, script designed as the masterRun.R script but including an initial optimisation process for the initialisation of the 4 MCMC chains used in

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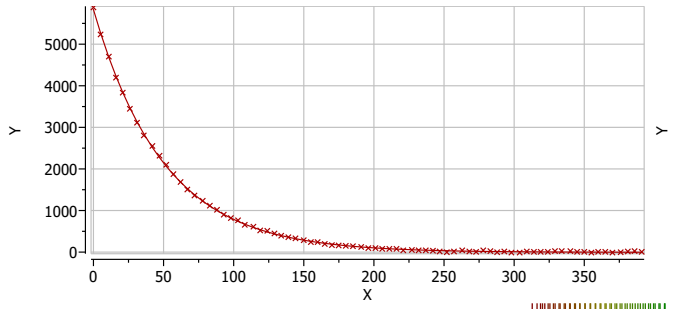

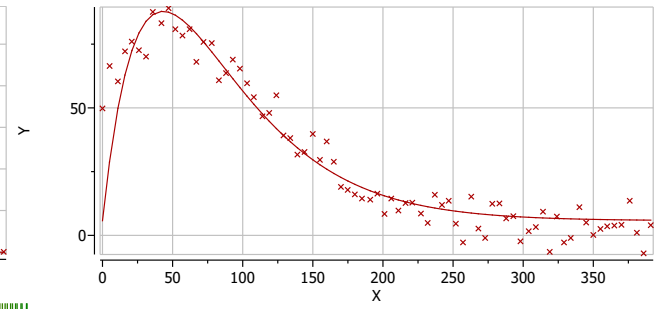

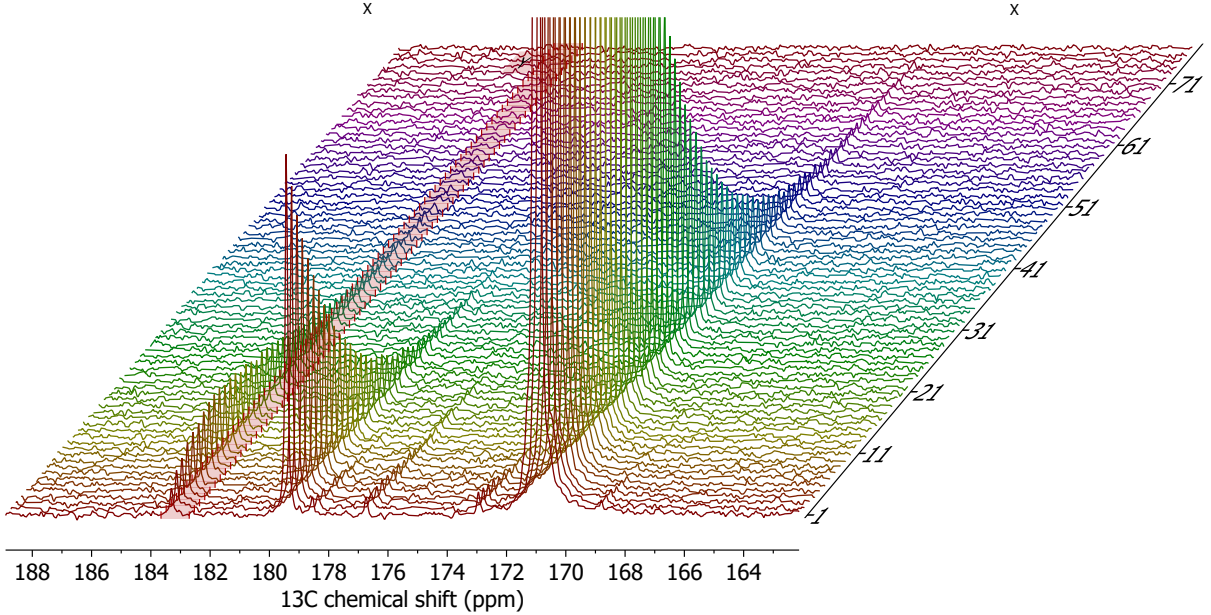

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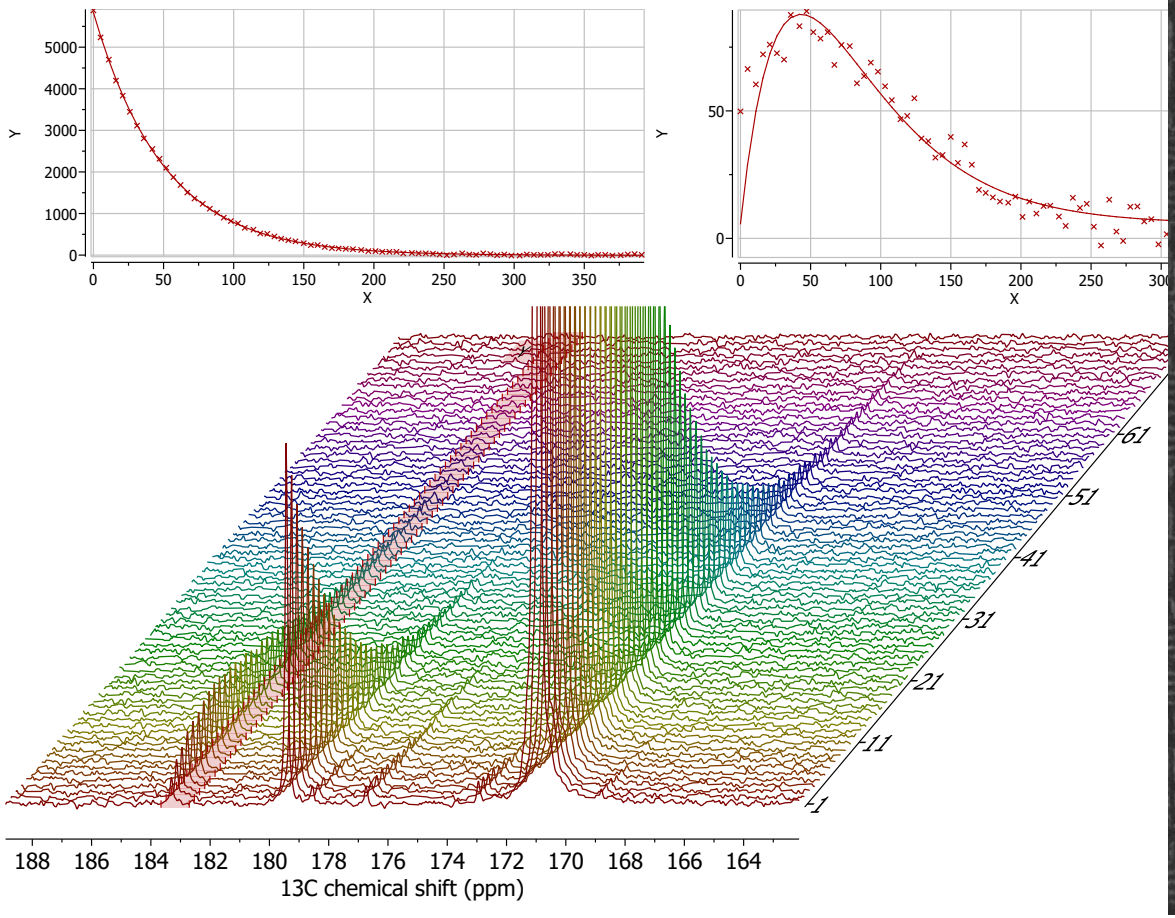

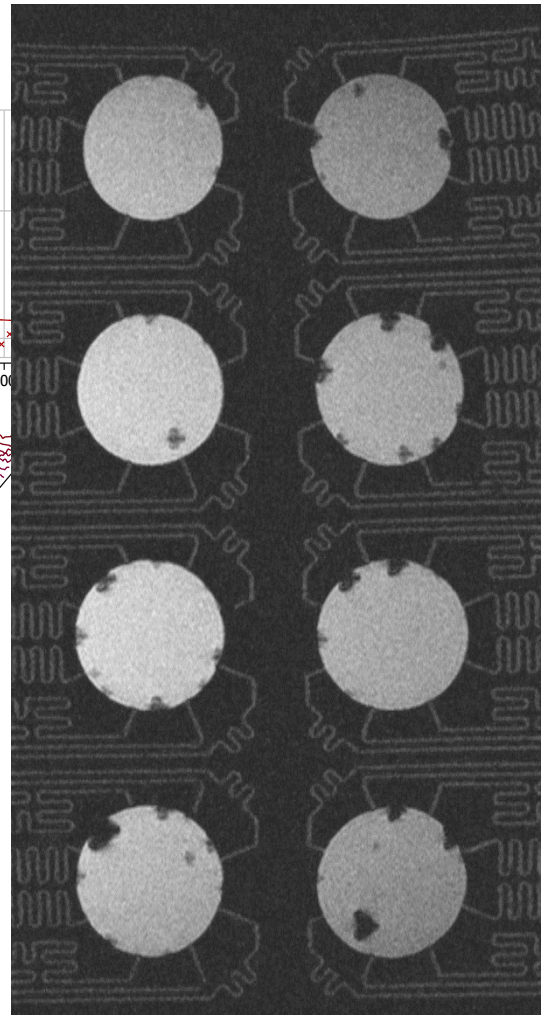

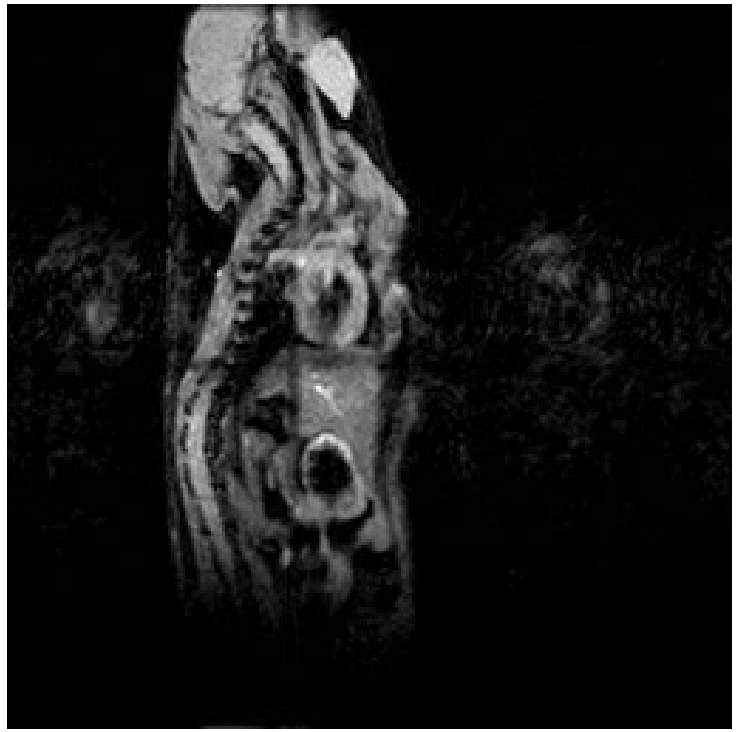

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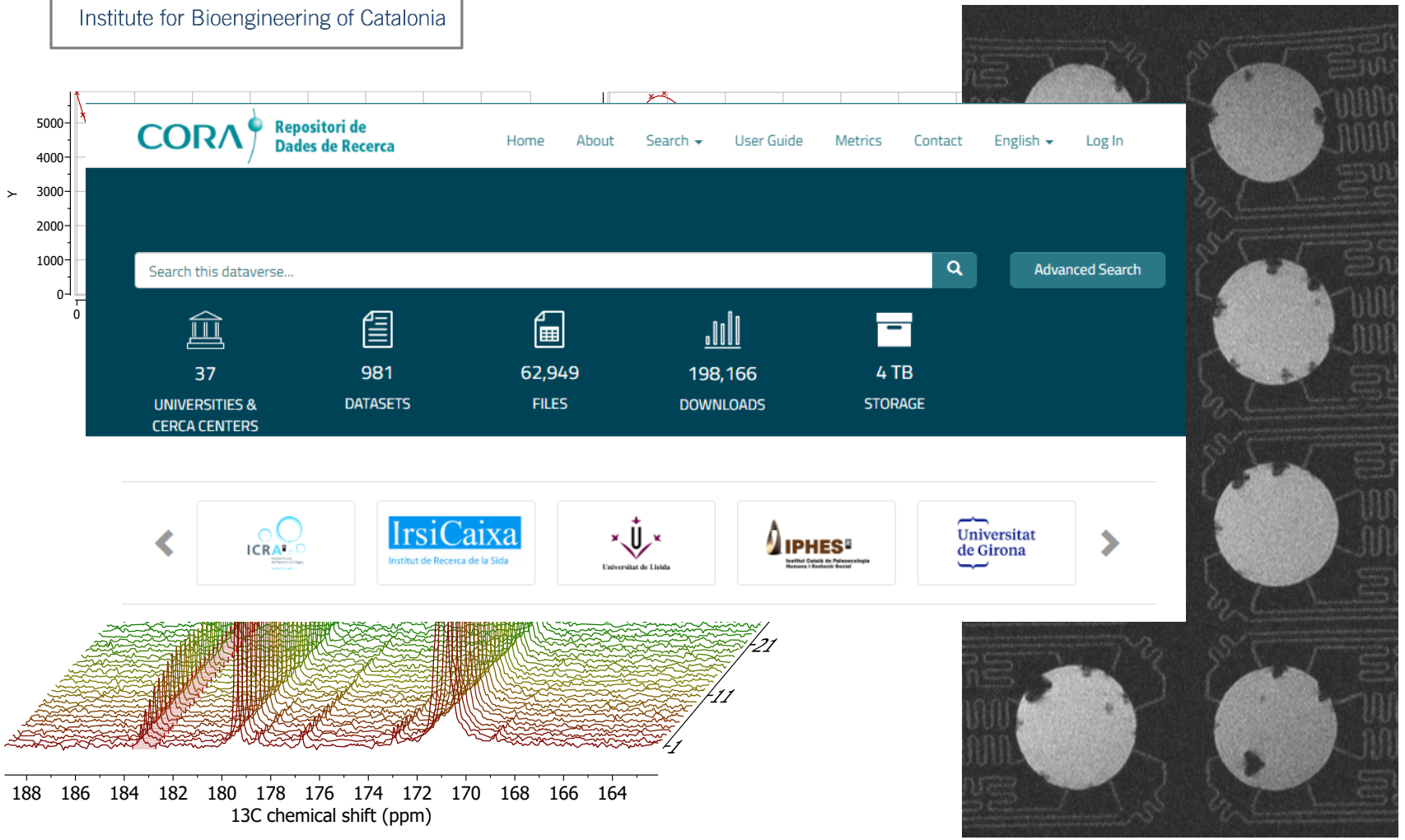

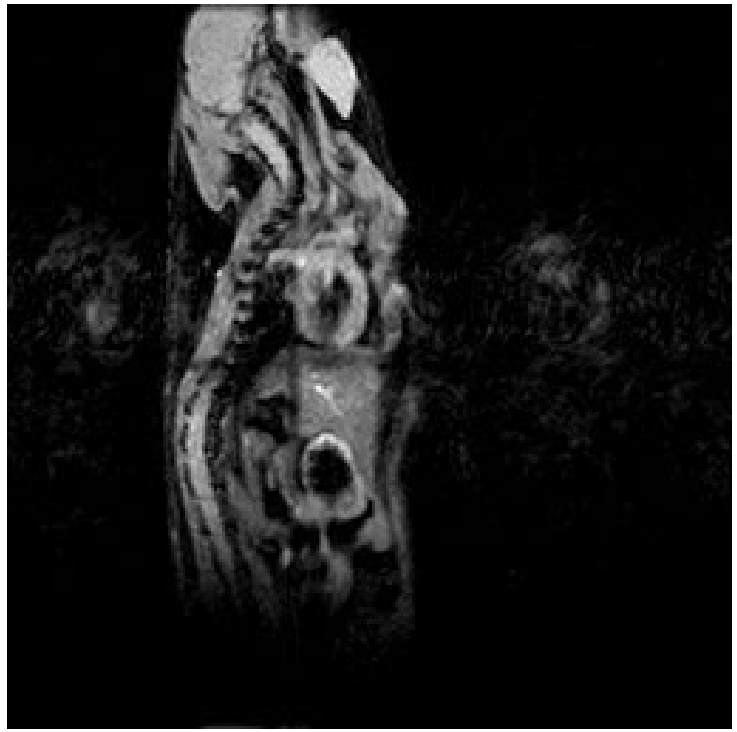

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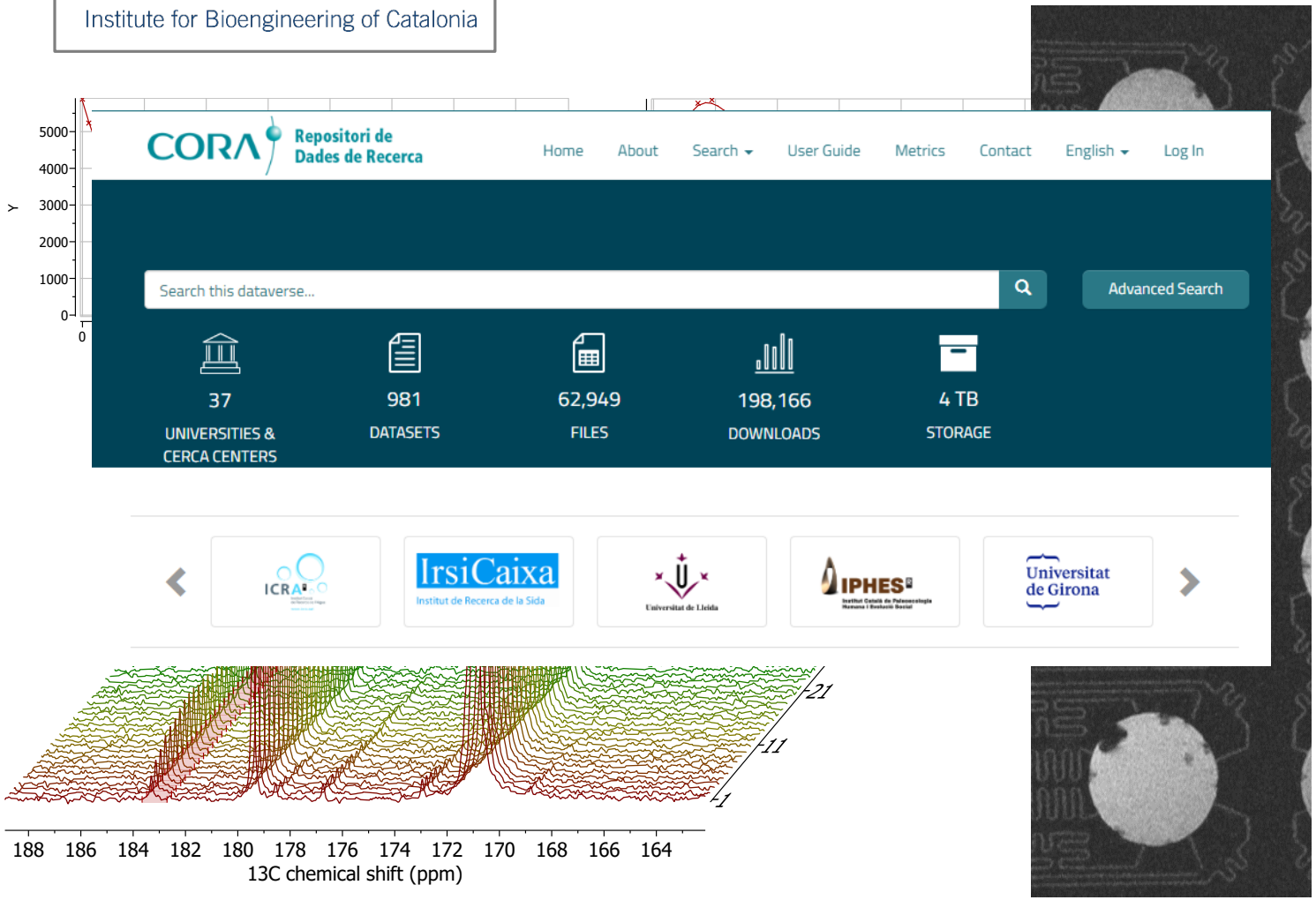

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DavidGomezCabeza Create FitDiffusion.ipynb — d6ab950 · 4 months ago — 11 Commits

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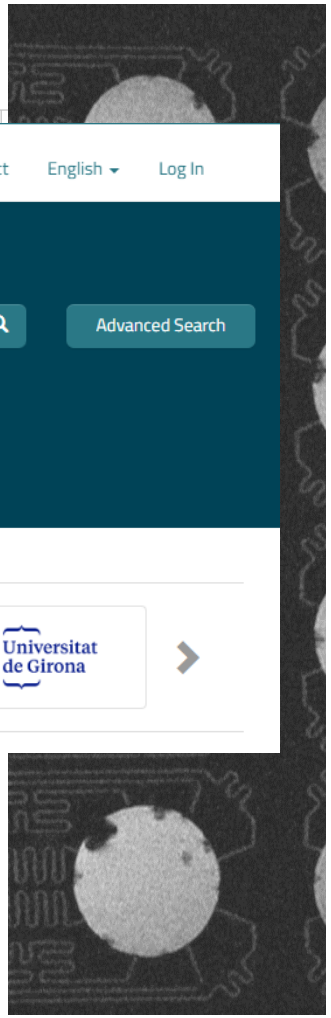
FastInjection.ipynb	CleanScripts	6 months ago
FitDiffusion.ipynb	Create FitDiffusion.ipynb	4 months ago
HydroGelPerfusion.ipynb	CleanScripts	6 months ago
PumpInjection.ipynb	CleanScripts	6 months ago
README.md	Update README.md	5 months ago

README

ScaffoldsDifPerfPaper_2023

This repository contains all the Python scripts developed to process the MRI data from the paper "Leveraging Magnetic Resonance Imaging to Study Biocompatible Scaffolds Perfusion for Lab-on-a-Chip Systems".

The MRI data generated and processed for this study can be found at https://doi.org/10.34810/data1028.



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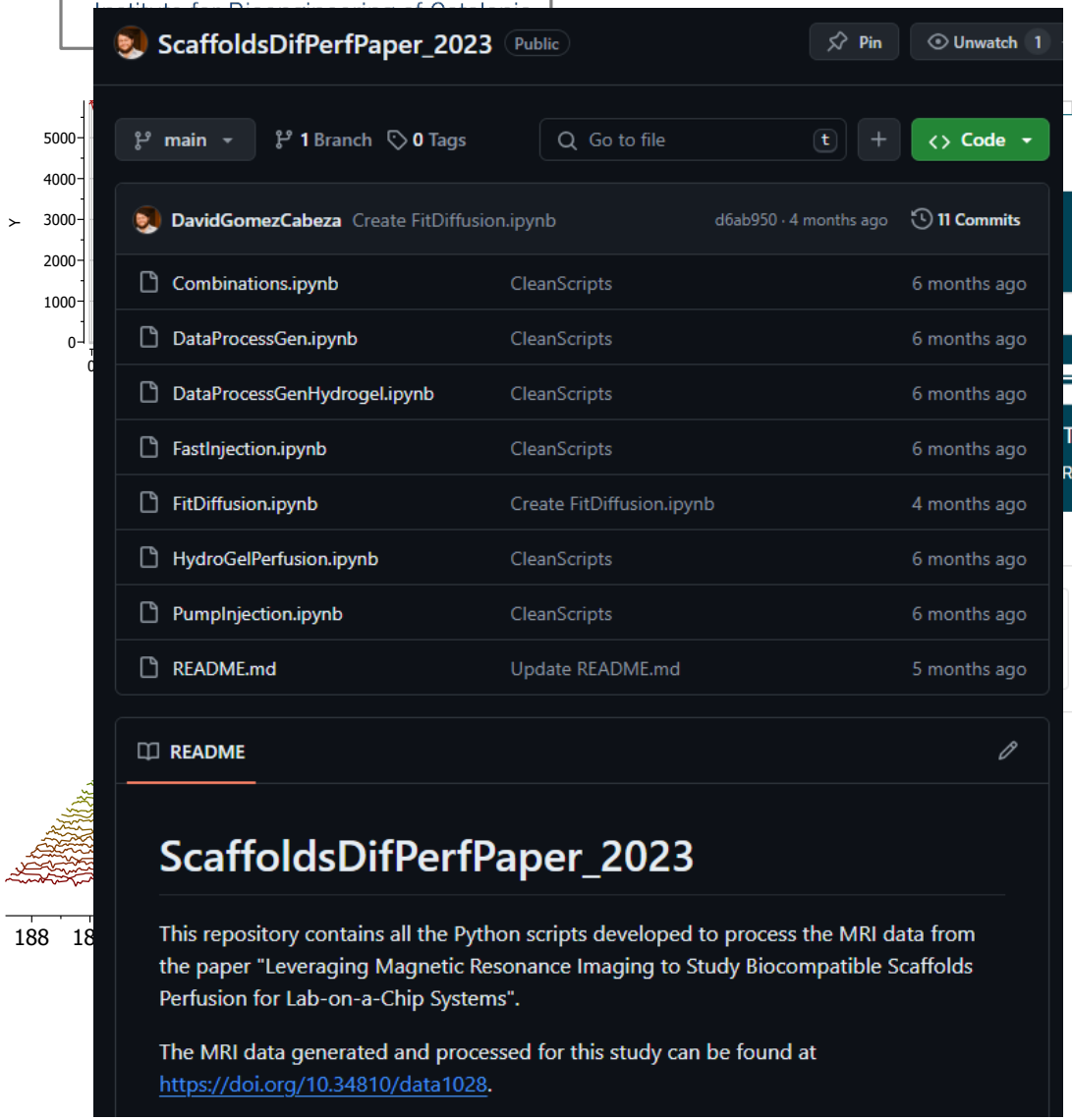

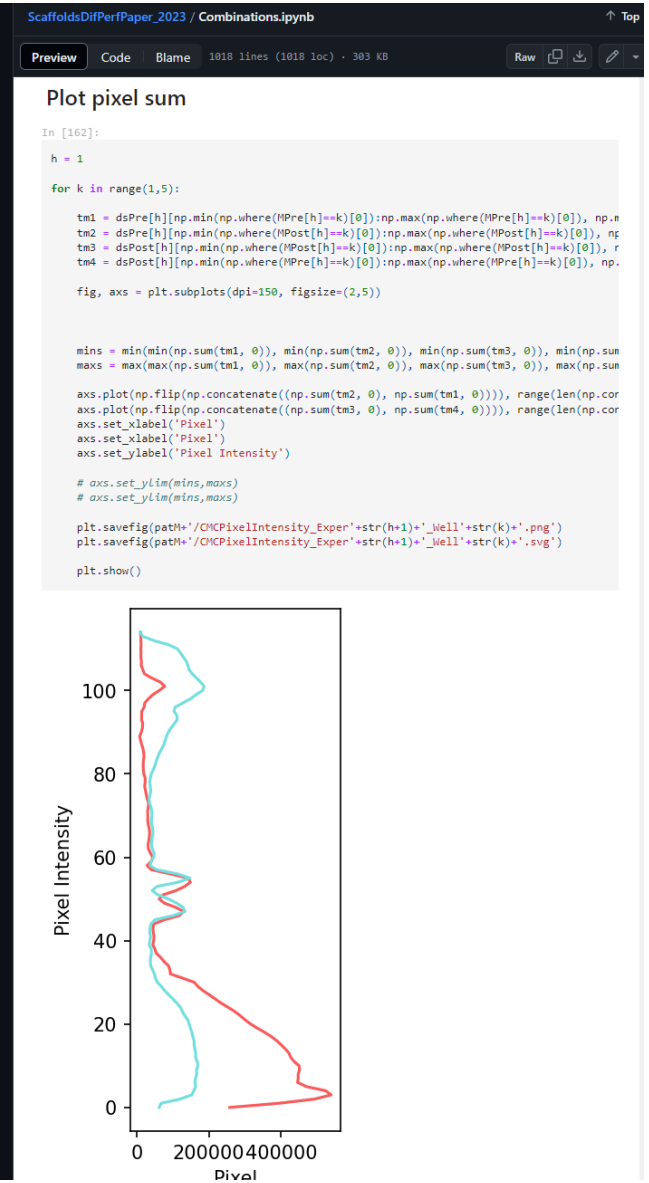

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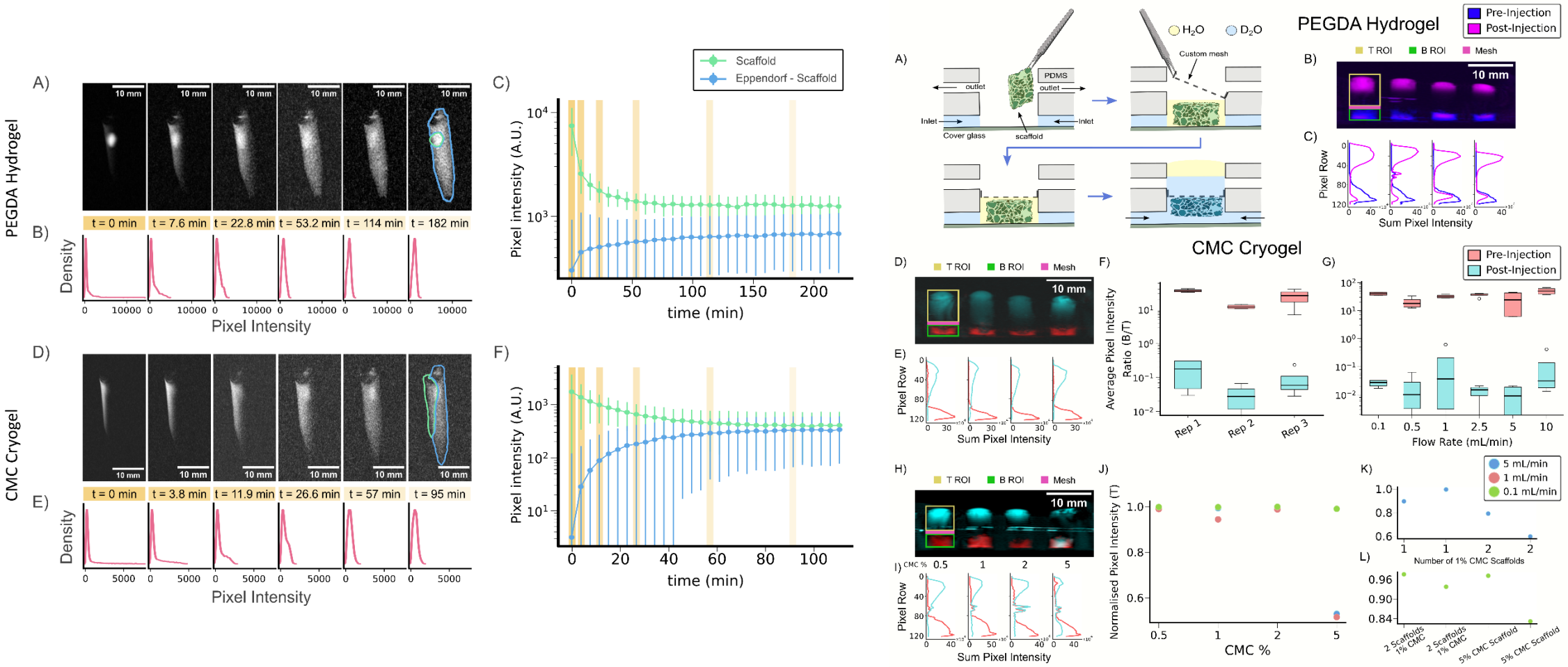

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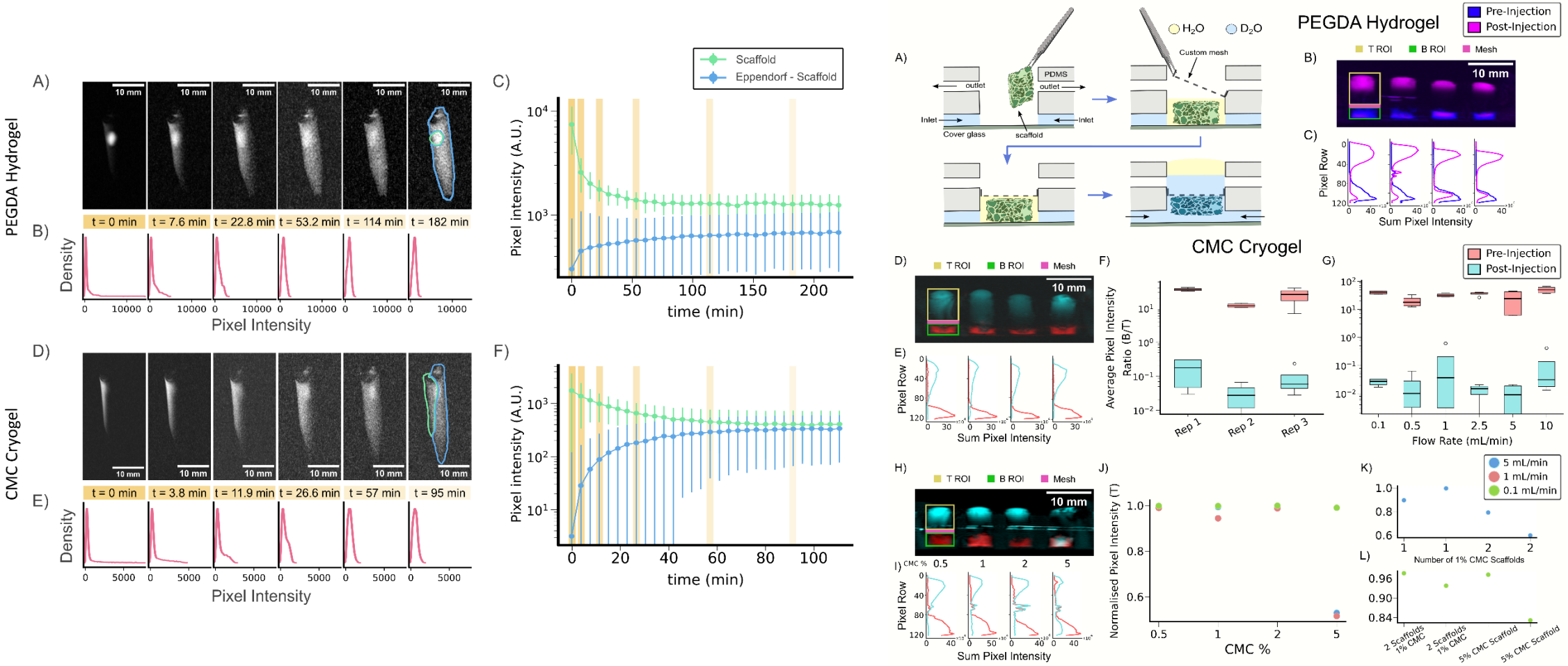
The final figures are important, but so is the raw data



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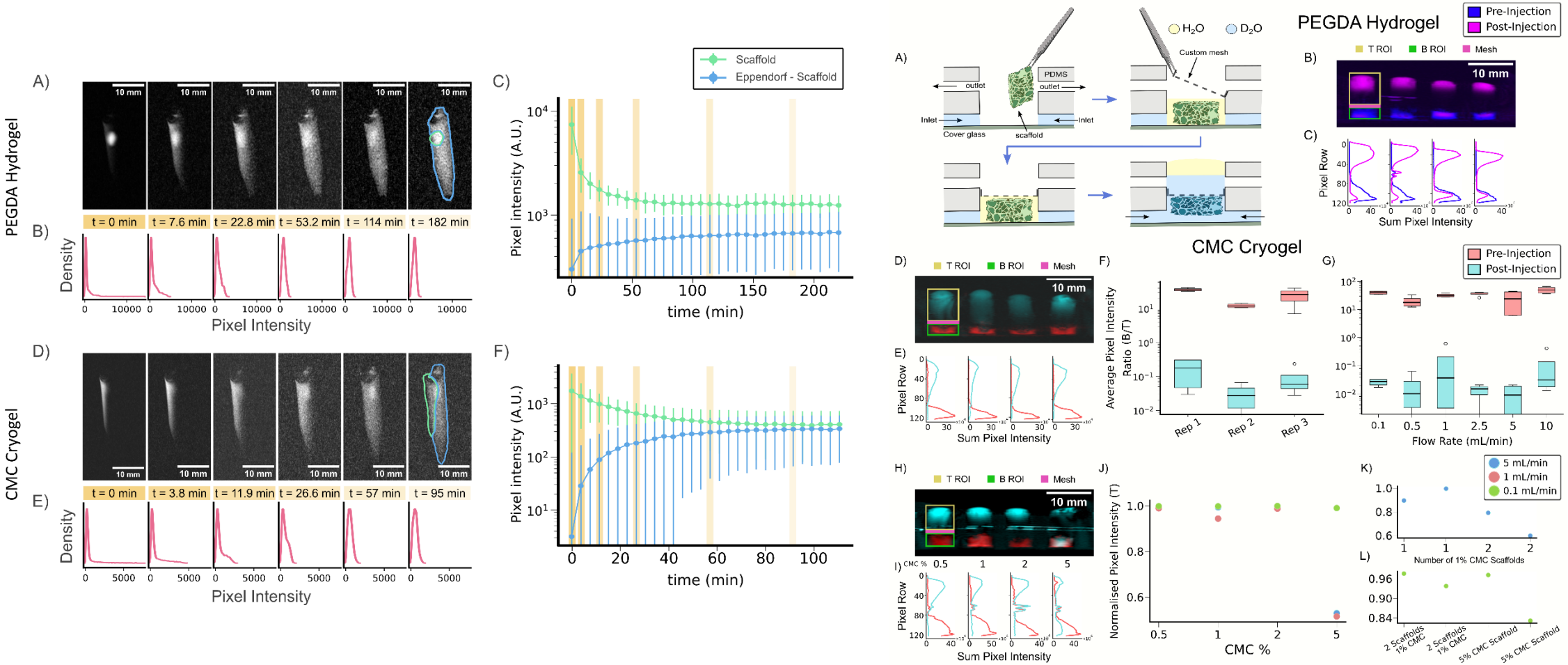
The final figures are important, but so is the raw data and the way we process this



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