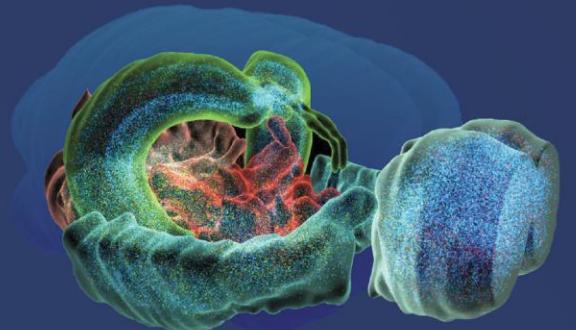
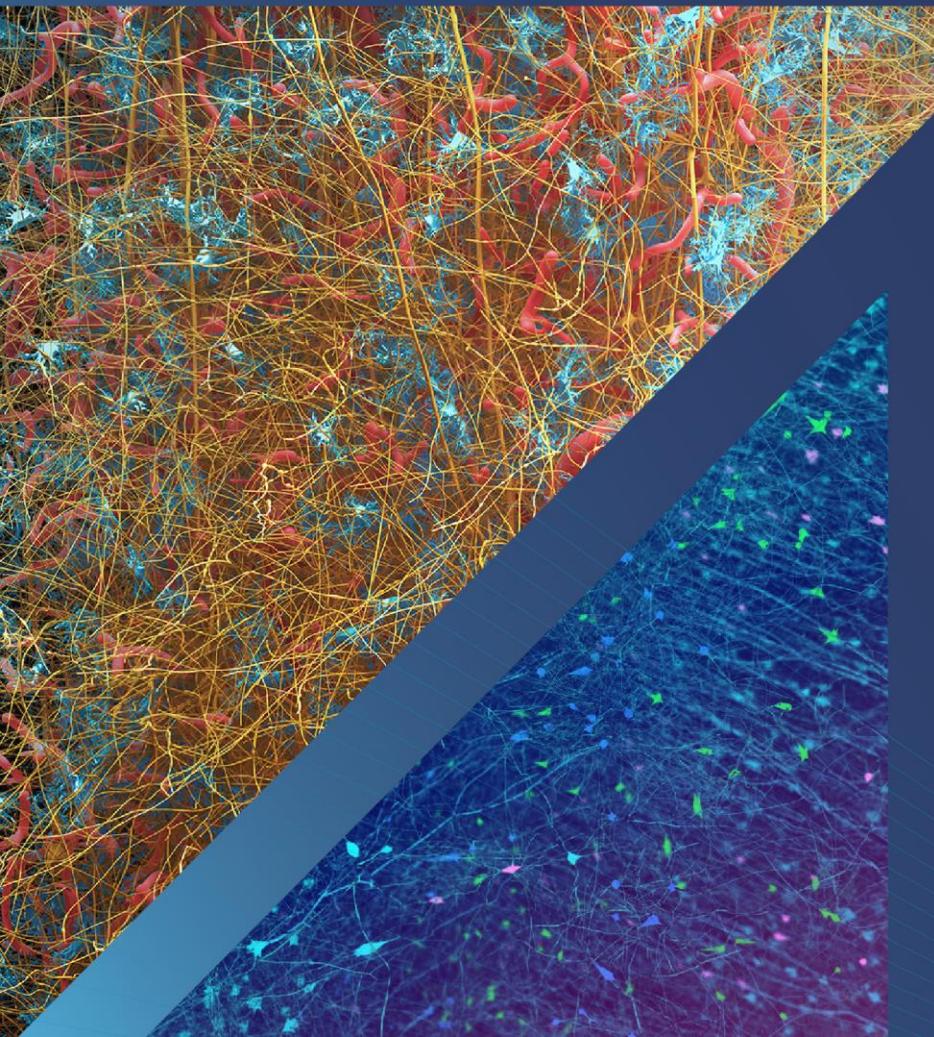
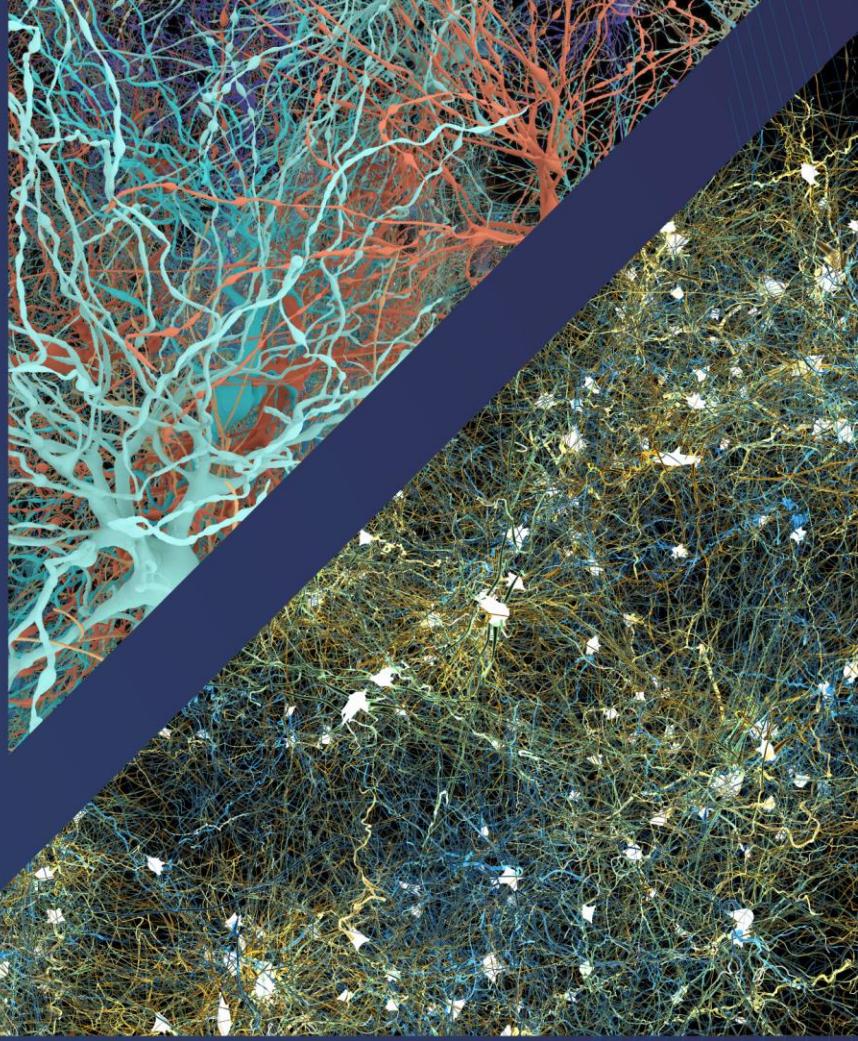


Blue Brain Project



Digitally reconstructing and
simulating the mouse brain

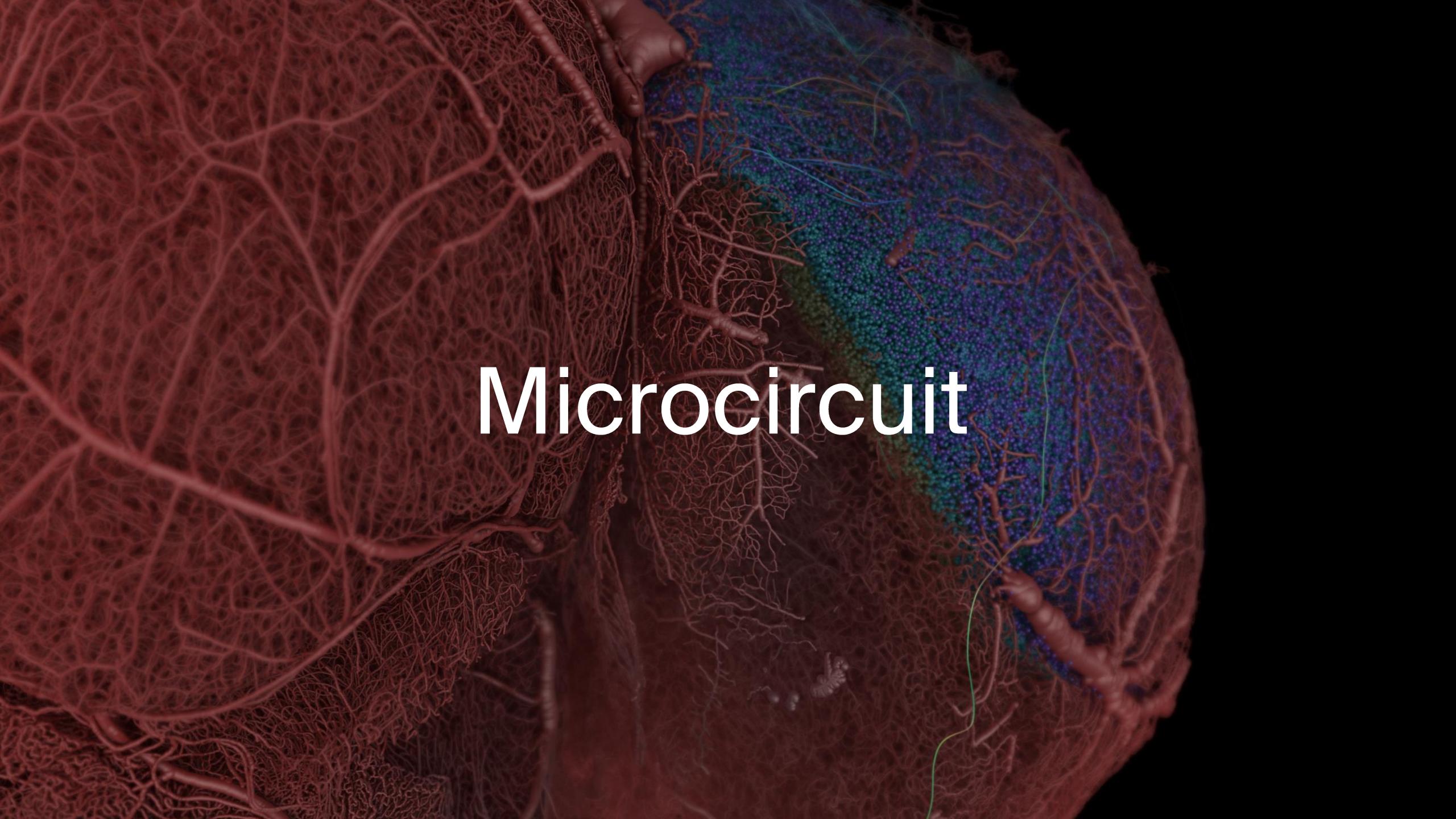




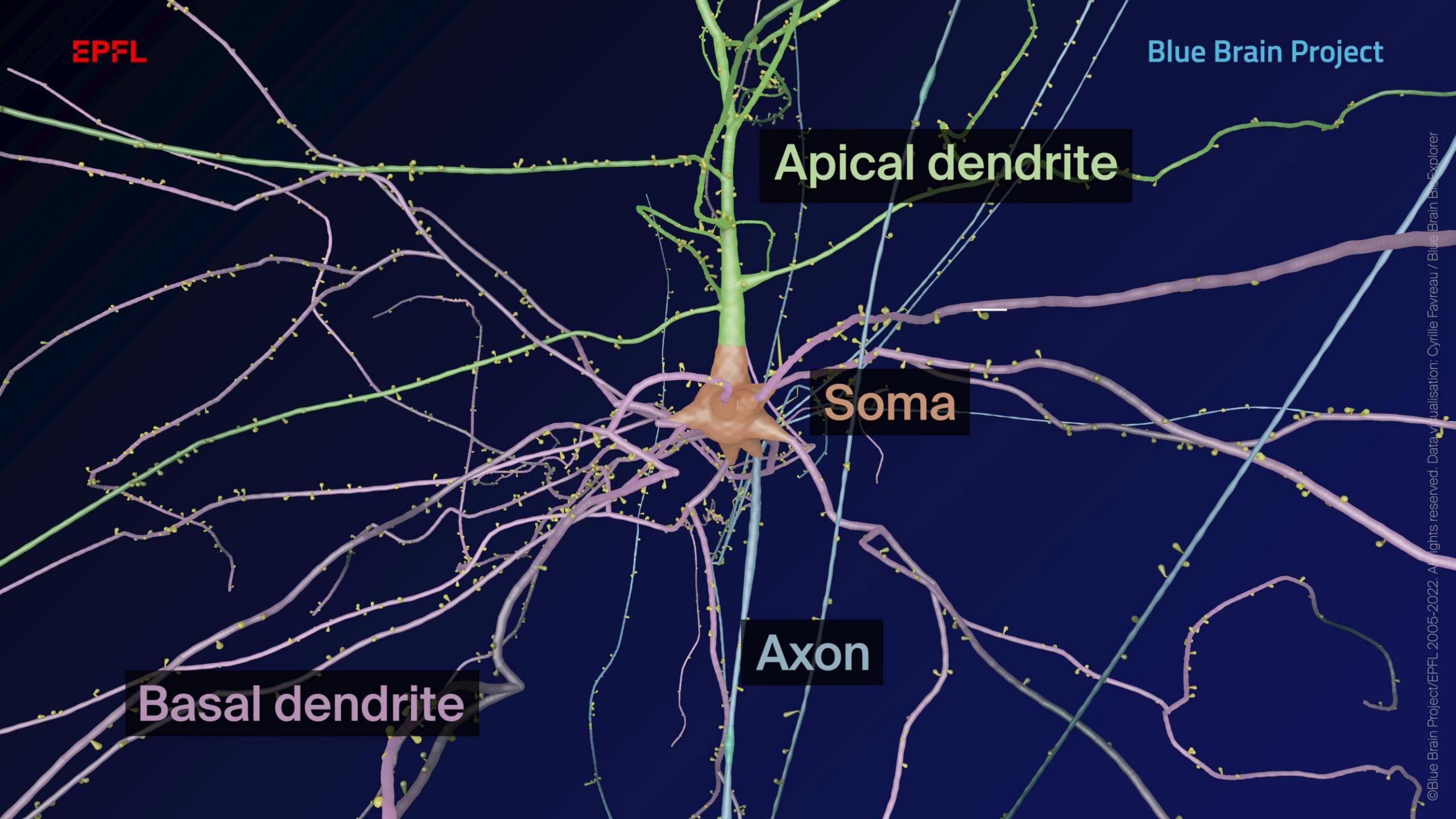
EPFL's Blue Brain Project is a Swiss brain research Initiative led by Founder and Director Professor Henry Markram.

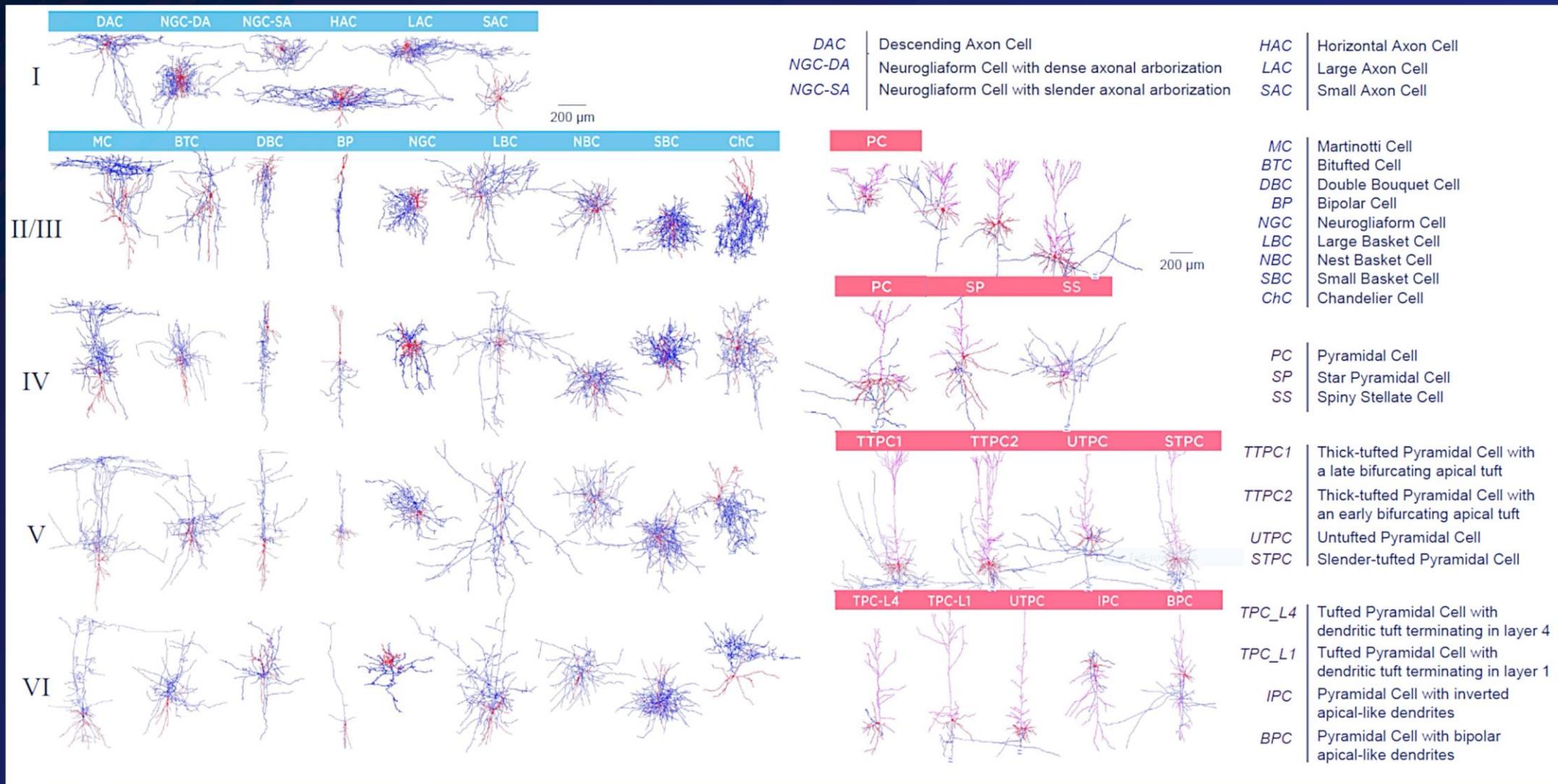
The aim of Blue Brain is to establish simulation neuroscience as a complementary approach alongside experimental, theoretical and clinical neuroscience to understanding the brain, by building the world's first biologically detailed digital reconstructions and simulations of the mouse brain.

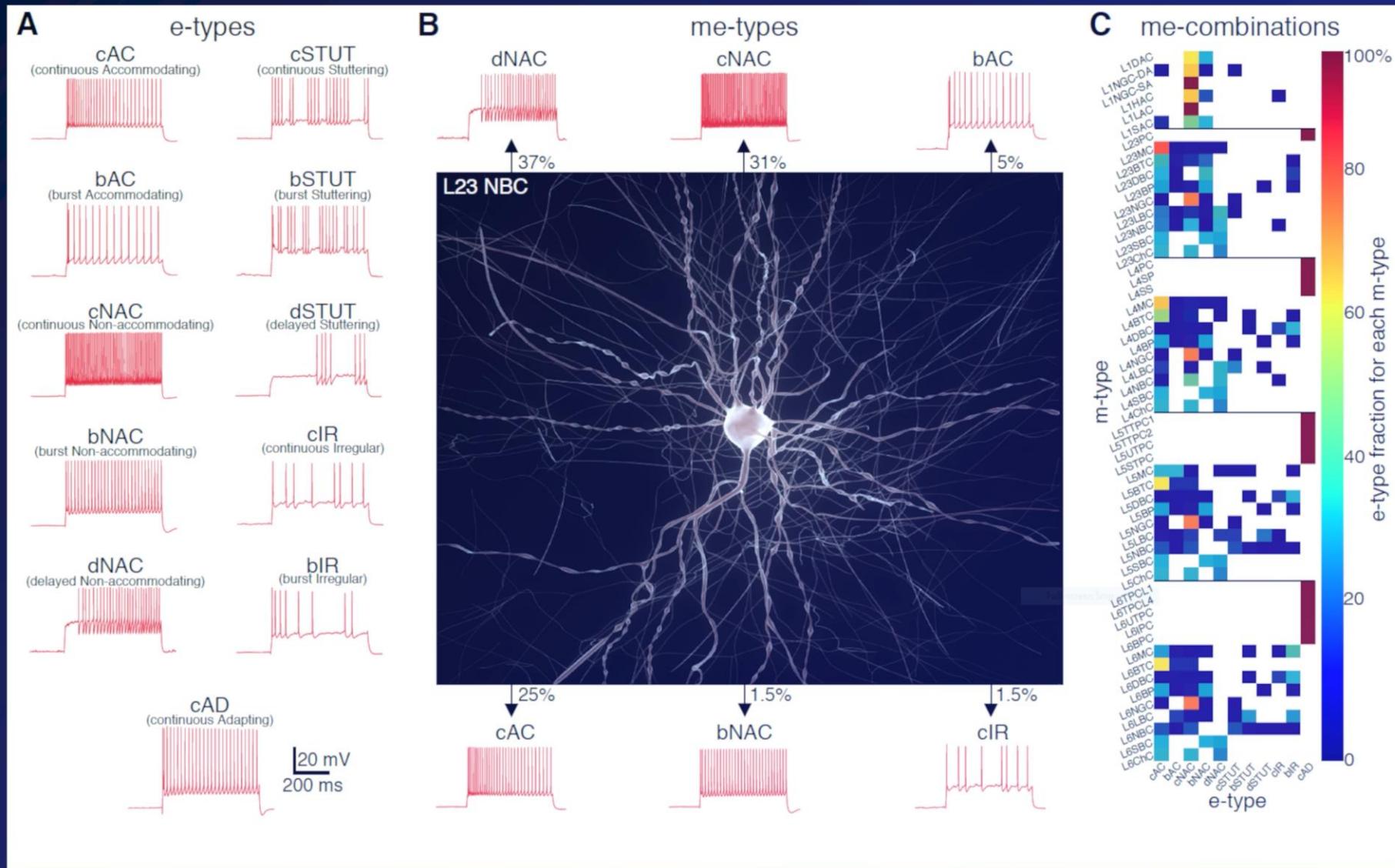


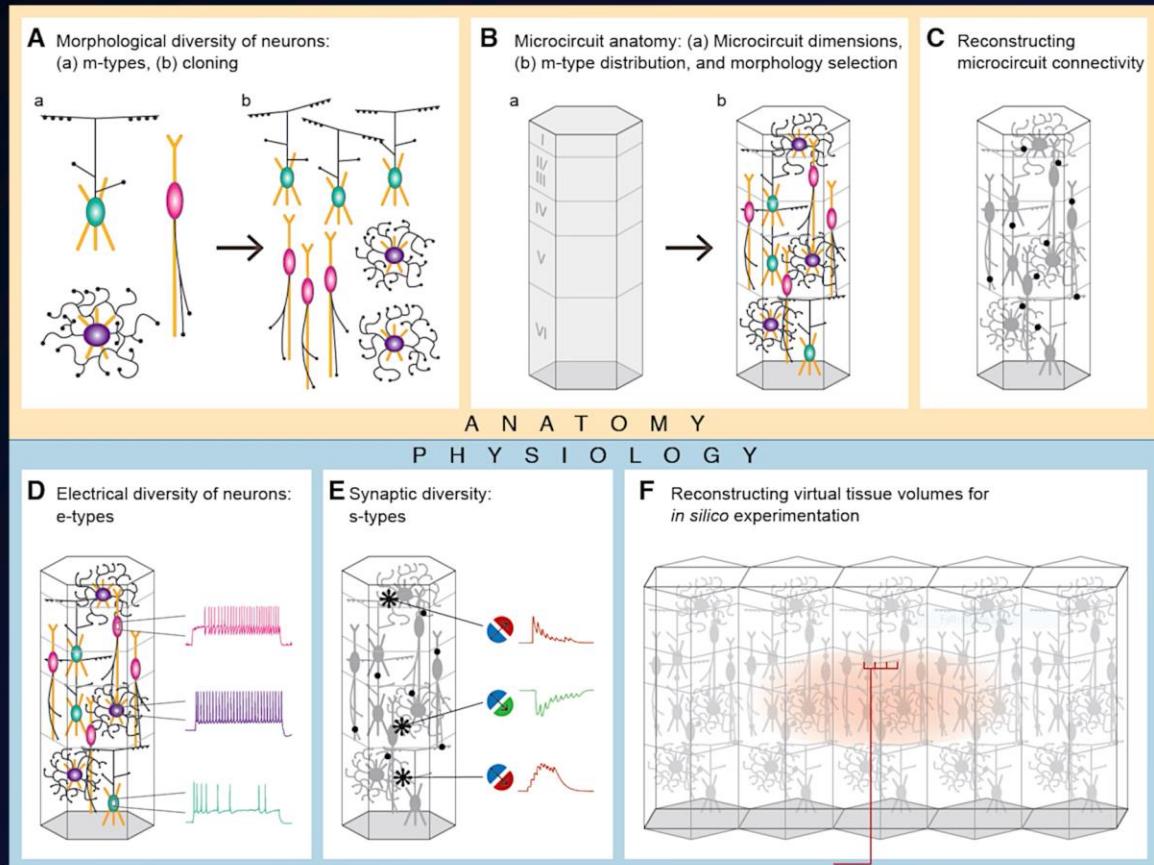
A 3D rendering of a brain microcircuit. The image shows a complex network of red blood vessels forming a dense web across the surface. Interspersed among the vessels are clusters of blue and green spherical objects, representing neurons or glial cells. A single green line traces a path through the tissue, highlighting a specific circuit. The overall color palette is dominated by shades of red, brown, and green against a dark background.

Microcircuit





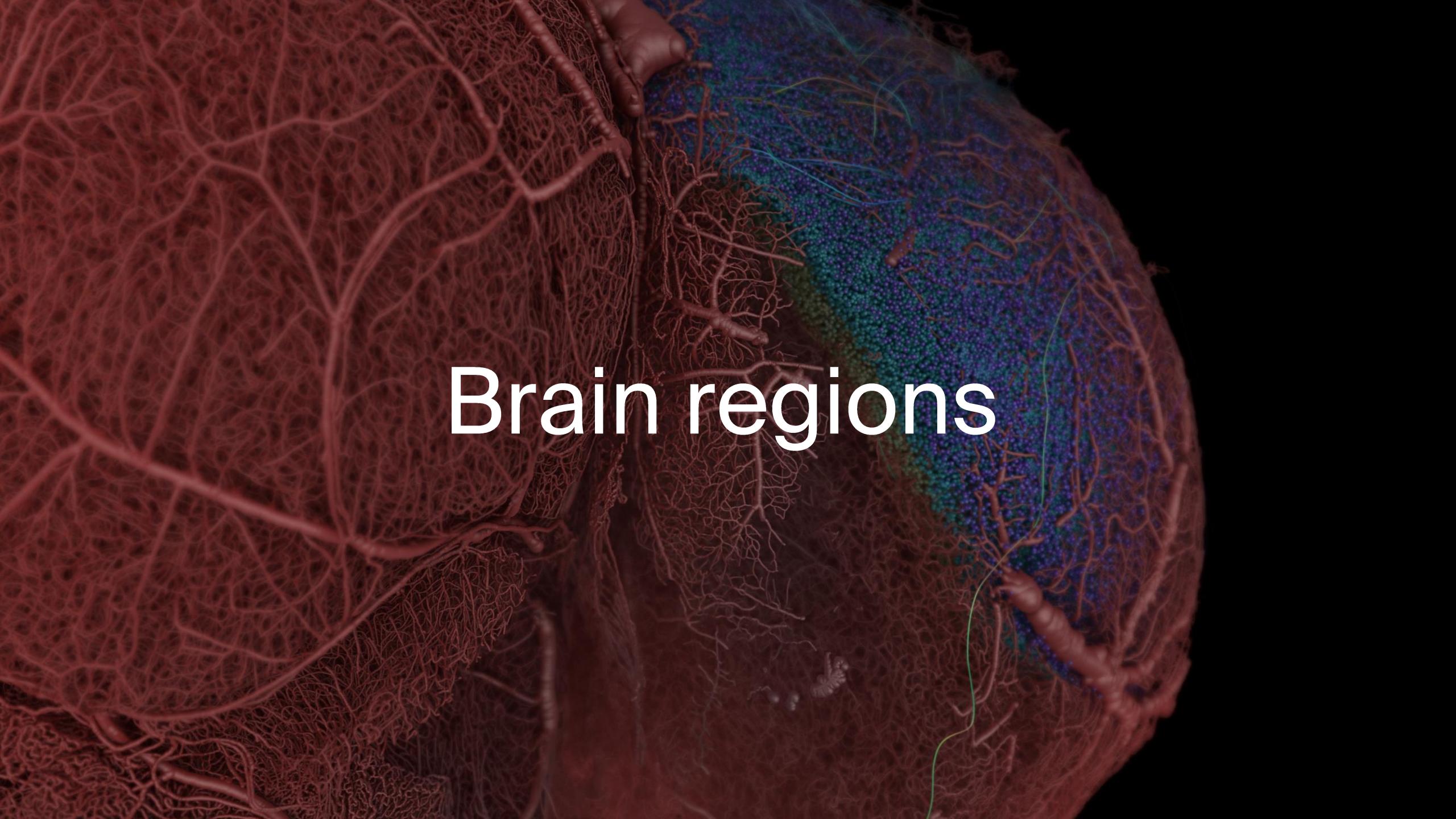




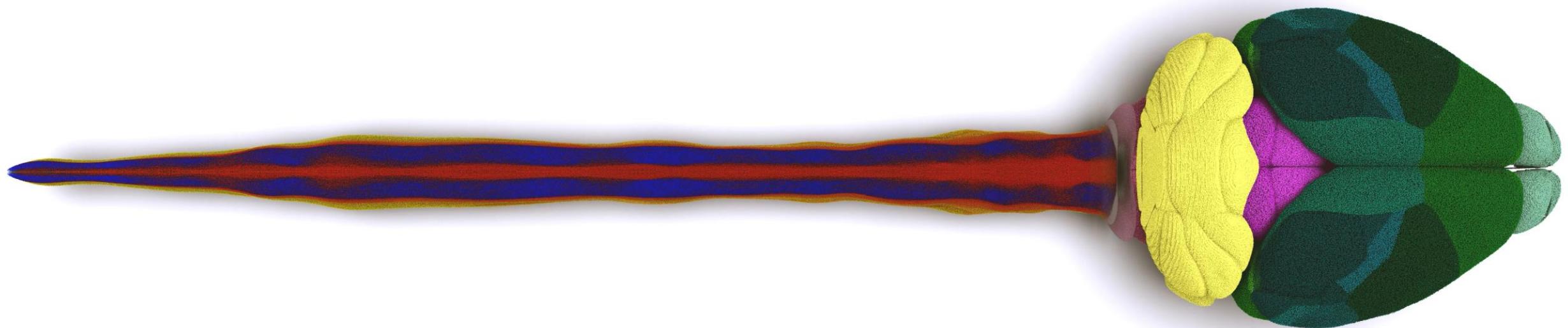
EPFL

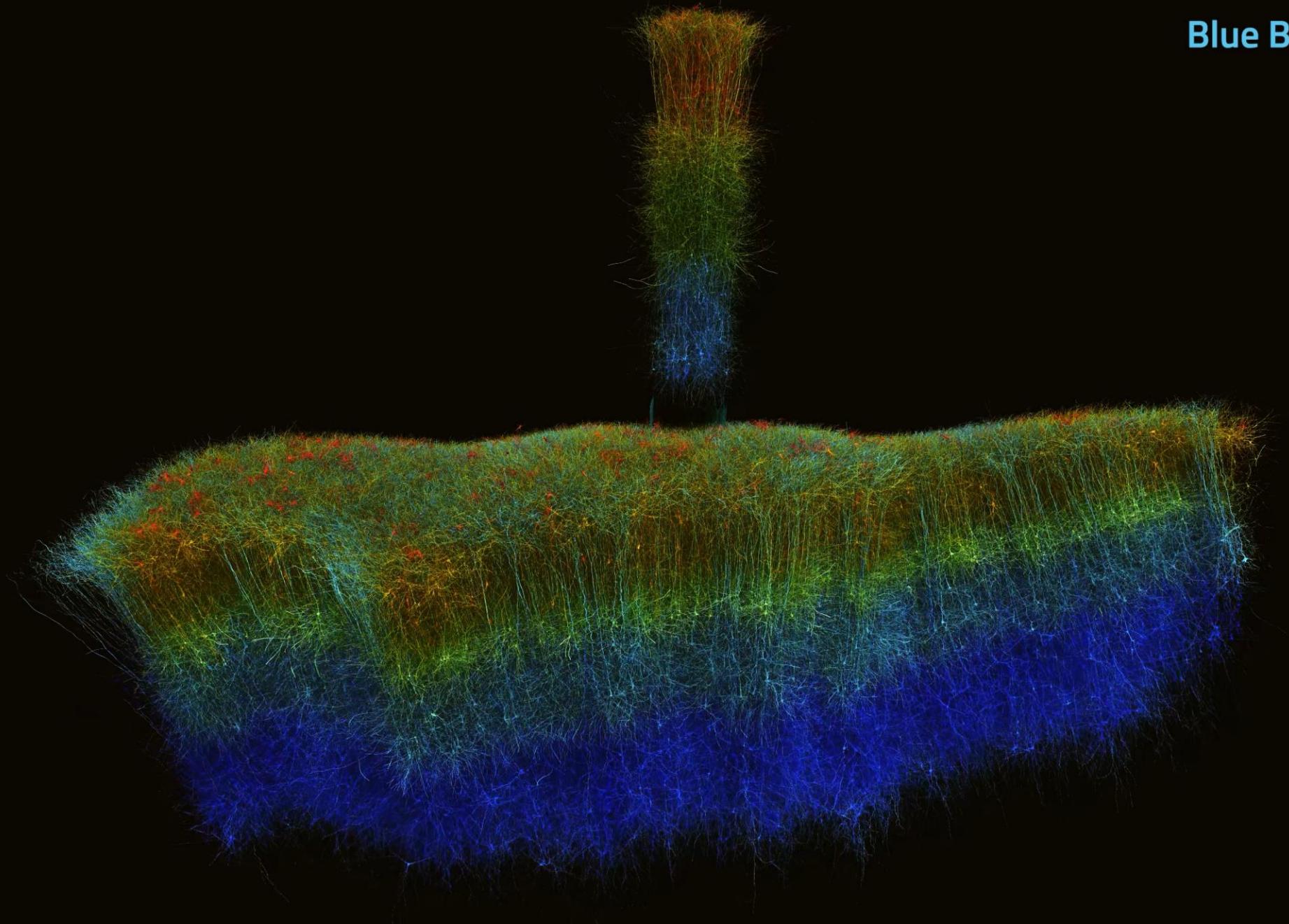
Blue Brain Project

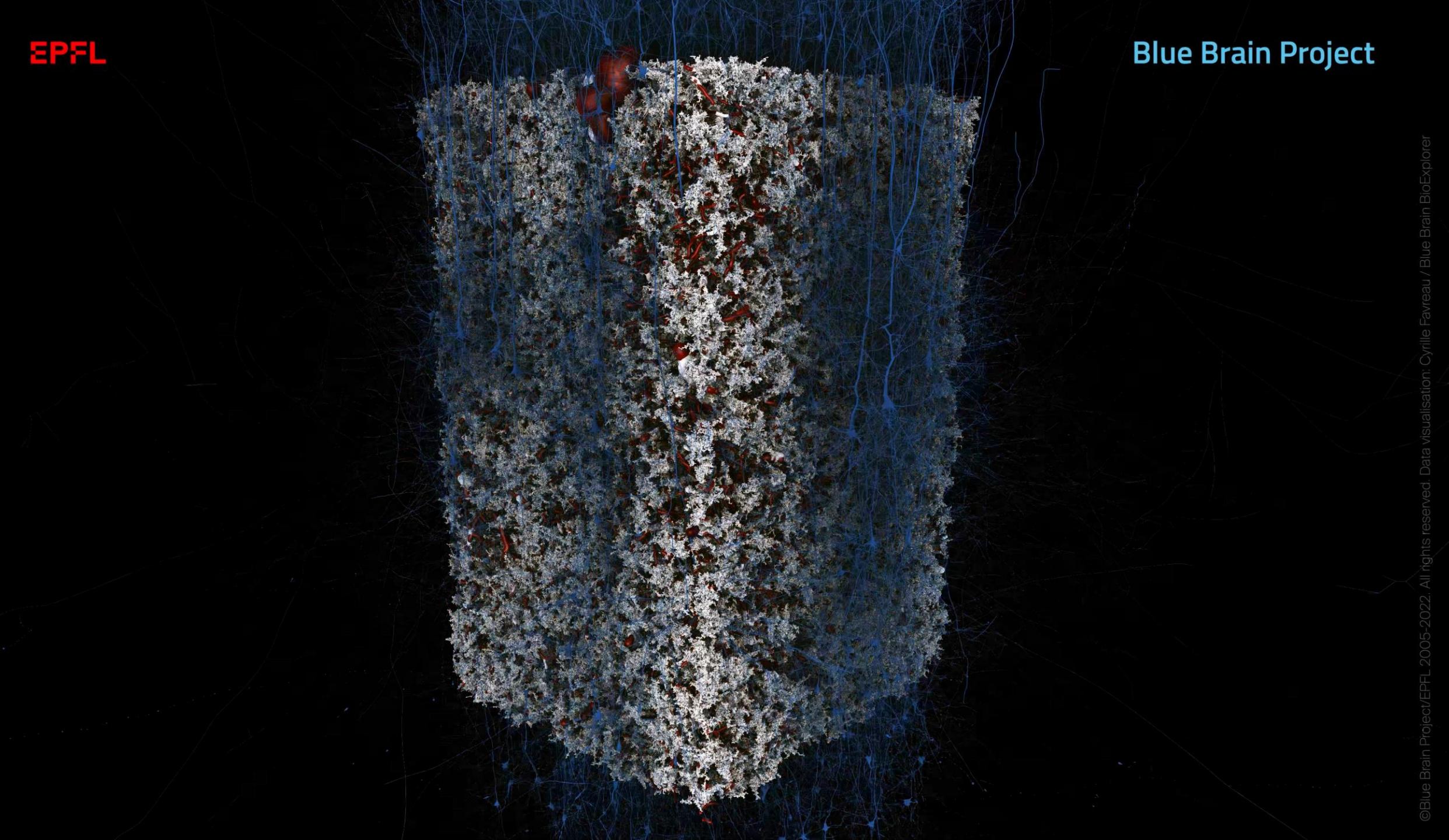


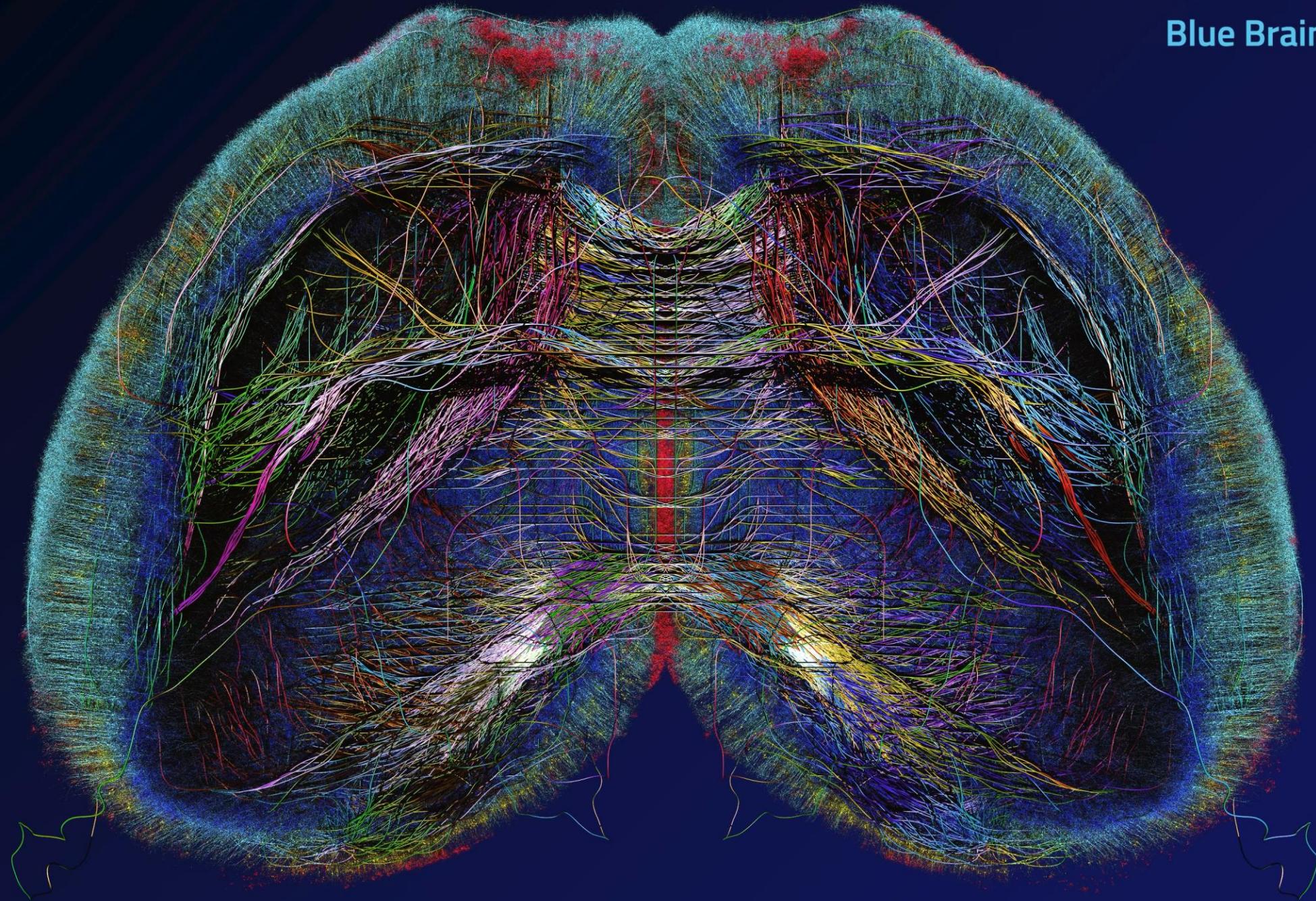
A 3D rendering of a brain from a lateral perspective. The brain is primarily colored in shades of brown and reddish-brown, representing the vascular network. A small, localized cluster of blue and green dots is visible on the right hemisphere, indicating a specific brain region or area of interest. A thin green line traces a path from this highlighted cluster towards the brainstem.

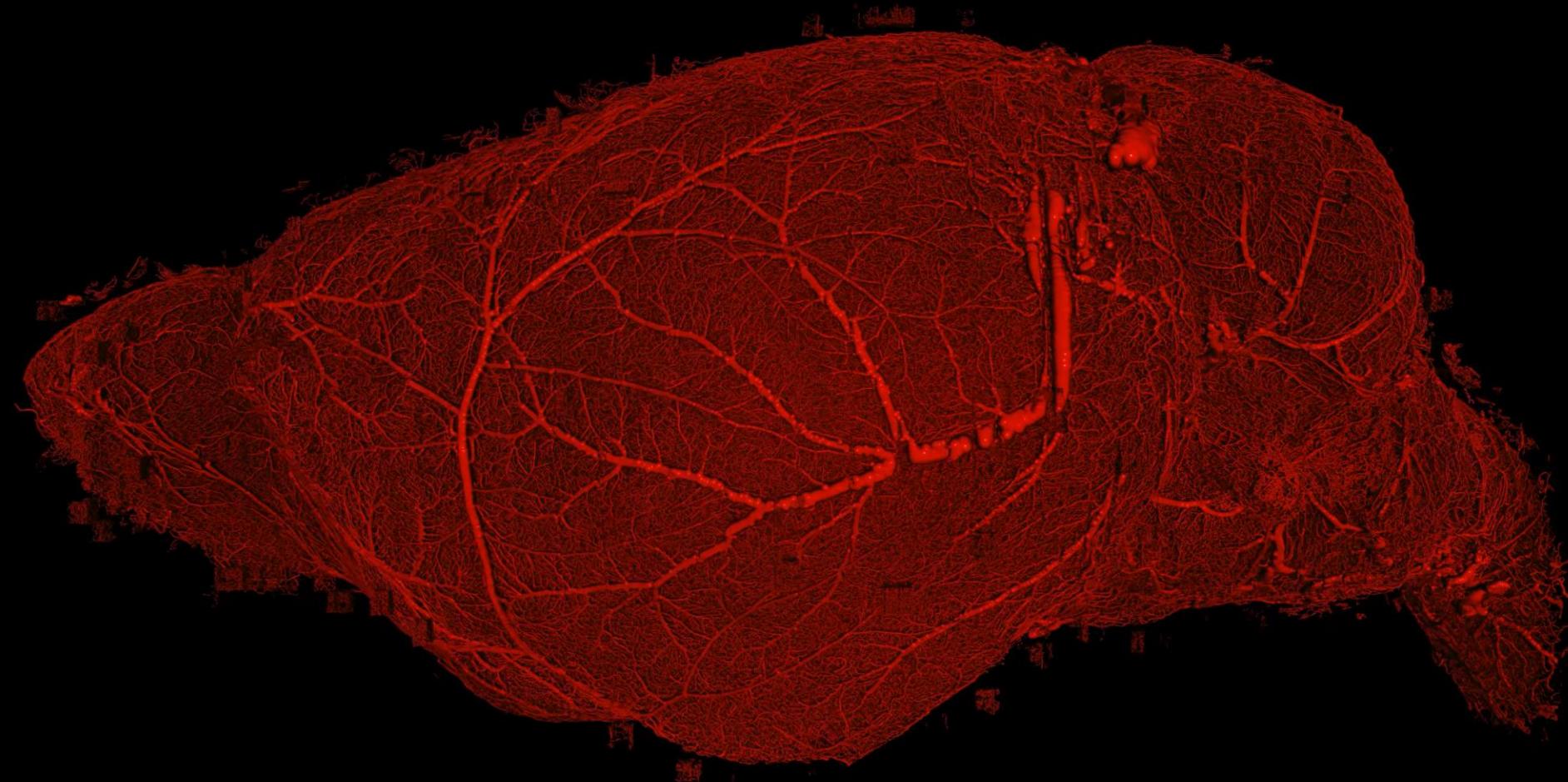
Brain regions

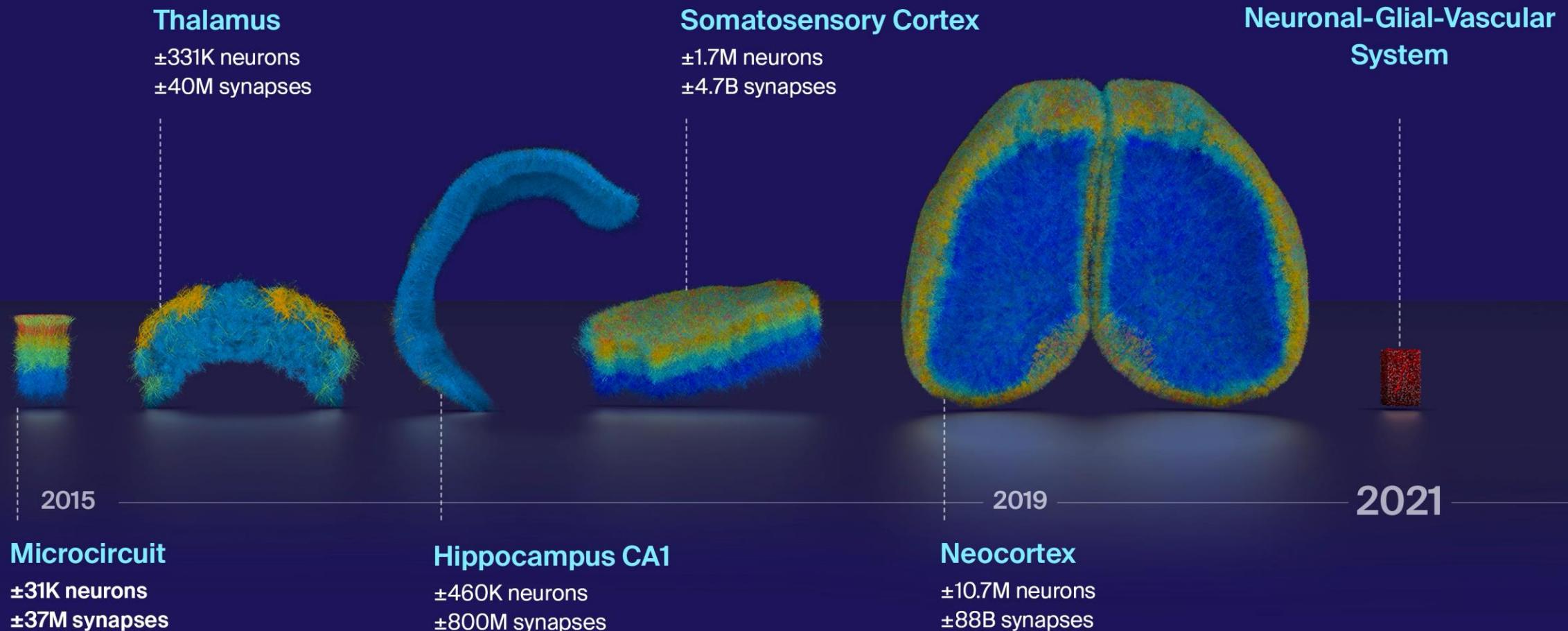








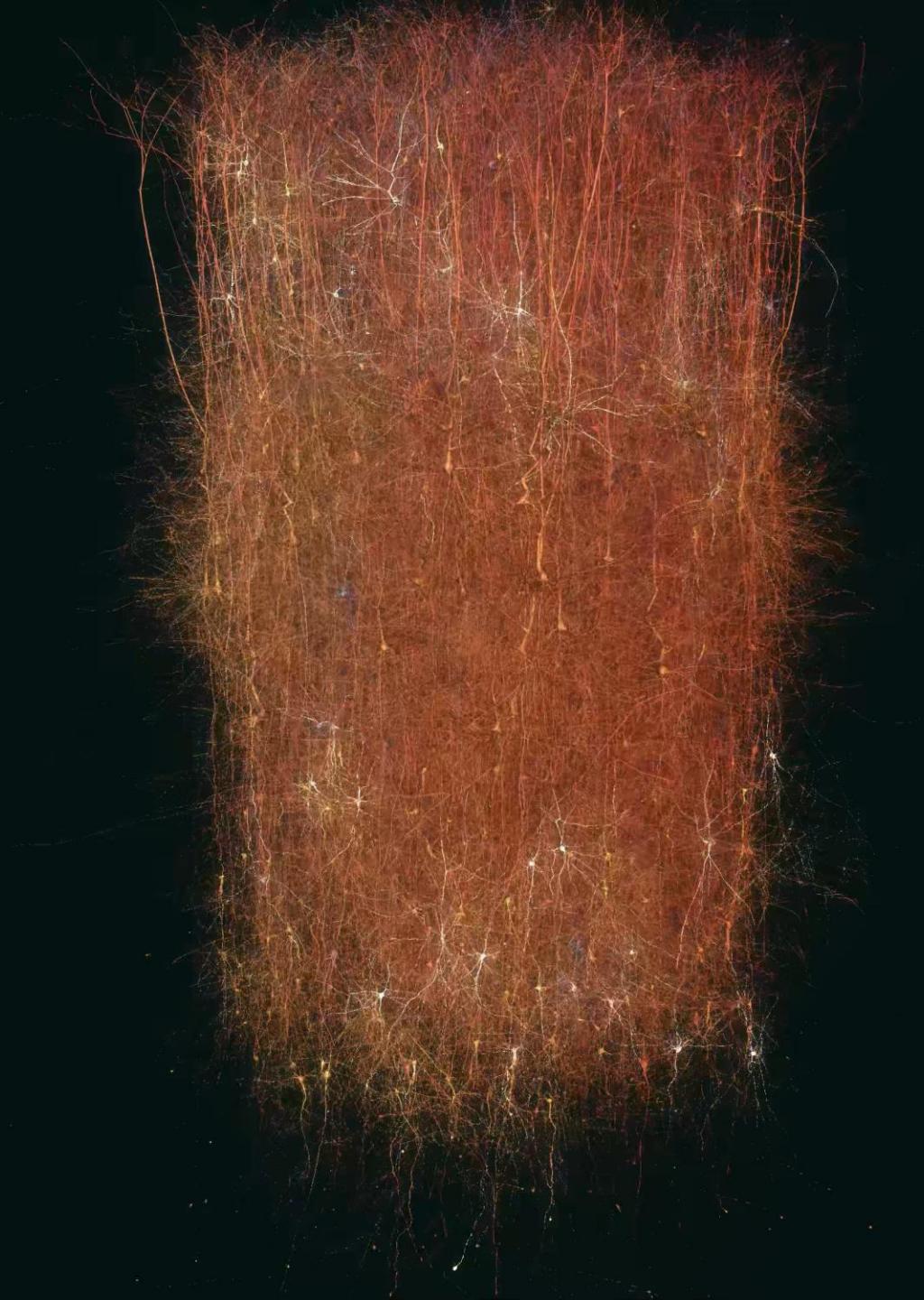


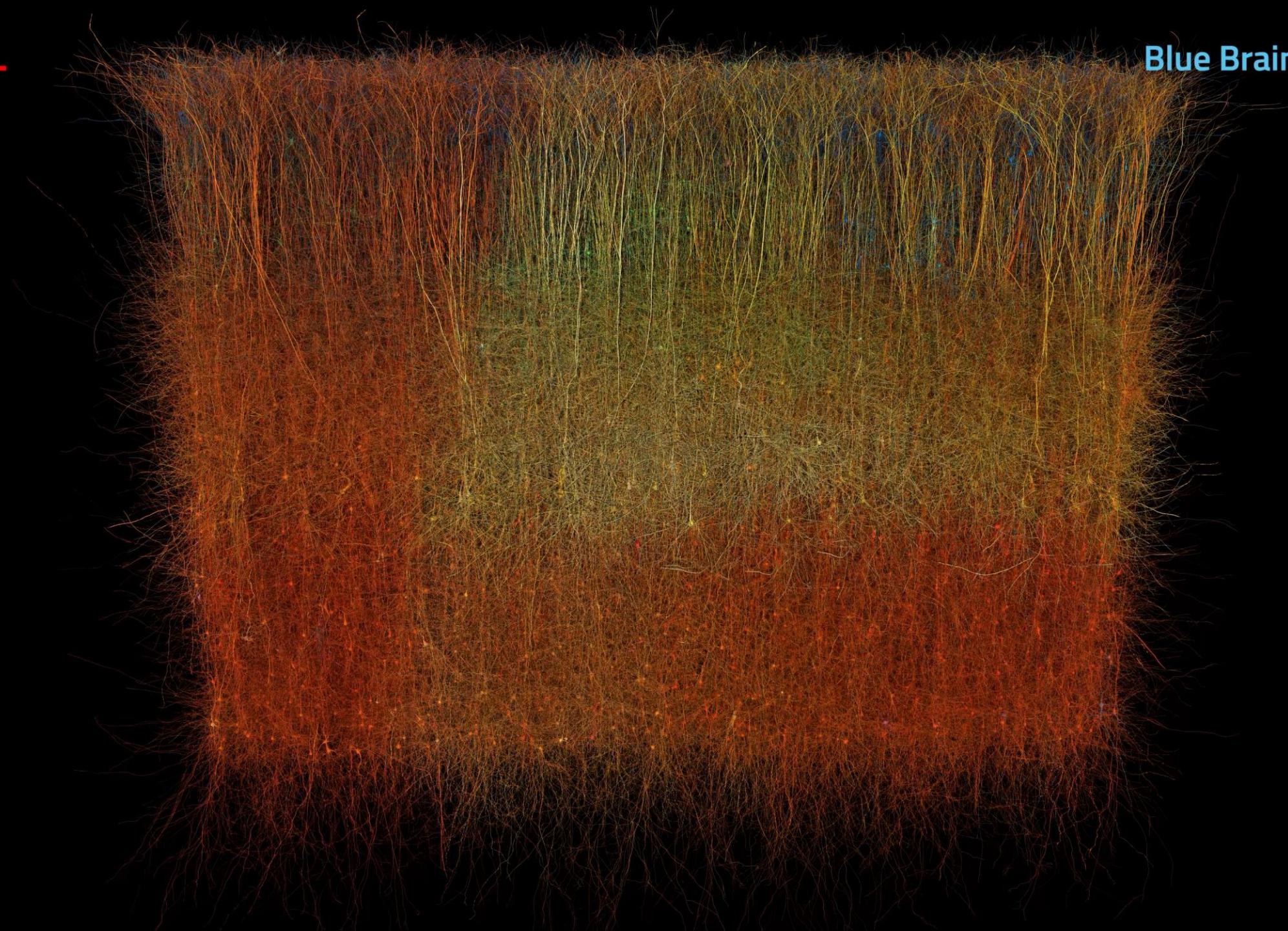


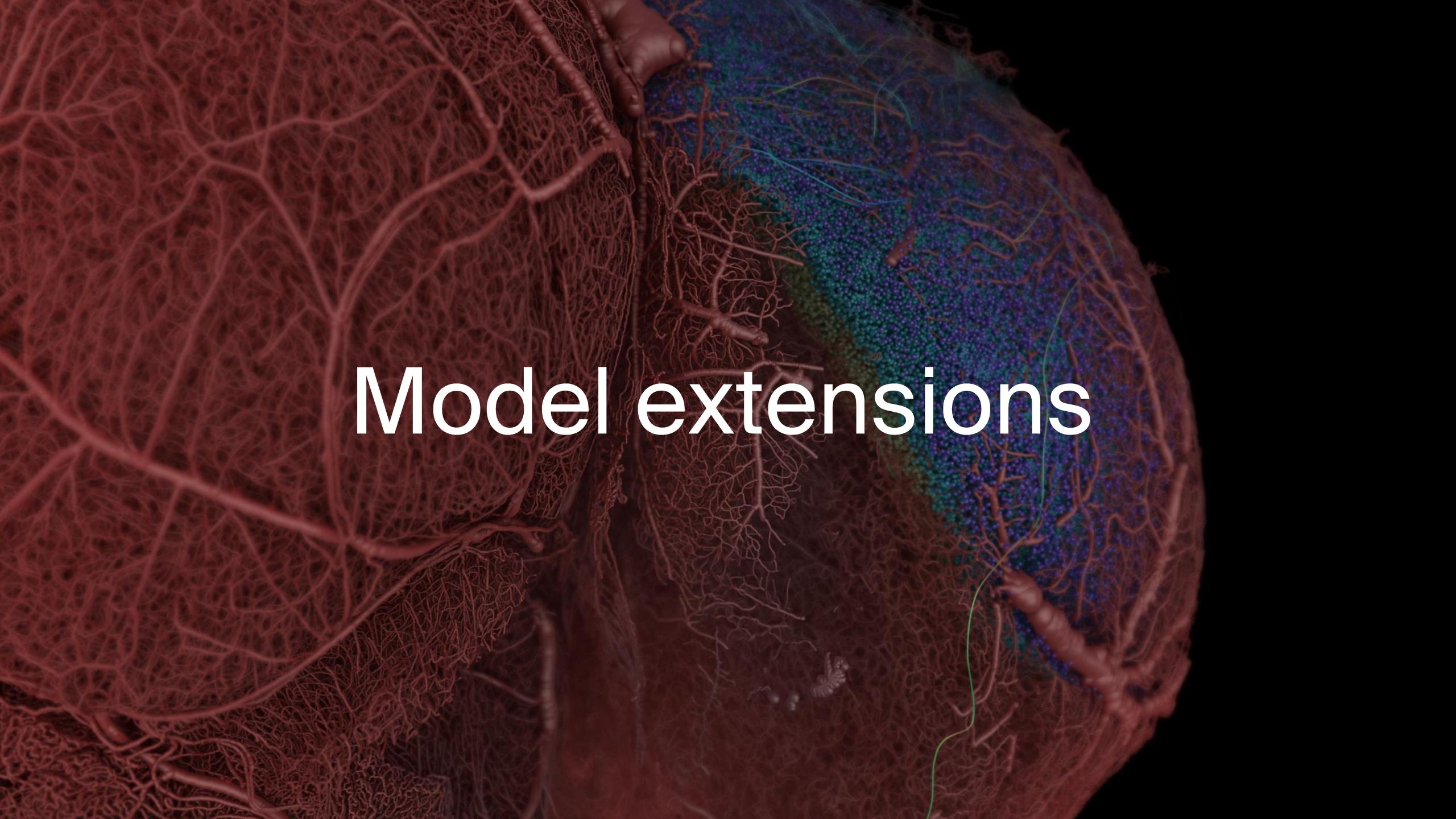
Digitally reconstructing and simulating the brain



Brain simulation







Model extensions

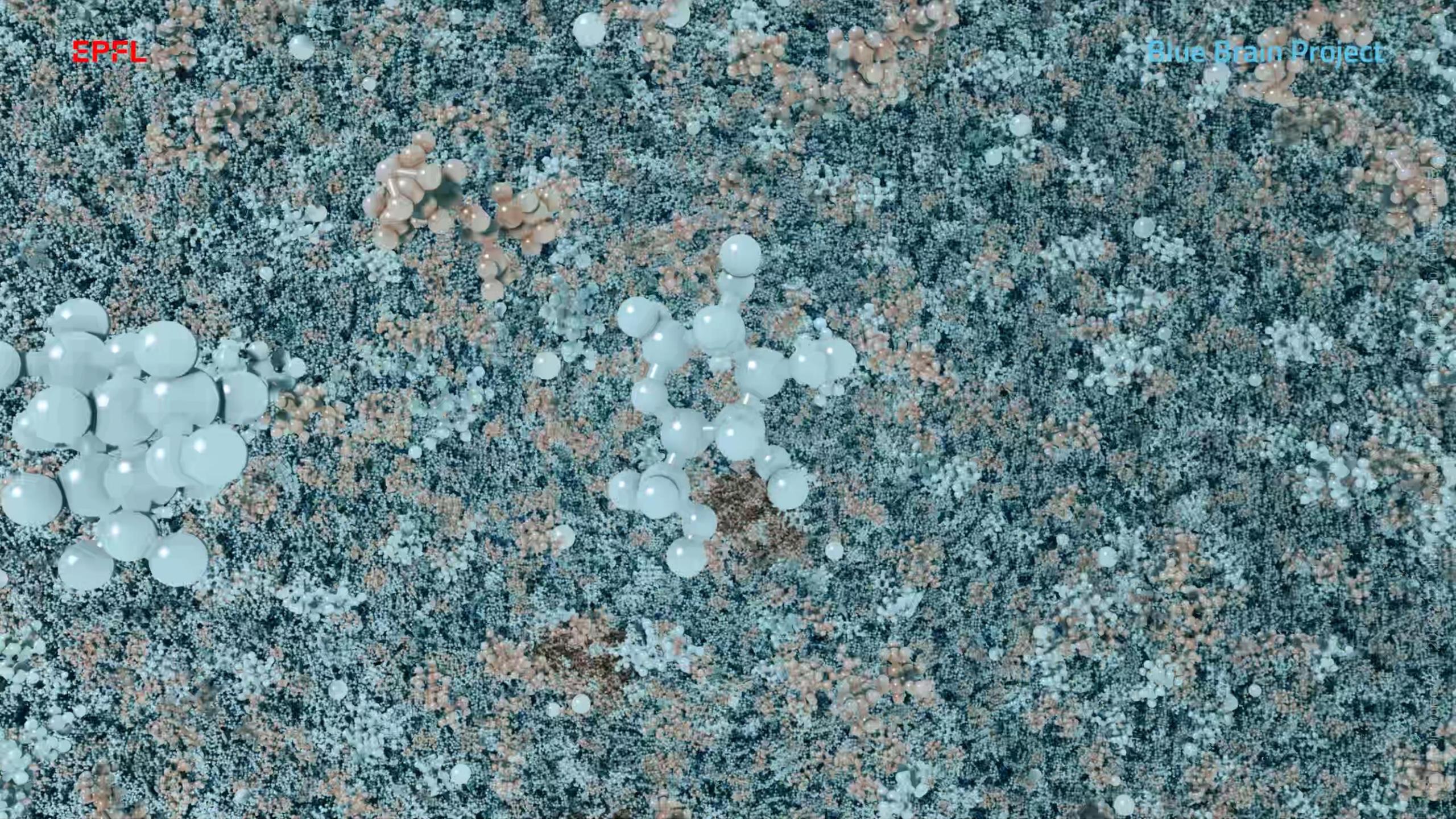
Astrocyte

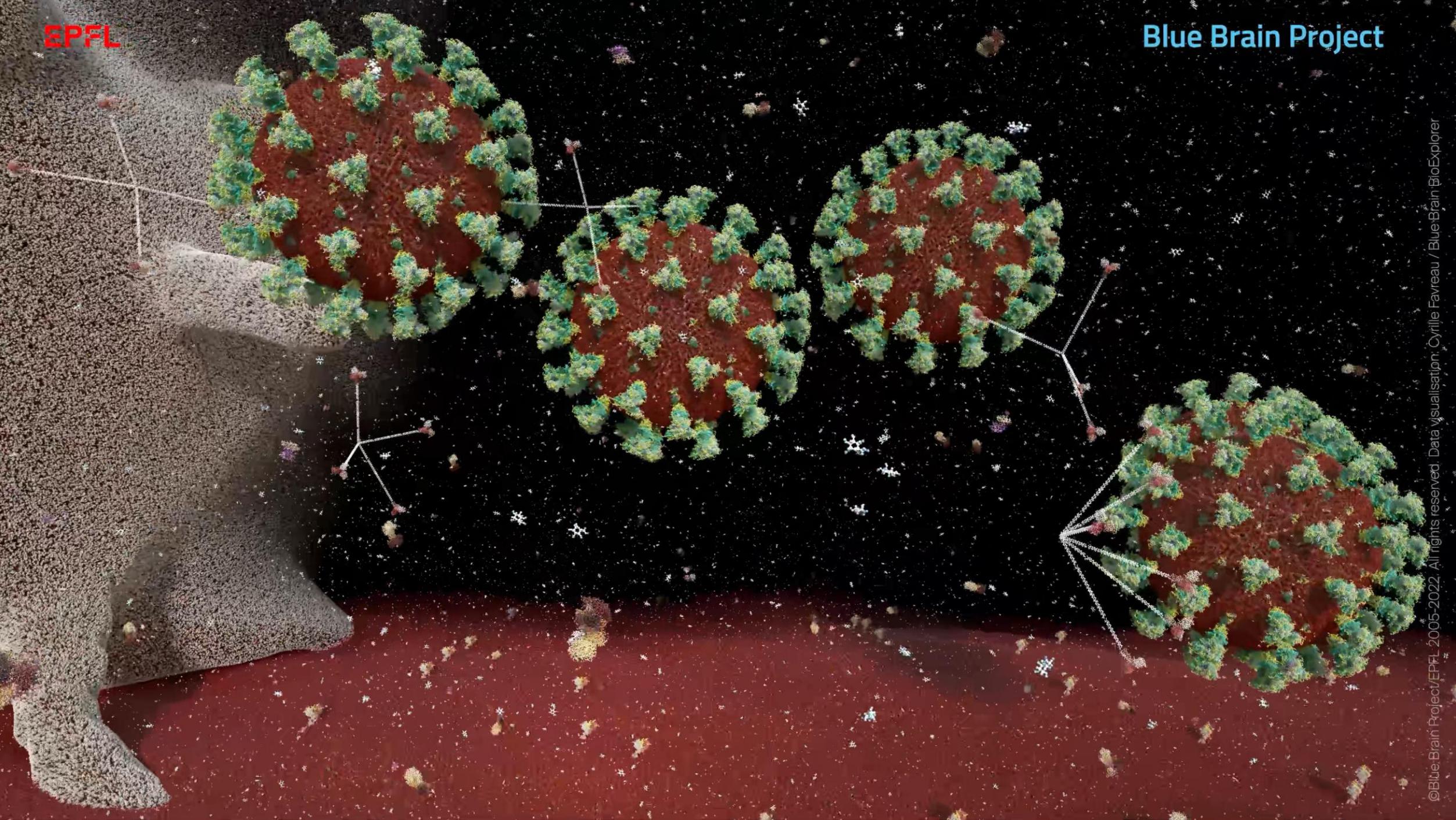
Neuron

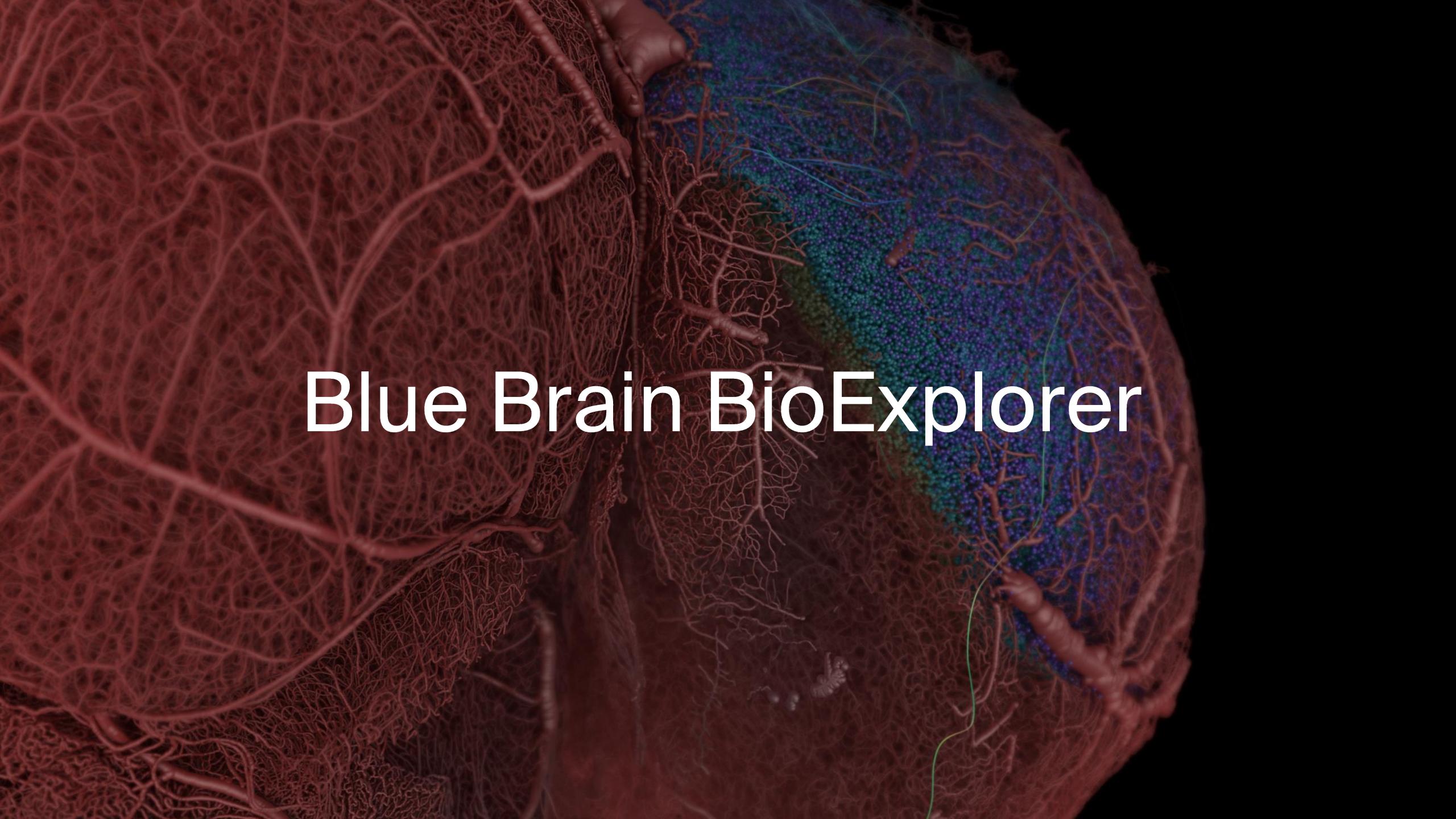
Vasculation

EPFL

Blue Brain Project



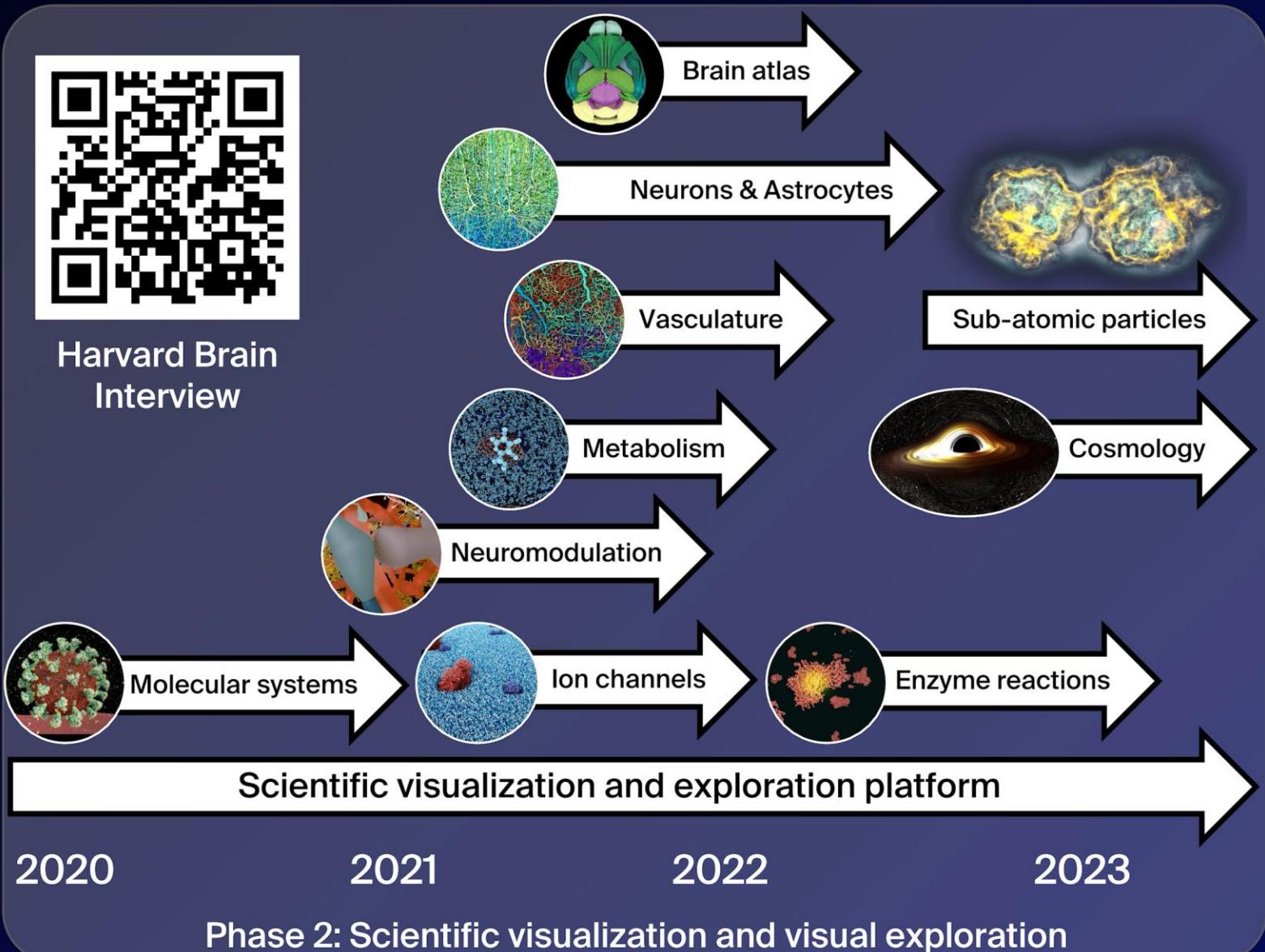
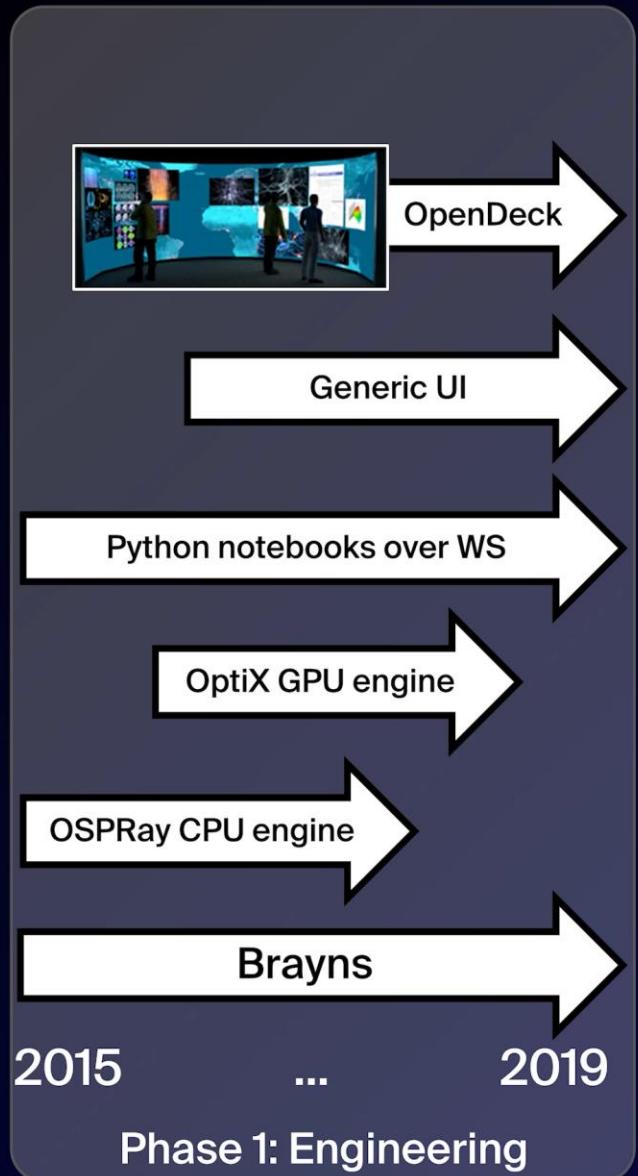




Blue Brain BioExplorer

Blue Brain BioExplorer timeline

Blue Brain Project



BlueBrain / BioExplorer Public

Code Issues 1 Pull requests Actions Projects Wiki Security Insights

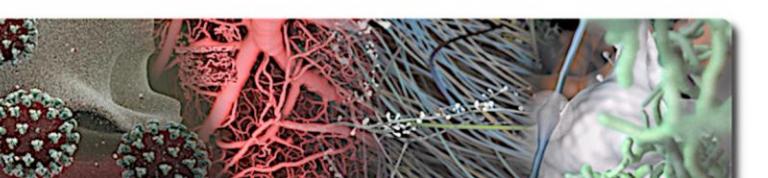
master 3 branches 12 tags Go to file Code

 favreau	Merge pull request #189 from favreau/master ...	✓ dsb917d last week 959 commits
 .github/workflows	Documentation on how to create and use a Docker image for the Pos...	7 months ago
 CMake	Added Xmp metadata to generated images	5 months ago
 bioexplorer	Version 1.5.0 preparation	2 weeks ago
 docs	Version 1.5.0 preparation	2 weeks ago
 extras	Documentation and copyright update	last month
 storage/database	Documentation and copyright update	last month
 .clang-format	Full refactoring of protein loading	3 years ago
 .gitignore	Minor UI fixes	2 years ago
 ARCHITECTURE.md	Documentation improvements: Minor spelling mistakes	7 months ago
 AUTHORS.txt	Set license to GPL	3 years ago
 CMakeLists.txt	Version 1.5.0 preparation	2 weeks ago
 CONTRIBUTING.md	Banner and README update	2 years ago
 DOCKER.md	Minor documentation and notebook edits	6 months ago
 Dockerfile	Documentation and copyright update	last month
 LICENSE.md	Made Licence file compatible with Github	2 years ago
 README.md	Contact update in the README	last week
 docker-compose.yml	Fixed docker issues	2 years ago

README.md

Blue Brain BioExplorer

This project is managed by GitHub Actions. You can trigger CI/CD jobs directly from the GitHub interface.



Contributors: favreau (Cyrille Favreau), jplanasc (Judit)

Languages: C++ 40.1%, Jupyter Notebook 27.4%, TypeScript 18.5%, Python 12.0%, CMake 1.3%, Dockerfile 0.3%, Other 0.4%

Releases: 1.5.0 (Latest) 2 weeks ago + 7 releases

Packages: No packages published

Contributors: 2

languages

Activities Firefox Web Browser 23 sept. 11:27 bluebrain/bioexplorer - Docker Hub - Mozilla Firefox

bluebrain/bioexplorer - Docker Hub - Mozilla Firefox https://hub.docker.com/r/bluebrain/bioexplorer

Explore Repositories Organizations Get Help favreau Manage Repository Using 0 of 1 private repositories. Get more

bluebrain/bioexplorer ☆

By bluebrain • Updated a day ago

This Image contains the Blue Brain BioExplorer rendering backend

Pulls 72

Container

Overview Tags

Blue Brain BioExplorer

Description

The Blue Brain BioExplorer (BBBE) is a tool for scientists to extract and analyse scientific data from visualization. BBBE is built on top of Blue Brain Brains, the Blue Brain rendering platform.

Architecture

The BioExplorer application is built on top of Brains, the Blue Brain rendering platform. The role of the application is to use the underlying technical capabilities of the rendering platform to create large scale and accurate 3D scenes from Jupyter notebooks.

General components

Assemblies

Docker Pull Command

```
docker pull bluebrain/bioexplorer
```

Owner

bluebrain



Scientific use-cases

Activities Firefox Web Browser

BioExplorer - Mozilla Firefox

bluebrain/bioexplorer -> BioExplorer

192.168.1.26:5002/?host=192.168.1.26:5000

23 sept. 11:31

BioExplorer_simplest_example - Jupyter Notebook - Mozilla Firefox

Home Page - Select or cr -> BioExplorer_simplest_e

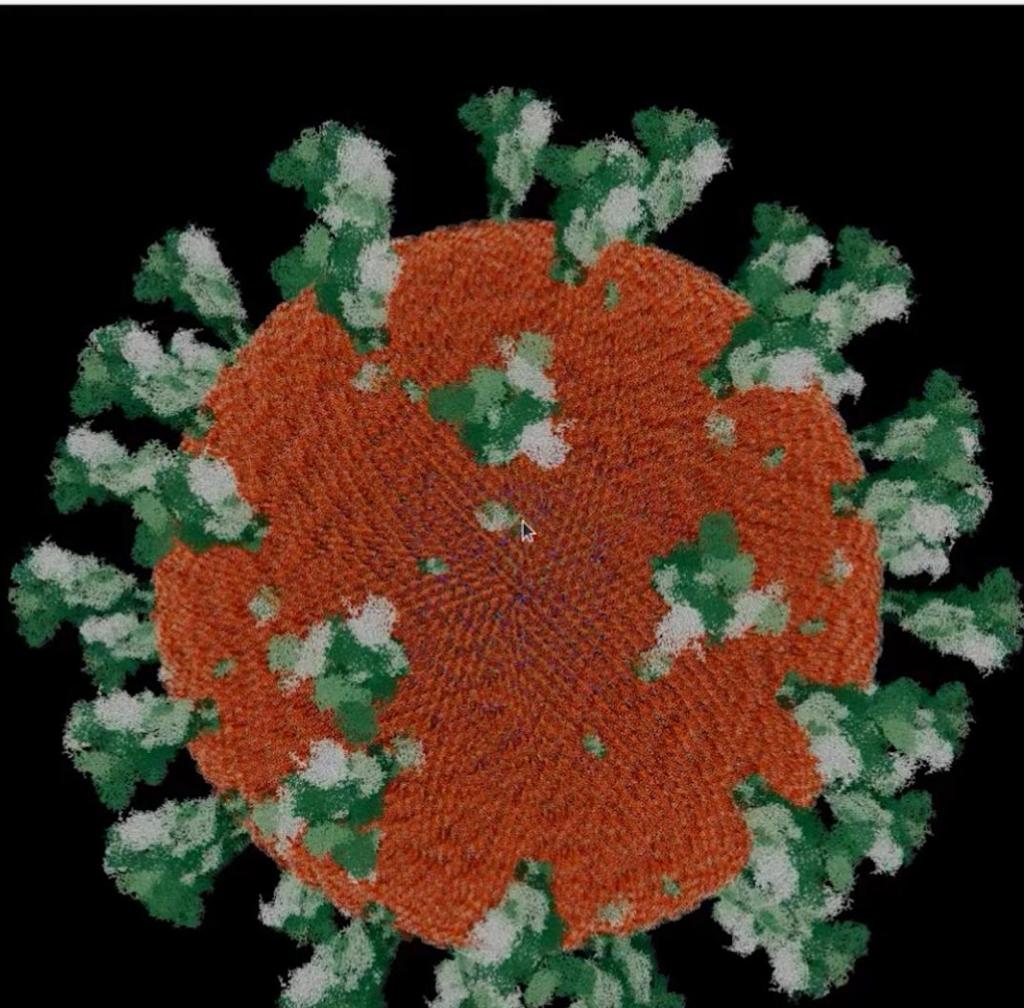
192.168.1.26:5001/notebooks/BioExplorer_simplest_examp ***

jupyter BioExplorer_simplest_example (untrusted)

File Edit View Insert Cell Kernel Widgets Help

Not Trusted Python 3

SSD



Blue Brain BioExplorer

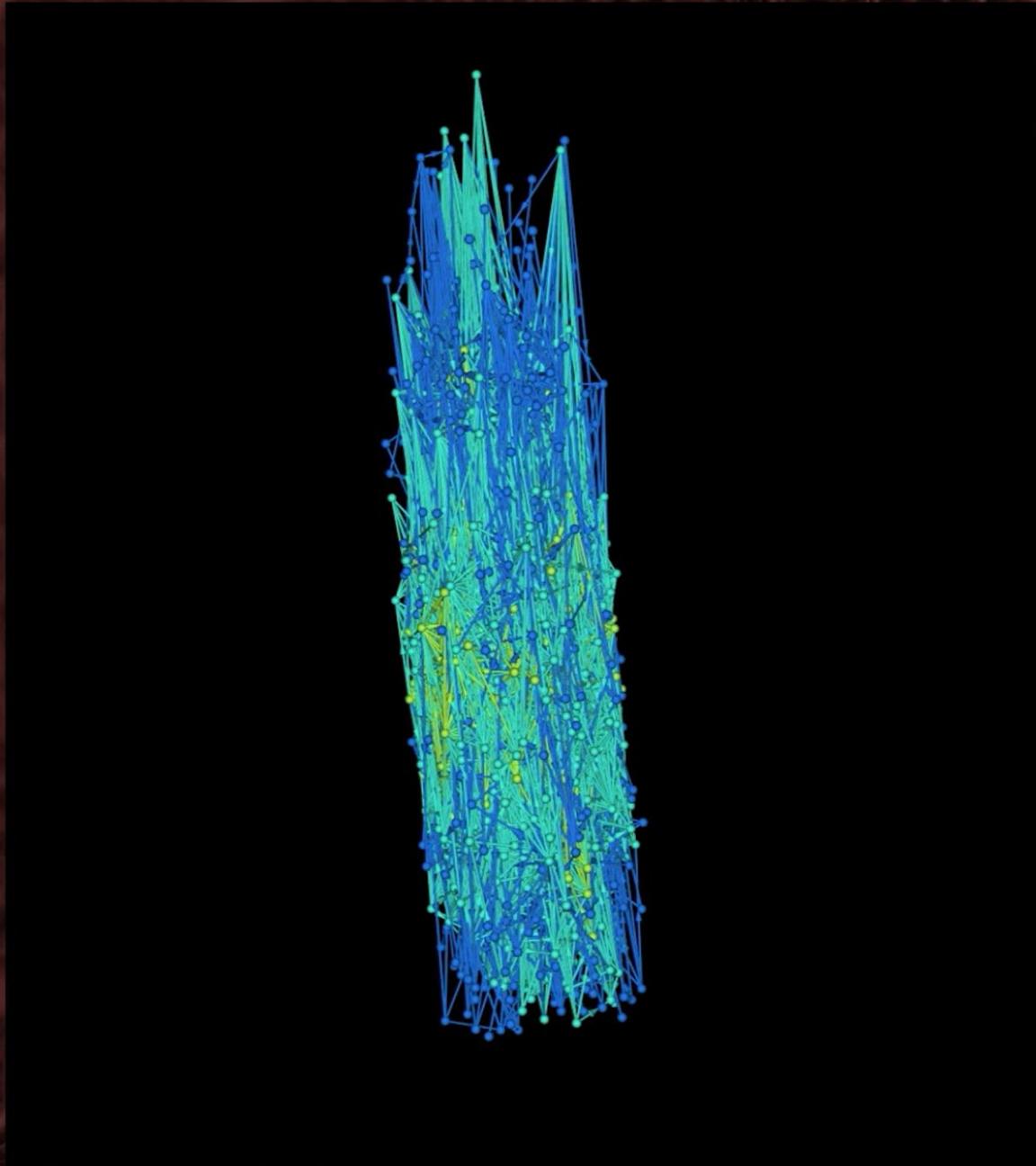


Simplest script to create a visualization of a Coronavirus

```
In [1]: from bioexplorer import BioExplorer  
be = BioExplorer('192.168.1.26:5000')  
  
In [2]: name='Coronavirus'  
be.add_coronavirus(name=name, resource_folder='../tests/test_files/')
```

```
In [ ]: status = be.set_protein_color_scheme(  
assembly_name=name, name=name + '_' + be.NAME_PROTEIN_S_CLOSED,  
color_scheme=be.COLOR_SCHEME_GLYCOSYLATION_SITE,  
palette_name='Paired', palette_size=2)
```

```
In [ ]: status = be.set_protein_color_scheme(  
assembly_name=name, name=name + '_' + be.NAME_PROTEIN_S_CLOSED,  
color_scheme=be.COLOR_SCHEME_CHAINS,  
palette_name='Set3', palette_size=4)
```



Jupyter Topology Viewer Last Checkpoint: 03/26/2018 (autosaved)

In [21]:

```
1 import viztools
2 topology_file_path = "/home/jkarlso/Work/tw_data/transmission_response_matrices.h5"
3 animation_file_path = "/home/jkarlso/Work/tw_data/transmission_response_matrices.h5.anim"
4 tv = viztools.TopologyViewer('128.178.97.68:5000')
5 tv.init_topology(topology_file_path, animation_file_path)
6 tv.draw_gui()
```

Neuron type filter

Layer	E-Type	M-Type
Any	Any	L6_BPC L6_MC L6_BTC L6_DBC L6_BP L6_NGC L6_LBC L6NBC L6_SBC L6_ChC
I	bNAC cNAC	
II	cSTUT	
IIIIV	cACintcIR	
IV	cIR	
V	cADpyrbAC	
VI	bAC dNAC bIR	

Order filter

- Order 0 (checked)
- Order 1 (checked)
- Order 2 (checked)
- Order 3 (checked)
- Order 4 (checked)
- Order 5 (checked)
- Order 6 (checked)
- Order 7 (checked)
- Order 8 (checked)

Order colors

Order 0	#555555	[Solid black]
Order 1	#0080ff	[Blue]
Order 2	#16fedf	[Cyan]
Order 3	#a8ff4c	[Green]
Order 4	#217701	[Yellow]
Order 5	#ffb500	[Orange]
Order 6	#ff2400	[Red]
Order 7	#b80000	[Dark red]
Order 8	#880000	[Maroon]

View

Neuron radius: 10.0

Connections visible

Directions visible

Brain circuits

Quality

5

4

3

2

1

0

Display size

Performance

Data size

Python
NotebookUser
InterfaceRockets
Plug-in

BioExplorer

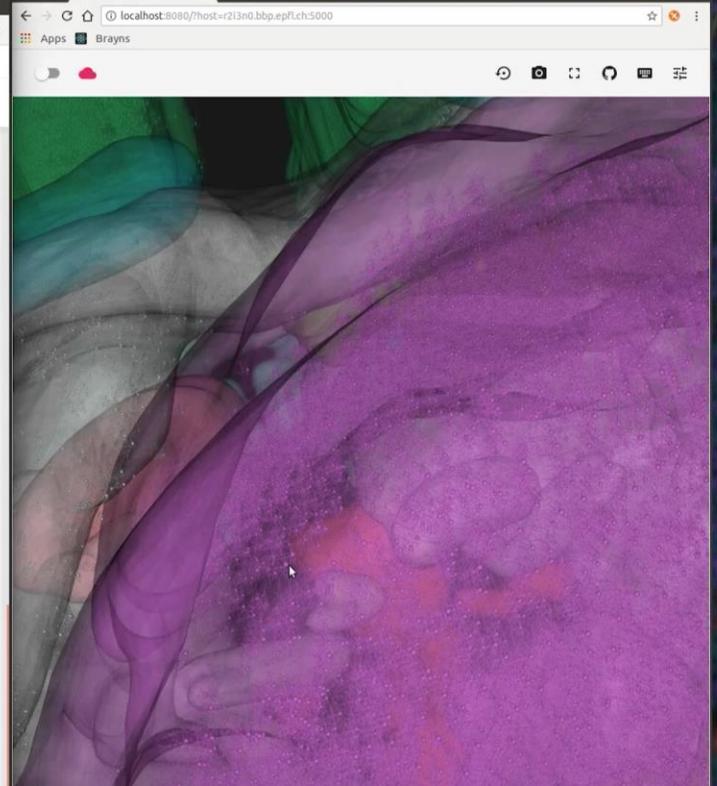
NVIDIA
OptiX Engine
(GPU)Intel
OSPRAY Engine
(CPU)

In [140]:

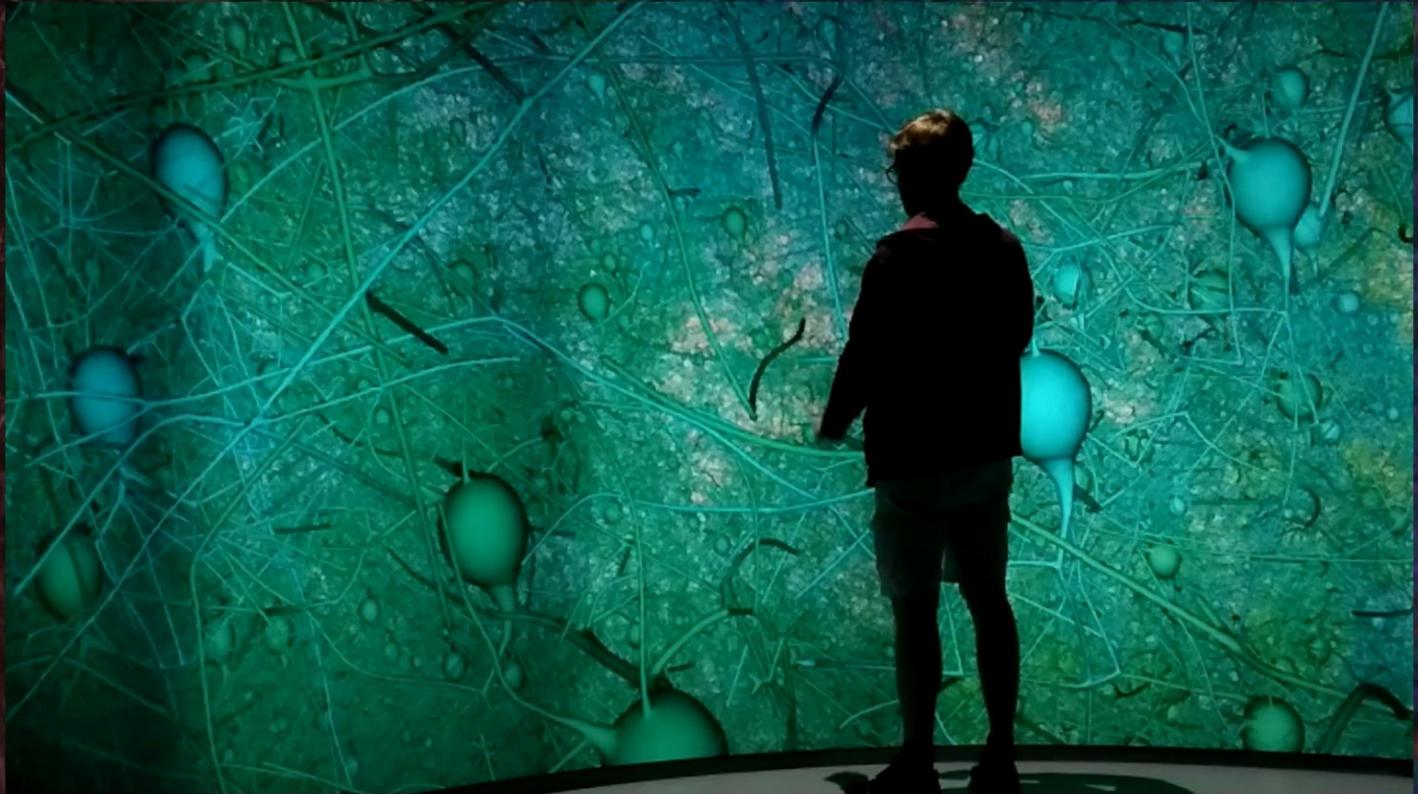
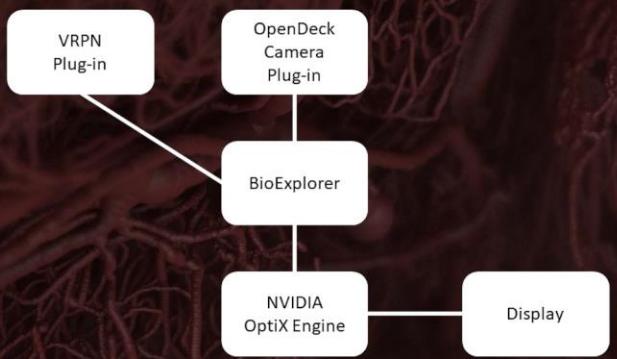
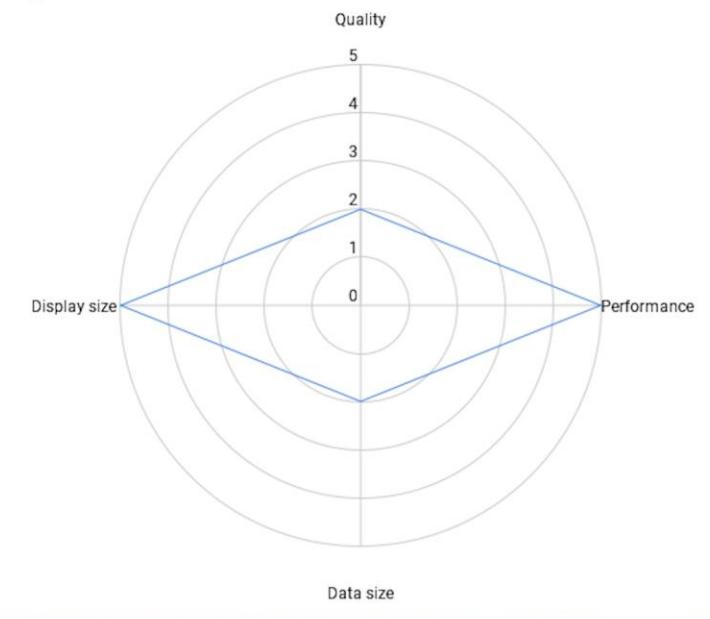
```
display(widgets.Label("Visible Regions:"))
display(regions_selector)
```

Visible Regions:

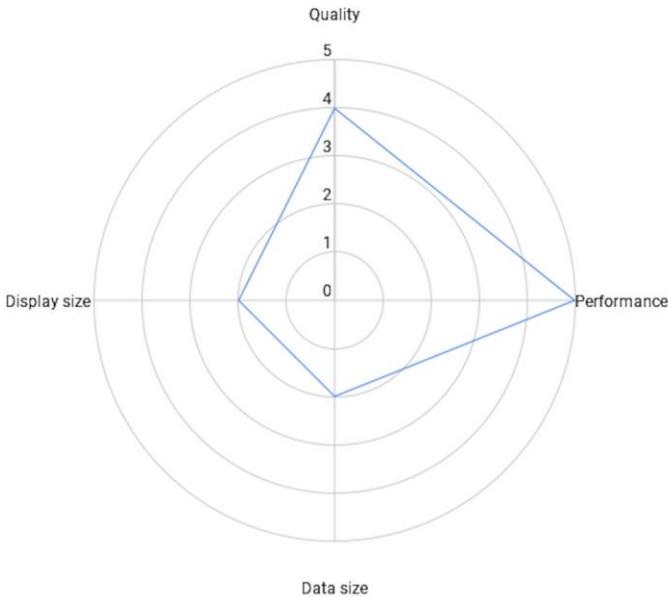
- Midbrain, sensory related
- Substantia nigra
- Primary somatosensory area, lower limbo
- superior colliculus commissure
- Perirhinal area, layer 6a
- Basomedial amygdalar nucleus, posterior part
- Supramammillary nucleus
- Accessory sympathetic group
- Mammillary body
- Retrosplenial area, dorsal part, layer 6b
- Primary somatosensory area, barrel field
- Agranular insular area, dorsal part, layer 2/3
- Basomedial amygdalar nucleus, anterior part
- superior cerebellar peduncles
- Dorsal raphe nucleus
- Anterior pretectal area, ventral zone, layer 2
- Midbrain, motor related
- Isocortex
- Agranular insular area, posterior part, layer 6a
- Midbrain



OpenDeck



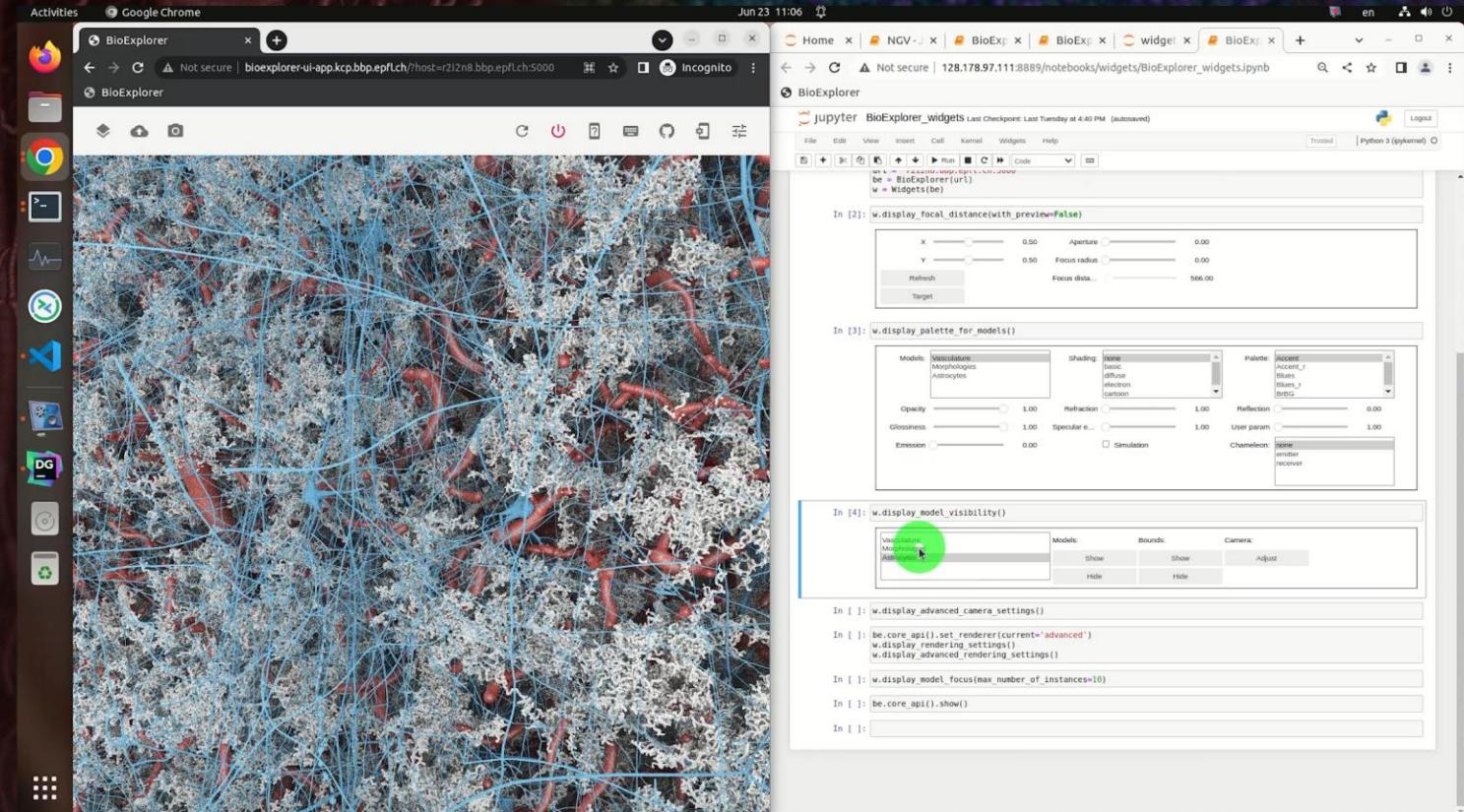
MOOC



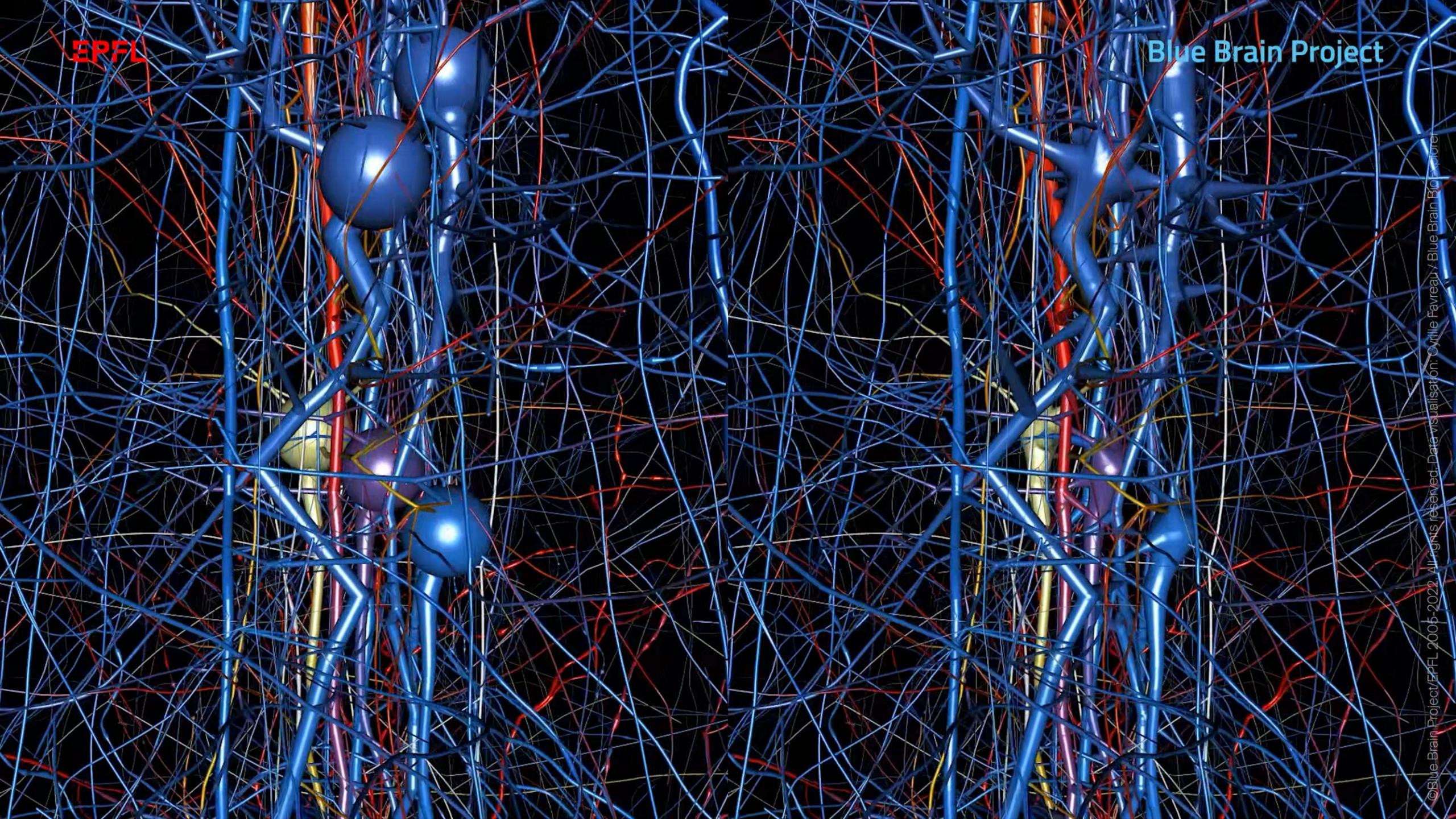
User Interface

Rockets
Plug-in

BioExplorer

Intel
OSPRAY Engine
(CPU)





Activities Google Chrome

CacheLoader.cpp - BioExplorer - Visual Studio Code

File Edit Selection View Go Run Terminal Help

EXPLORER OPEN EDITORS BIOEXPLORER Glycans.h Membrane.cpp Membrane.h MeshBasedMembrane.cpp MeshBasedMembrane.h Molecule.cpp Molecule.h Node.cpp Node.h Protein.cpp Protein.h RNASequence.cpp RNASequence.h Uniquid.cpp Uniquid.h common CommonTypes.h Defines.h GeneralSettings.cpp GeneralSettings.h Logs.h Types.h Utils.cpp Utils.h fields io DBConnector.cpp DBConnector.h CacheLoader.cpp CacheLoader.h OOCManager.cpp OOCManager.h meshing BioExplorerPlugin.cpp BioExplorerPlugin.h tests CMakeLists.txt OUTLINE TIMELINE

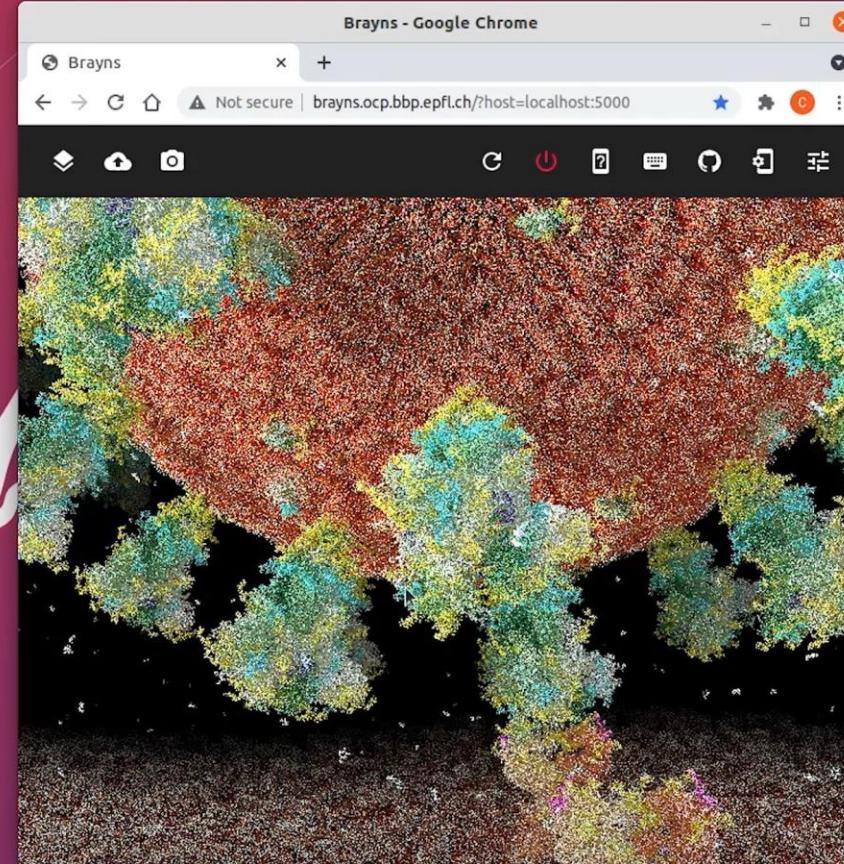
CacheLoader.cpp -> {} bioexplorer > CacheLoader::importModel(std::stringstream &, const int32_t) const

```
359
360     bool first{true};
361     for (const auto& tf : transformations)
362     {
363         if (first)
364         {
365             modelDescriptor->setTransformation(tf);
366             first = false;
367         }
368
369         const ModelInstance instance(true, false,
370             tf);
371         modelDescriptor->addInstance(instance);
372
373         modelDescriptor->setVisible(
374             GeneralSettings::getInstance()
375             ->getModelVisibilityOnCreation());
376
377     }
378
379     return nullptr;
380 }
381 std::vector<ModelDescriptorPtr>
382 CacheLoader::importModelsFromFile(
383     const std::string& filename, const int32_t brickId,
384     const LoaderProgress& callback, const PropertyMap&
385     properties) const
386 {
387     4036, 4037, 4066, 4067, 4068, 4069, 4994, 4995, 4996, 4997, 5026, 5027,
388     5028, 5029, 5058, 5059, 5060, 5061, 5090, 5091, 5092, 5093, 6018, 6019,
389     6020, 6021, 6050, 6051, 6052, 6053, 6082, 6083, 6084, 6085, 6115, 6116,
390     6117]
391 [140736286393472] [DEBUG] [BIO_EXPLORER] Visible bricks : [2946, 2947,
392     2949, 2978, 2979, 2980, 2981, 3010, 3011, 3012, 3013, 3042, 3043,
393     3044, 3045, 3070, 3071, 3072, 3073, 4002, 4003, 4004, 4005, 4034, 4035,
394     4036, 4037, 4066, 4067, 4068, 4069, 4994, 4995, 4996, 4997, 5026, 5027,
395     5028, 5029, 5058, 5059, 5060, 5061, 5090, 5091, 5092, 5093, 6018, 6019,
396     6020, 6021, 6050, 6051, 6052, 6053, 6082, 6083, 6084, 6085, 6114, 6115,
397     6116, 6117]
398 [140736286393472] [DEBUG] [BIO_EXPLORER] Adding model: 4790
399 [140736286393472] [DEBUG] [BIO_EXPLORER] Bricks to load : [6114]
400 [140736286393472] [DEBUG] [BIO_EXPLORER] SELECT nb_models, buffer FROM P
401 ublic.brick WHERE guid='6114' AND version=1
402 [140736286393472] [DEBUG] [BIO_EXPLORER] Adding model: 4791
403 [140736286393472] [DEBUG] [BIO_EXPLORER] Adding model: 4792
```

PROBLEMS 15 OUTPUT TERMINAL 2:cppdbg:braynsS + ^ x

Brayns - Google Chrome

Brayns Not secure | brayns.ocp.bbp.epfl.ch/?host=localhost:5000





... Cosmology ...

Blue Brain BioExplorer for sub-atomic worlds

Particles Composition and Interactions Using the Nuon Model

René Brun

CERN, Geneva, Switzerland.

DOI: [10.4236/jmp.2023.145036](https://doi.org/10.4236/jmp.2023.145036) PDF HTML XML 126 Downloads 965 Views

Abstract

The Standard Model in Particle Physics has been able to make many predictions confirmed later with a flow of experimental results. With the discovery of the Higgs boson at the LHC, one is full of admiration for the people contributing to this model fifty years ago and its predictions that have been confirmed gradually. The original particle quark constituent model has evolved with the deep inelastic experiments to a quark and gluons system, then to a more general system with virtual quarks. This work is the result of observations while working at CERN in Geneva with many different experiments at the ISR, SPS, LEP, LHC colliders. A new model based on nuons is introduced, that allows accurate evaluations of the particle masses (mesons and baryons) and magnetic moment, computes very accurately the kinematics distributions for particles and jets observed in the p-p collisions at the LHC (elastic and inelastic) and at lower energy machines. This new model looks at a first glance in contradiction with the quark model because it can build the elementary particles with nuons only, *i.e.* electrons and neutrinos. However, all the existing physics involved in electron, positron and neutrino interactions may be used to explain interactions between composite particles such as protons or heavy ions.

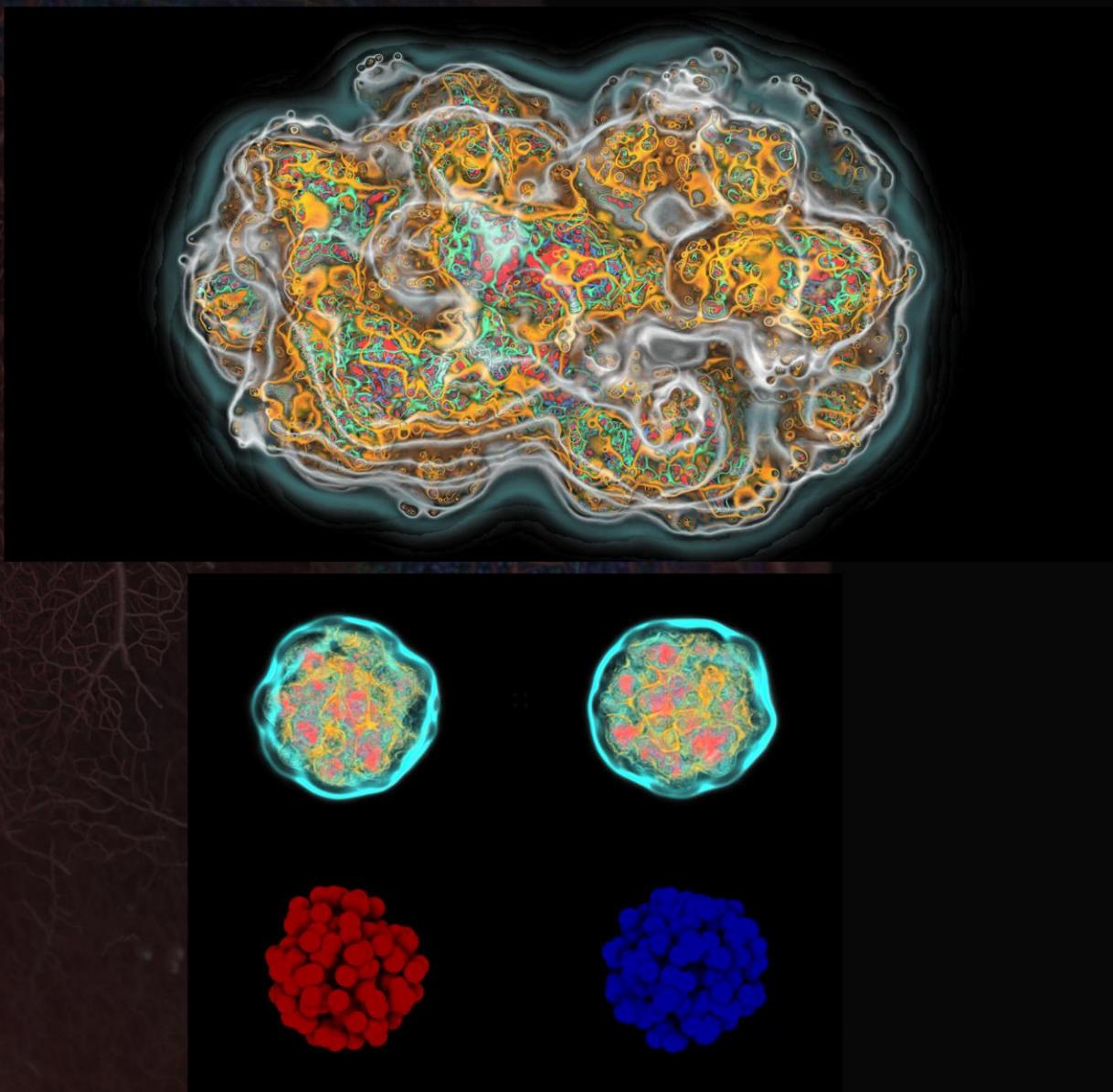
Keywords

Standard Model, Particle Masses, Particles Interactions, Elastic Scattering, Deep Inelastic, Jets, Charge Density

Share and Cite:

Brun, R. (2023) Particles Composition and Interactions Using the Nuon Model. *Journal of Modern Physics*, **14**, 623-665.

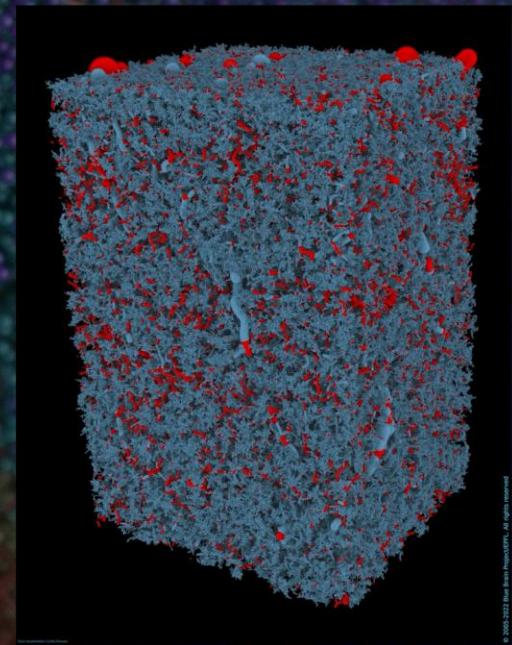
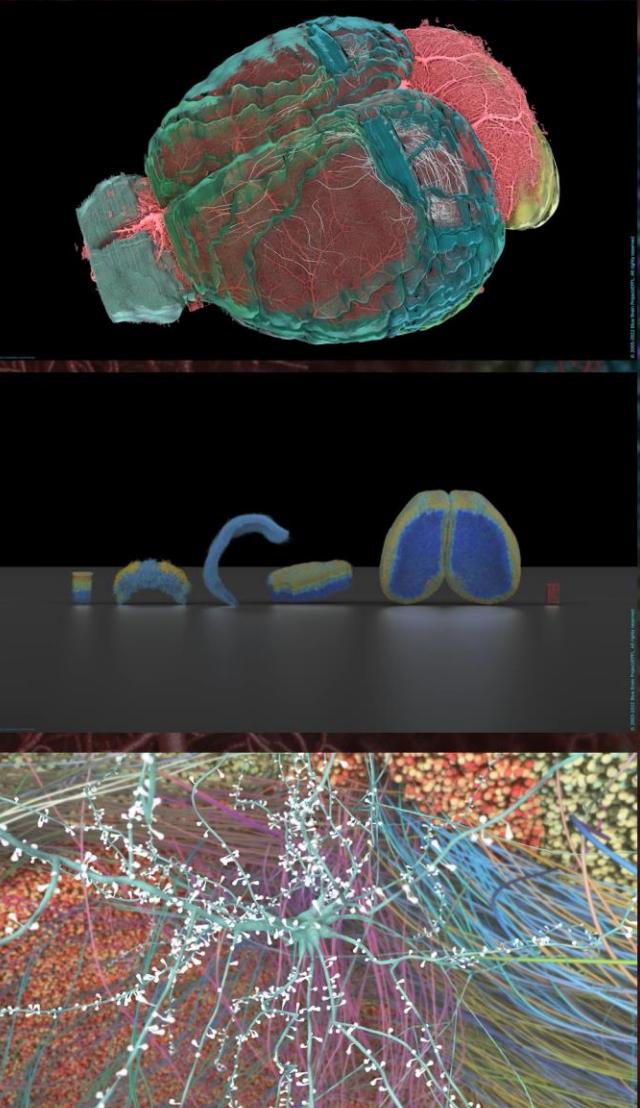
doi: [10.4236/jmp.2023.145036](https://doi.org/10.4236/jmp.2023.145036).





Science outreach

EPFL

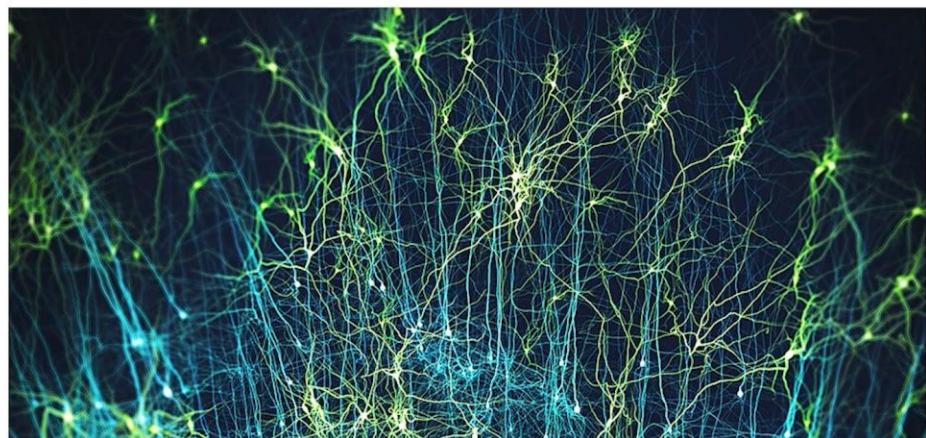


Blue Brain Project

Barcelona Centre of Contemporary Culture - 2022-2023



Hôpitaux
Universitaires
Genève



24 mai 2022 - 27 novembre 2022

Les HUG ont le plaisir d'accueillir [l'exposition photographique Blue Brain Project de l'EPFL](#).

Le Blue Brain Project est une initiative suisse de recherche sur le cerveau fondée et pilotée par le Pr Henry Markram. Son but est de créer, pour la première fois au monde, des reconstructions numériques et des simulations biologiquement détaillées du cerveau de la souris. La visualisation scientifique est un élément clé de la recherche du Blue Brain Project. Les images exposées montrent quelques exemples de ces visualisations.



Hôpitaux Universitaires de Genève - 2022





Greg Dunn Brainbow Hippocampus in Color (détail), 2014
© Greg Dunn and Brian Edwards



Jeremy Shaw Phase Shifting Index 2020 Installation vidéo avec son
Courtesy Jeremy Shaw et König Galerie, Berlin

L'exposition Neurones, les intelligences simulées bénéficie du soutien de

Talan  **MARSH**  **Centre Pompidou** 

En partenariat avec **ARTÉ**, **20 minutes** et **les Irrocksables**

Expositions présentées du 29 février au 20 avril 2020

L'exposition Jeremy Shaw bénéficie du soutien de

EDF  **KÖNIG GALERIE**  **Brillux** 

Modélism / Créations #4 bénéficie du soutien de

ENEDIS  **Grand mécène** 

Centre Pompidou

Franck Riester
Ministre de la Culture

Serge Lasvignes
Président du Centre Pompidou

Bernard Bléthen

Délégué du Musée national d'art moderne / Centre de création industrielle

Frank Madlener

Délégué de l'Institut de recherche et coordination acoustique / musique

Présent Monsieur Cyrille Favreau
de bien vouloir assister à l'inauguration des expositions

dans le cadre de Mutations / Créations #4

Neurones, les intelligences simulées

et

Jeremy Shaw

Phase Shifting Index

Mardi 25 février 2020

18h – 20h30

Galeries 3 et 4, niveau 1

Accès par l'entrée 2, face à la place Stravinsky

Fermé le 21h, dernier accès à 20h30

Cliquez sur le lien pour accéder à la bande annonce de Neurones, les intelligences simulées

Cliquez sur le lien pour accéder à la bande annonce de Jeremy Shaw

Programmation de l'Ircam associée :

- Forum Vertigo - Intelligence artificielle et création artistique
mercredi 26 et jeudi 27 février 2020, Petite salle, niveau -1

- Concert Ircam Live
jeudi 5 mars 2020, 20h30, Grande salle, niveau -1

Invitation valable uniquement ce jour, pour deux personnes, sur présentation à l'entrée



ircam
Centre
Pompidou

Centre Pompidou

entre neurosciences
et innovations artistiques

Centre Pompidou - Paris - February 2020

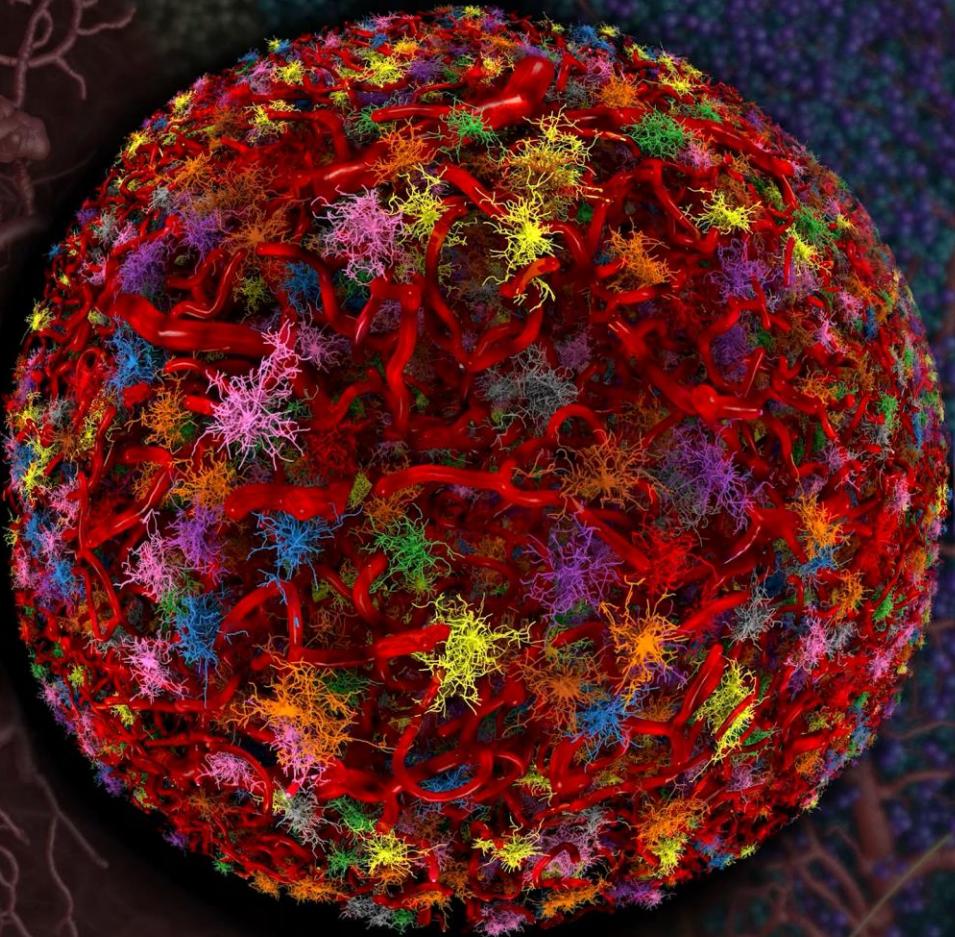
eCAL / eM+



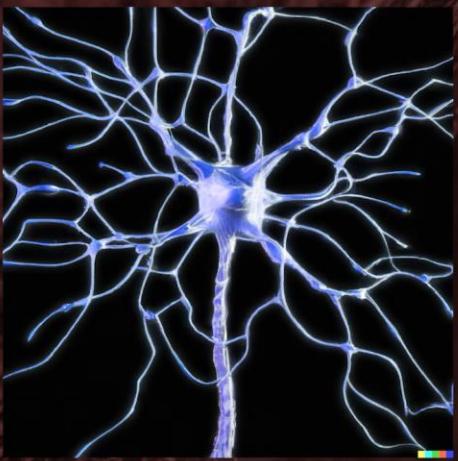
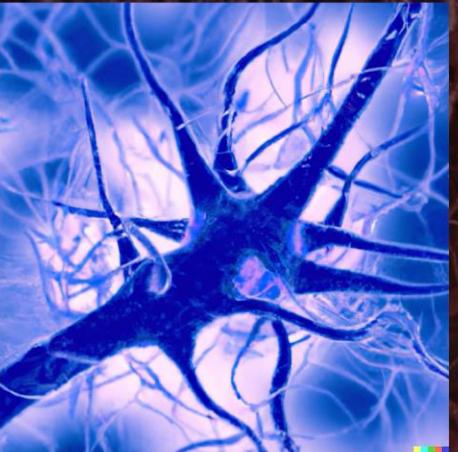
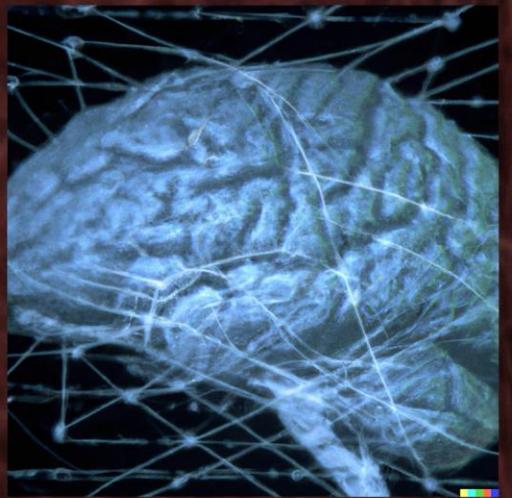
Prof Sarah Kenderdine

infinity
room

13.09.2019
→ 26.01.2020



EPFL 50th anniversary - December 2019



Generative AI vs High-fidelity visualization