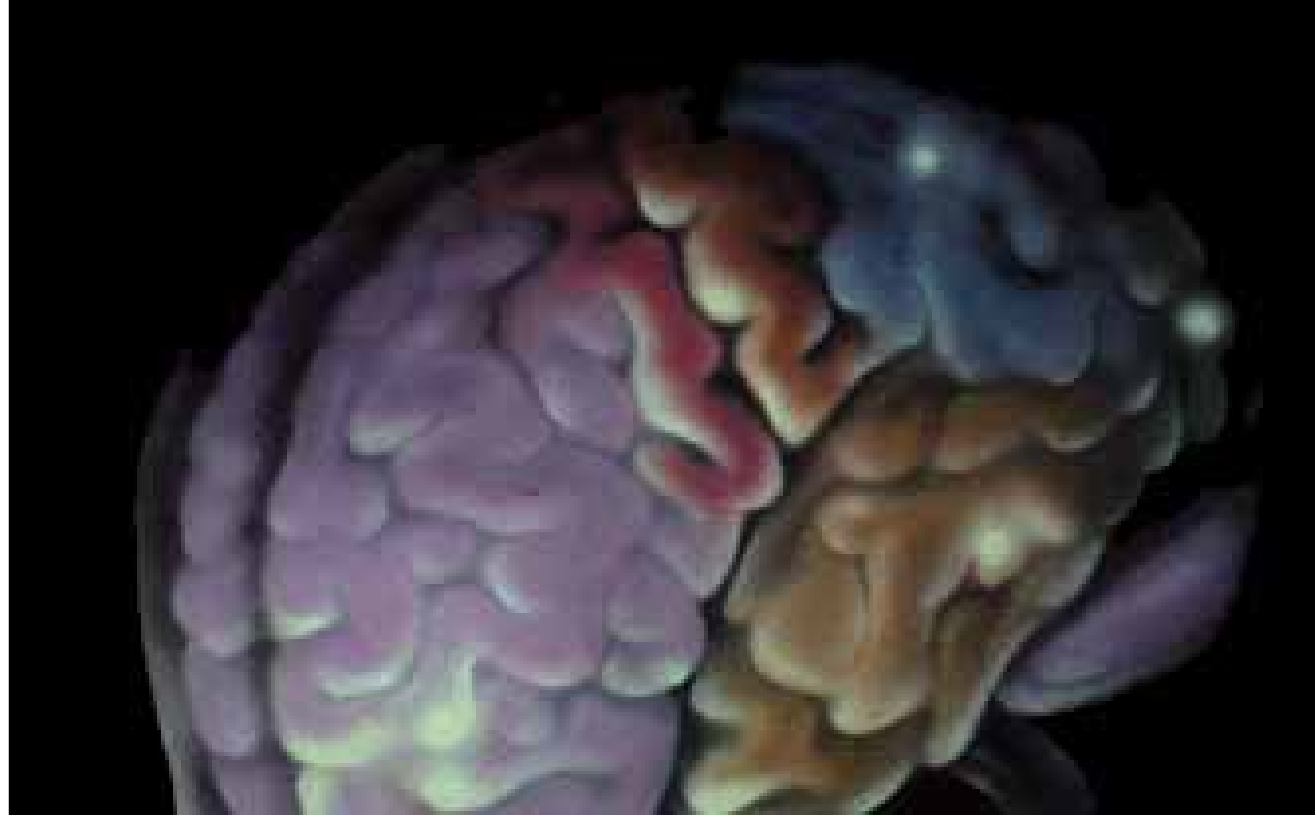


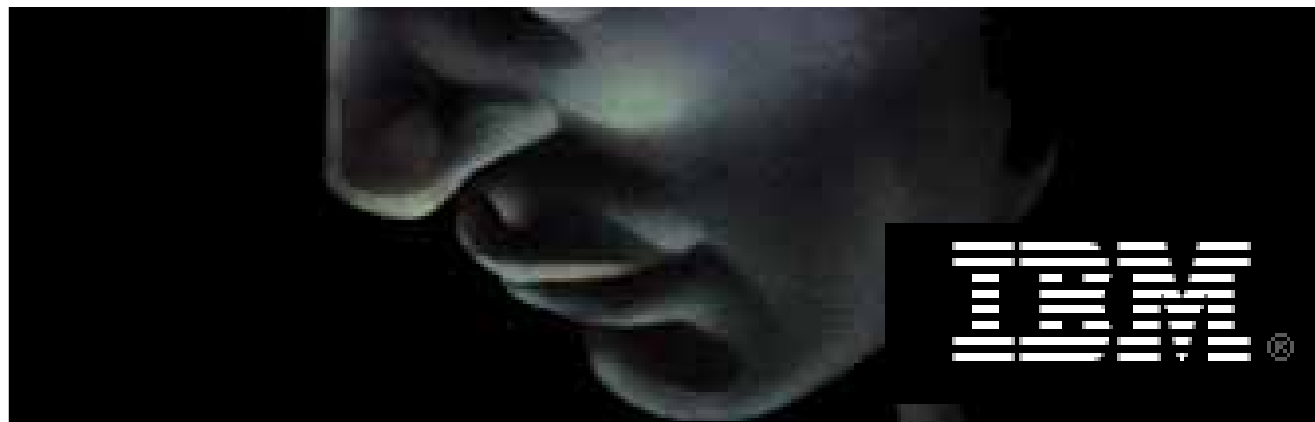


Blue Brain Project



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<http://bluebrainproject.epfl.ch>

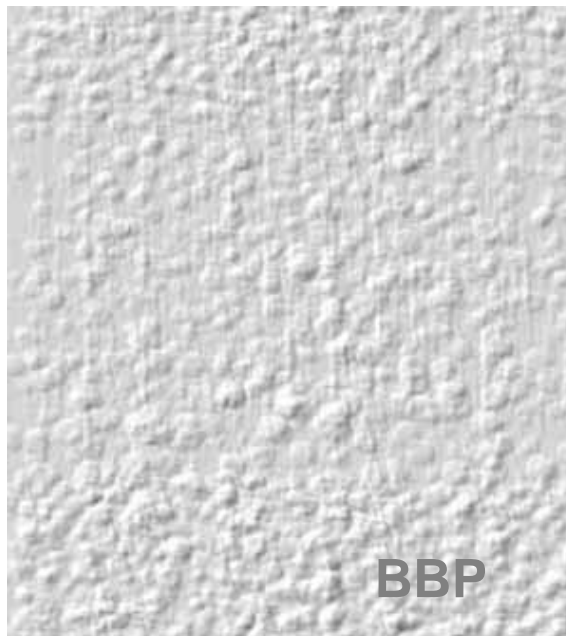
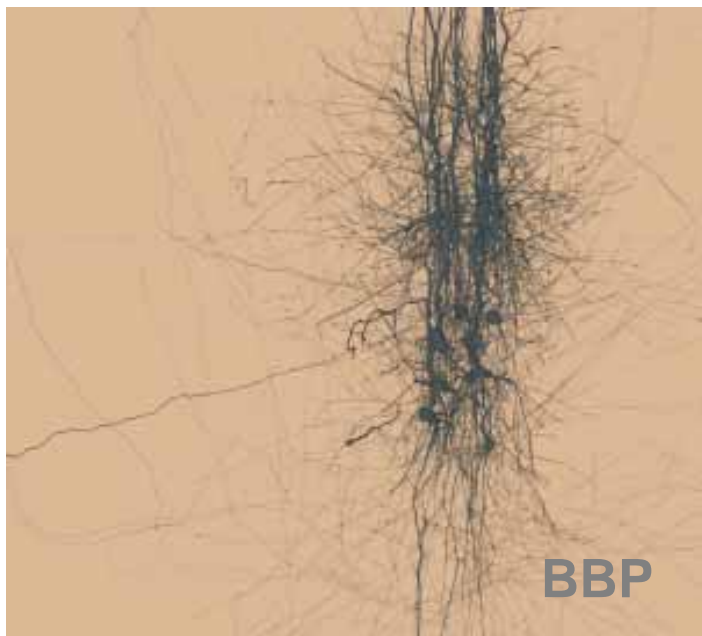
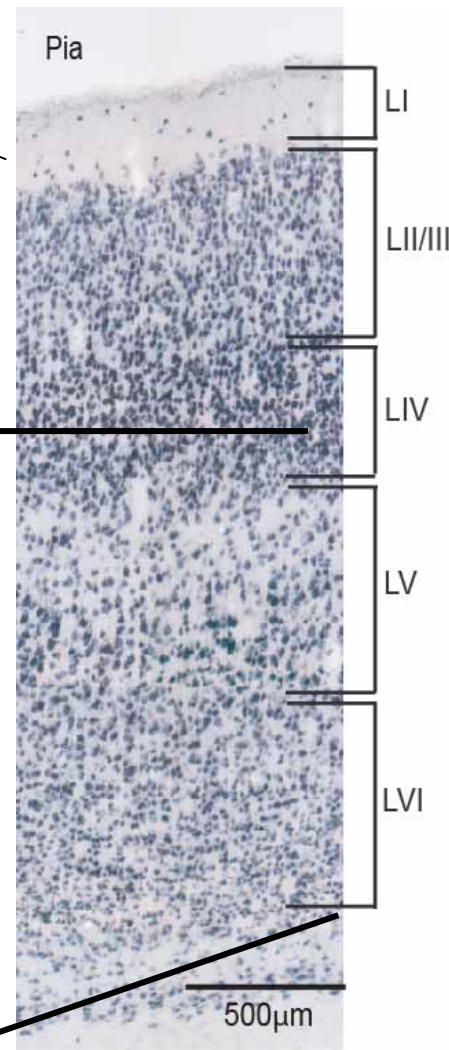
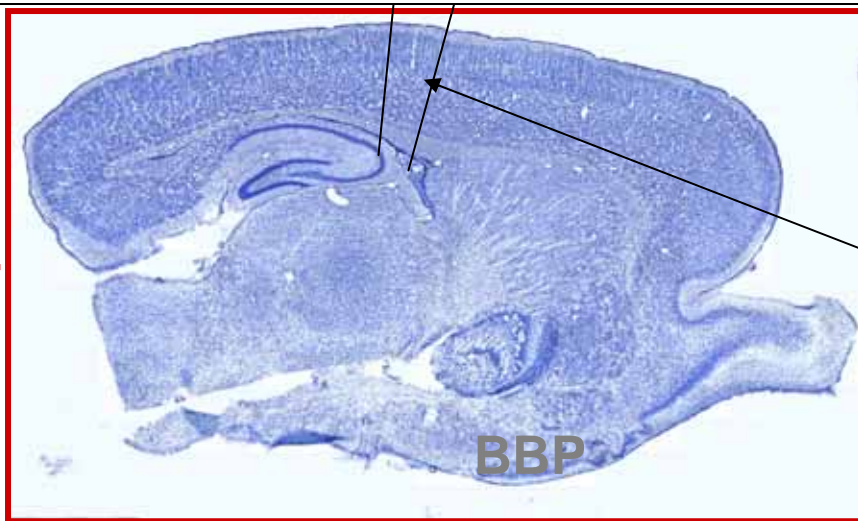
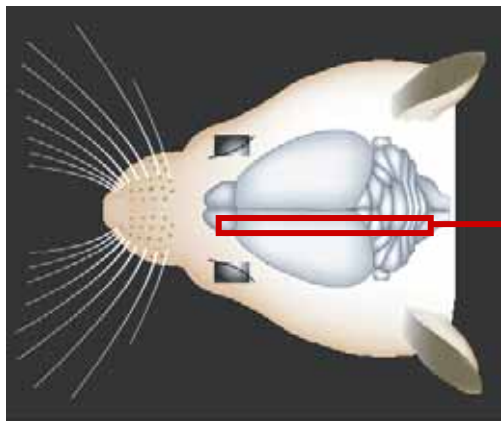
Reverse-Engineering the Brain



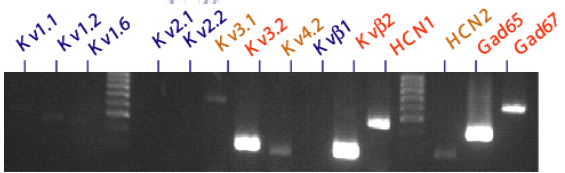
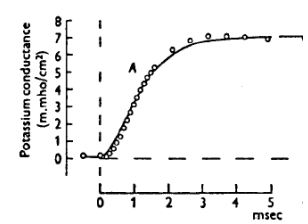
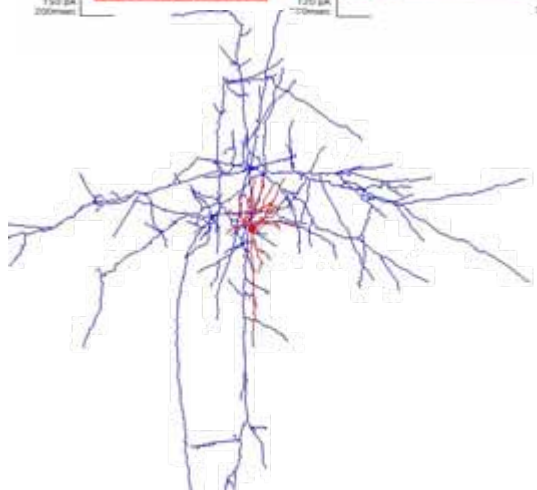
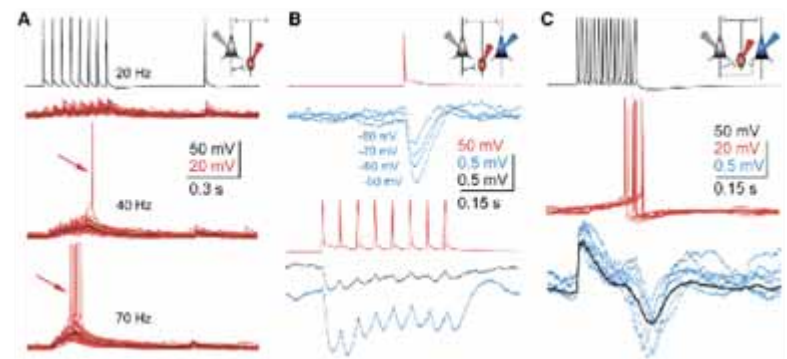
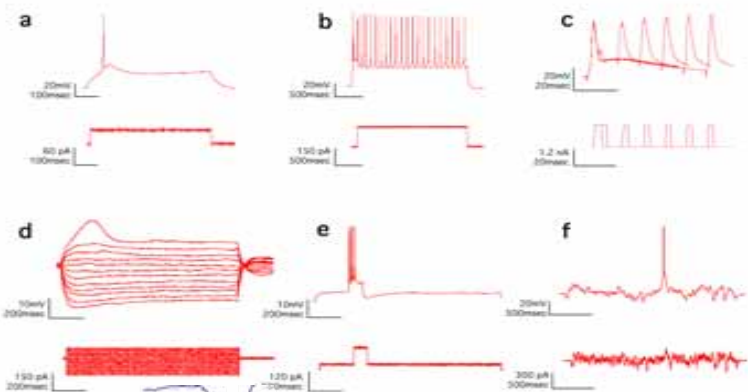
ÉCOLE POLYTECHNIQUE
FÉDÉRALE DE LAUSANNE
Brain Mind Institute



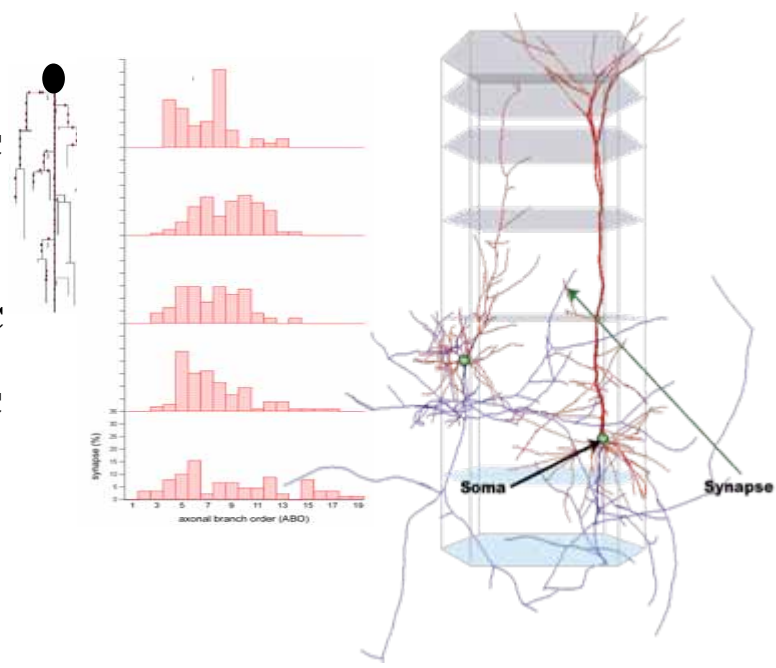
The Electrophysiologist's View



Accurate Models that Relate to Experiment

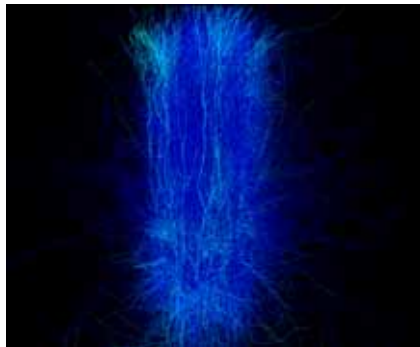
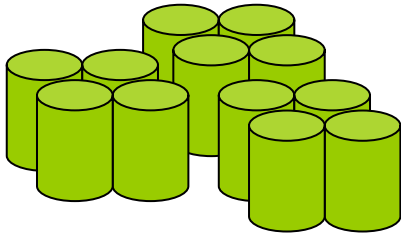


- LBC→PC
- SBC→PC
- NBC→PC
- BTC→PC
- MC→PC

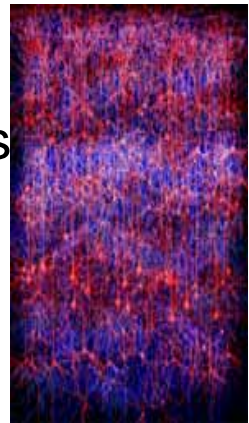


Create a faithful “in silico” replica at cellular level of a neocortical column of a young rat by the means of:

- reverse engineering the biology components
- forward constructing functional mathematical models



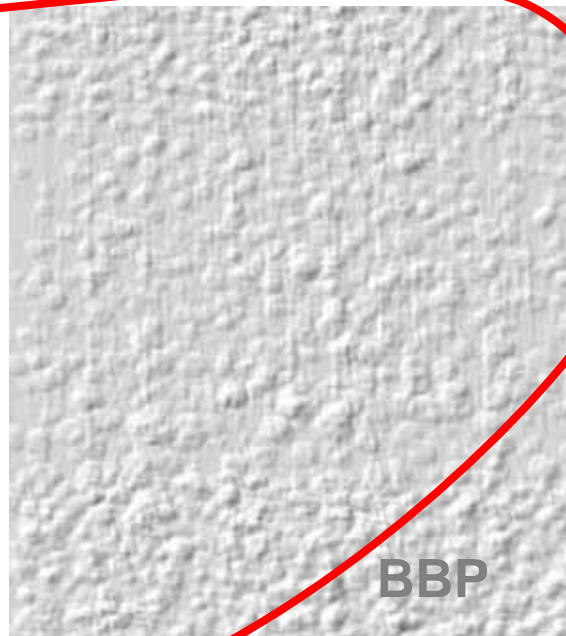
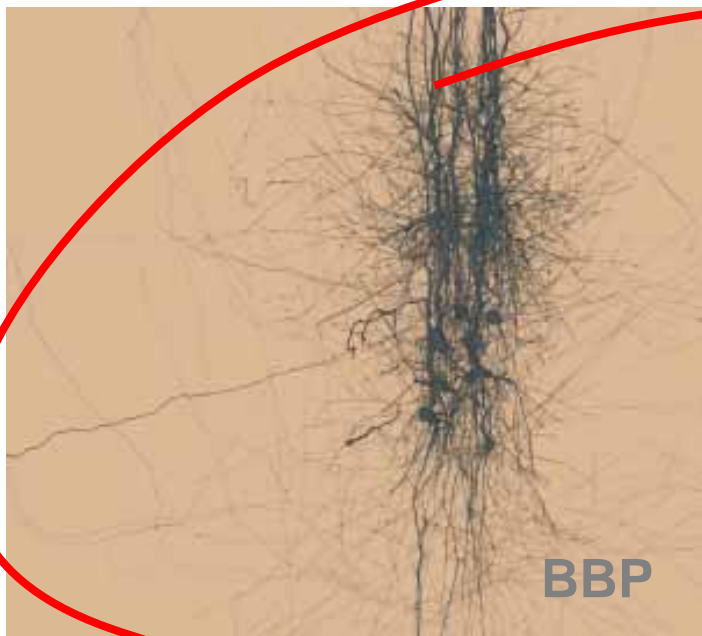
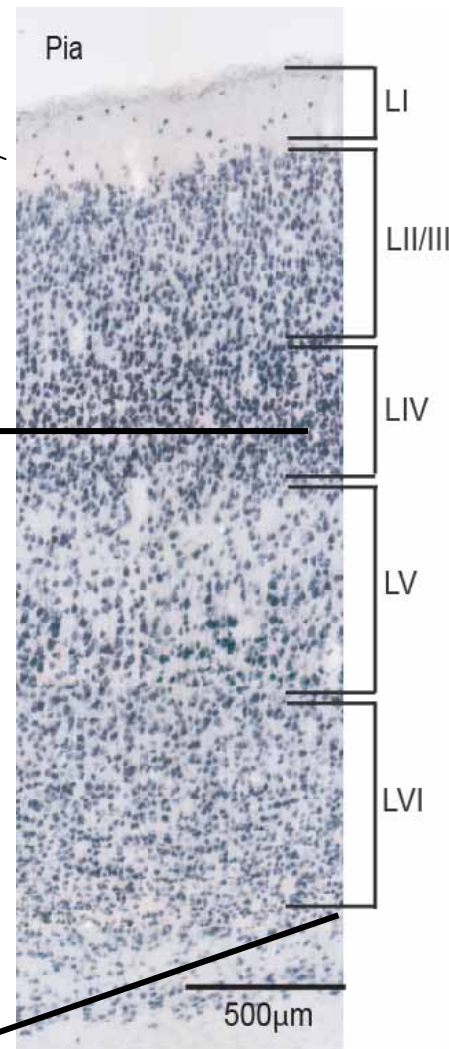
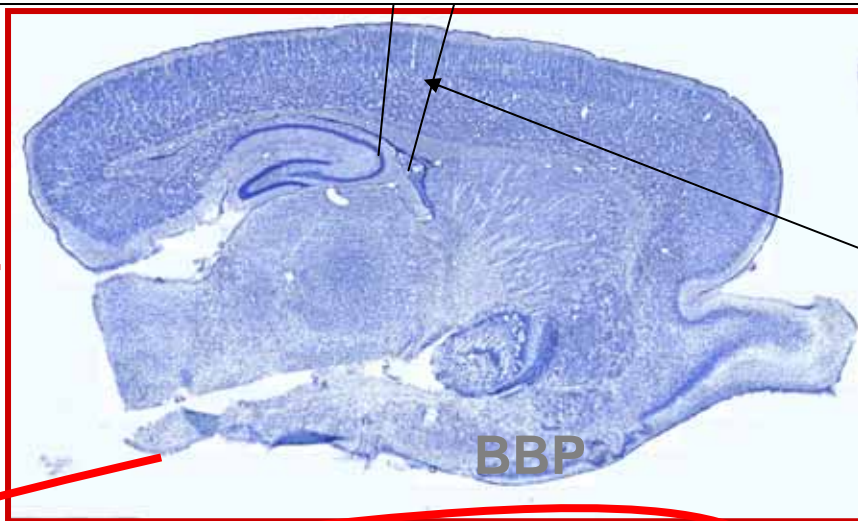
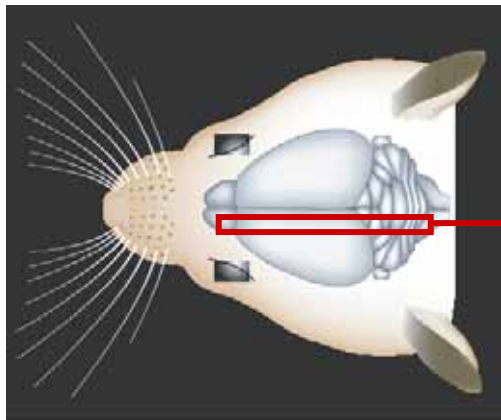
- **Building**
10,000 morphologically complex neurons
- **Constructing**
a circuit with 30,000,000 dynamic synapses
- **Simulating**
the column close to real-time





BBP

The Electrophysiologist's View - Revisited



BBP Phase I: « in vitro » vs. « in silico »



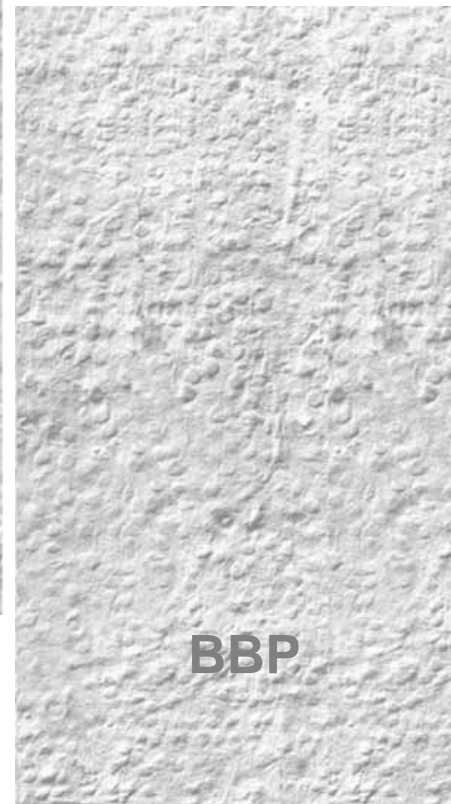
in silico



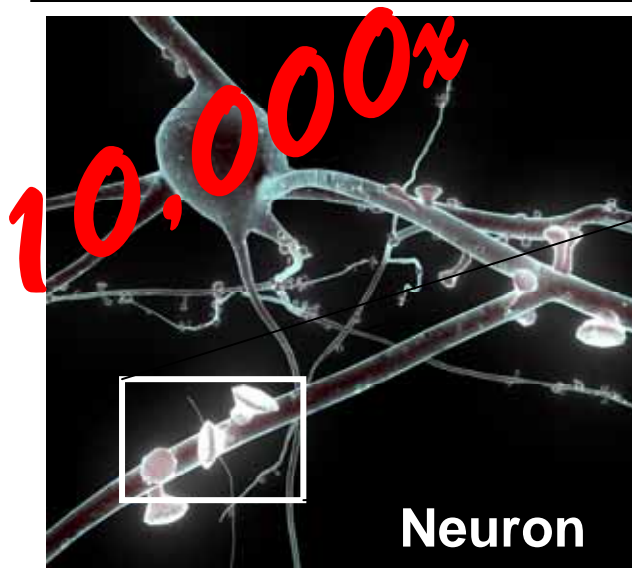
in vitro



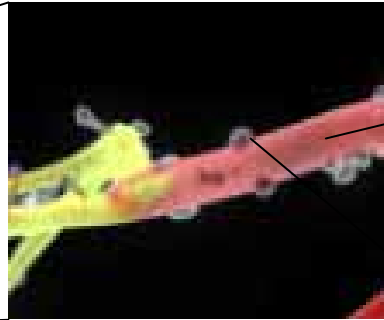
in silico



in vitro

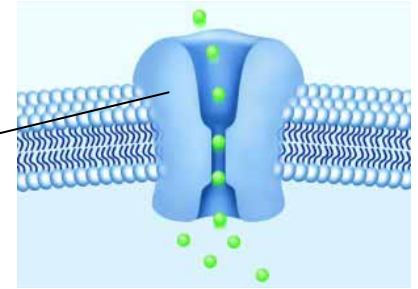


Compartment



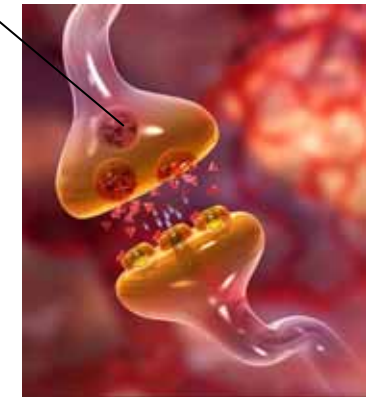
~350compartments/neuron

Channels



~20HH style channels/compartment

Synapses



~3,000/neuron

A Rat's Neocortical Column:

- ~1mm³
- 6 layers
- > 50 morphological classes
- ~340 morpho-electrical types
- ~200 types of ion channels
- 10,000 neurons
- 18 types of synapses
- 30,000,000 synapses

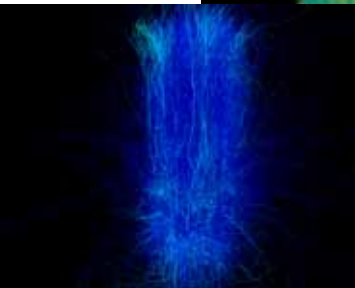
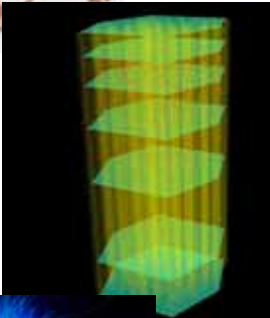
IT Challenge:

- 3,500,000 compartments
 - passive (cable, Gauss Elimination)
 - active HH style channels
- 30,000,000 synapses
 - dynamic
- → reporting 1 value/compartment → 140GB/biol sec

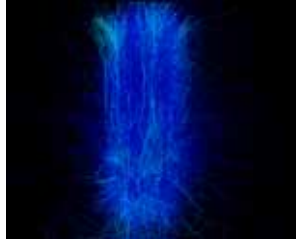


Dedicated 4 rack BG/L @ EPFL with 8192 processors, 2TB of distributed memory, 22.4 TFlop (peak)

- Used throughout all parts of the project
- Allows iteration of complete process within a week



- **Building: Run evolutionary algorithms for fitting of thousands of single cell models to data**
typical job size: 2048 procs
S. Druckmann et al., A Novel Multiple Objective Optimization Framework for Constraining Conductance-Based Neuron Models by Experimental Data, Frontiers in Neuroscience 2007
- **Constructing: Run dedicated algorithm to establish connectivity between cells**
typical job size: 8000 procs
J. Kozloski et al., Identifying, tabulating, and analyzing contacts between branched neuron morphologies, IBM Journal for Research and Development, Issue 52, Number 1/2, 2008
- **Simulating: Run simulation of cell networks**
typical job size: 8192 procs
M. Hines et al., Fully Implicit Parallel Simulations of Single Neurons. Journal of Computational Neuroscience, accepted



20,000X

A Rat's Neocortical Column

10,000 (10^4) neurons
30,000,000 (10^7) synapses

~1 neuron/core → 1:10-100 time penalty



4 rack BG/L

~ 10^4 cores

~ 10^{13} Flops (~10TeraFlops)

~ 10^{12} Bytes RAM (TeraBytes)



1,000X

A Rat's Brain

200,000,000 (10^8) neurons
 10^{11} synapses

~500 neurons/core → 1:5,000 - 50,000 time penalty

PetaScale HPC

~ 10^5 - 10^6 cores

~ 10^{15} Flops (PetaFlops)

~ 10^{14} Bytes RAM (~100TB)



A Human's Brain

10^{11} neurons
 10^{14} - 10^{15} synapses

ExaScale HPC

~ 10^{18} Flops (ExaFlops)

~ 10^{17} Bytes RAM (~100PB)

...but you wanted to give me 10^{23} – right?

10^{18} = ExaFlops

1 sec biological time = 1/2 day computation
→ unique brain research facility

10^{21} = ZettaFlops

1 sec biological time = few seconds computation
→ brain-scale plasticity simulations
→ desk-side brain simulations

10^{23} = 100 ZettaFlops

1 year biological time = 1 day computation
→ brain-scale developmental simulations
→ personalized models

But all this scaling is based on electrical models...

- Glial cells
- Vasculature
- Ligand-gated ion channels
- Second-messengers
- Receptors
- Organelles
- Bio-chemical pathways/cascades
- Proteins, Protein-interactions
- Genes

Hodgkin-Huxley → Langevin Description → Fokker-Planck → Master Equation → Ensembles of stochastic channels → Reaction/Diffusion Models → ...

What can we learn for Building Computers?

- The general recommendations from biology are clear
 - go analog (energy)
 - go local persistent memory (energy)
 - go sparse activity (energy density)
 - go 3D (integration, connectivity)
 - go distributed encoding (robustness)
- Along the way we will be able to extract principles for specific applications
 - generic building principles (structure, composition, connectivity)
 - specialization rules (circuit rewiring)
 - learning rules (local learning, homeostatic principles)
- We will have to go quite some way with computers that at least *look* like digital Von-Neumann machines to reverse-engineer biology and consolidate our knowledge in a model

The People Behind BBP

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- Prof. Phil Goodman (University of Nevada, Reno)

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- Dr. Charles Peck (IBM, Yorktown)
- Dr. Sean Hill (IBM, Lausanne)
- Dr. James Kozloski (IBM, Yorktown)

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- Dr. Philippe Rochat
- Dr. Konstantinos Sfyarakis

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- Rajnish Ranjan (EPFL, Lausanne)
- Imad Riachi (EPFL, Lausanne)
- Sandrine Romand (EPFL, Lausanne)
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- Afrasyab Bashir (EPFL, Lausanne)
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- Javier Sanchez Tamargo (EPFL, Lausanne)

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- Dr. Tania Rinaldi
- Dr. Gilad Silberberg
- Dr. Pablo de Heras (VisualBiotech, Lausanne)
- Haroon Anwar (OIST, Okinawa)
- Thomas Tränkler (Munich)

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- Prof. Georges Abou-Jaoudé (EPFL, Lausanne)
- Marco Belotti, assistant
- Alexandra Boussommier, student assistant