
**Cortical neural networks:
light-microscopy-based anatomical reconstruction,
numerical simulation and analysis**

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Collaborators



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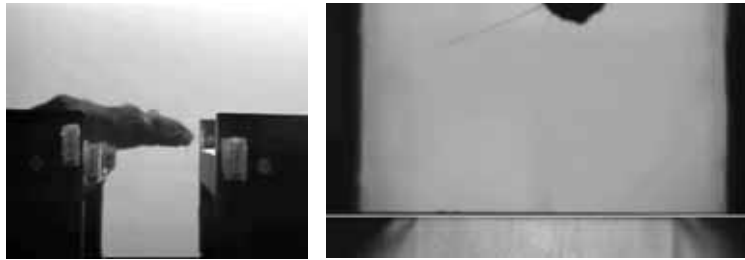
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Motivation

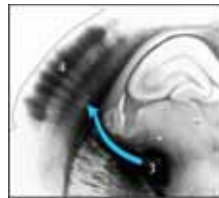
- Fundamental question in neuroscience:
How does the brain translate sensory input into behavior?
 - Describe and understand at cellular level, complete circuits that can drive behavior.
- Widely used model system: somatosensory whisker system in rodents



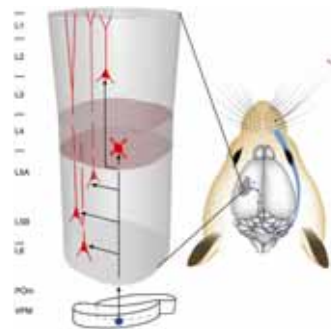
- Decision making; example: gap crossing
 - Reveal relation between structure and function (anatomy ↔ physiology)

Biological background: cortical column

- Somatosensory cortex processes information from whisker
- Information pathway:
whisker → brain stem → thalamus (VPM) → cortical column
- **Basic anatomical unit:** cortical column
- **1-to-1 whisker-column correspondence**
- Column divided into layers 1-6



Modified from V.C. Wimmer et al (2010): *Dimensions of a projection column and architecture of VPM and POm axons in rat vibrissa cortex.* Cereb Cortex, 20(10), 2265–2276



Modified from Helmstaedter et al. (2007): *Reconstruction of an average cortical column in silico.* Brain Res. Rev. 55(2): 193-203

Approach

Reconstruct cortical column



Numerically simulate its behavior

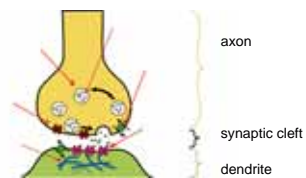
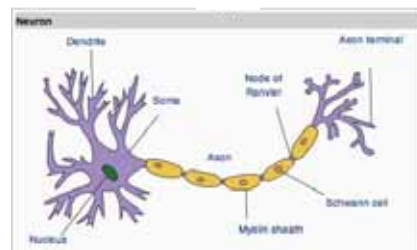


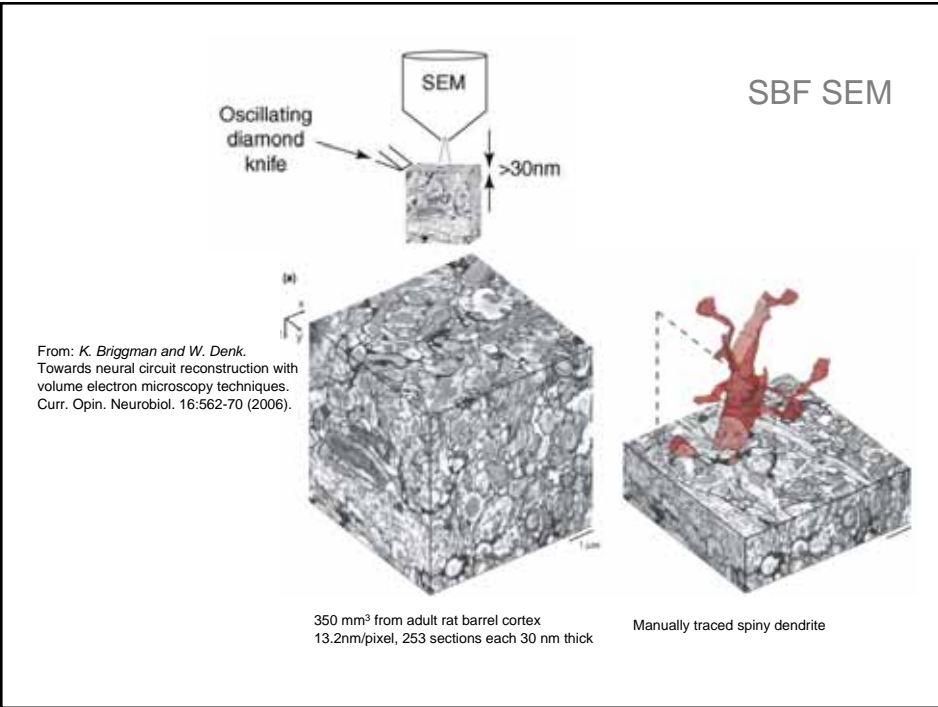
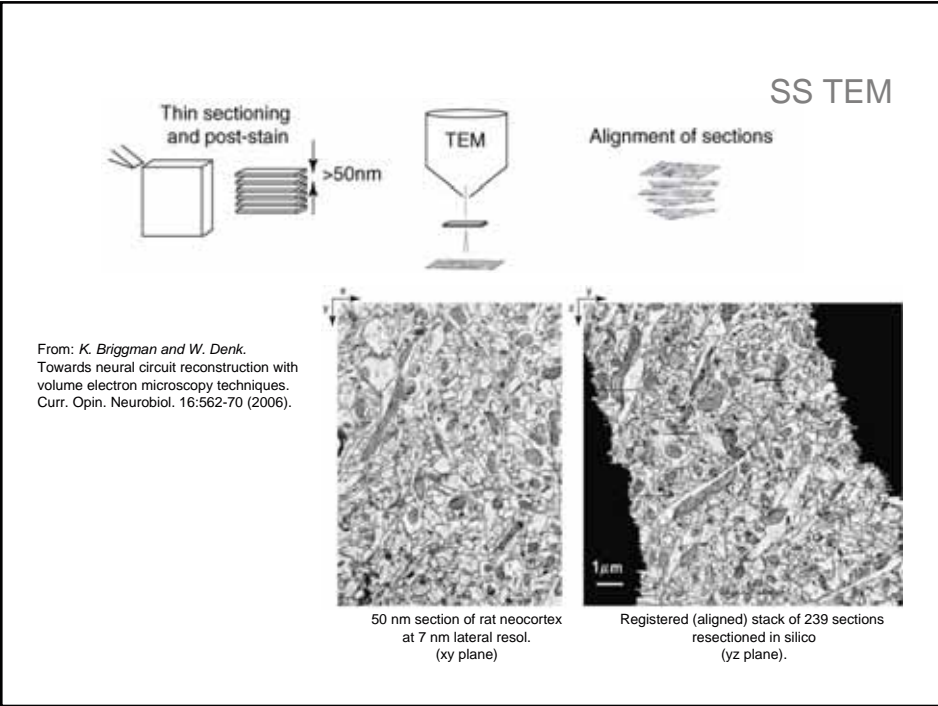
Analyze simulation results

Reconstruction

Ideal:

Dense reconstruction of all *neurons* and their *synaptic connections* within a cortical column of **1 individual**.

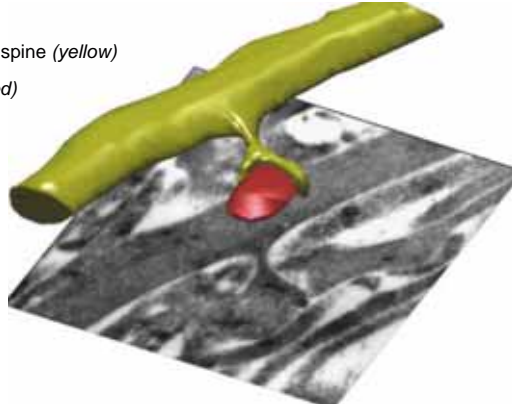




Synaptic connection

Reconstruction of

- dendrite segment with spine (*yellow*)
- pre-synaptic bouton (*red*)



From: K. Braun, Univ. Magdeburg

Reconstruction approach

Ideal:

Using electron tomographic technique perform dense reconstruction of all *neurons* and their *synaptic connections* within a cortical column of 1 individual

technically not feasible



Instead "Reverse engineering":

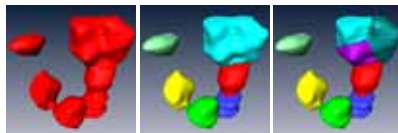
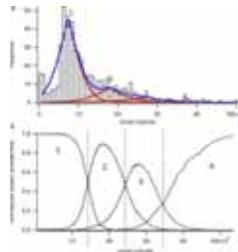
Using light microscopy, collect *somata* and *neurites* from *different sources* and *combine* them in a single model and establish rule-based connection

What anatomical data do we need?

- 3D neuron distributions
- 3D VPM axon reconstructions
- 3D dendrite reconstruction
for a representative sample of neurons of all occurring cell types
- Spatial frequencies of all cell types
- Spine- and bouton densities
(number of pre-/post-synaptic connection sites per μm axon/dendrite)

3D neuron distribution

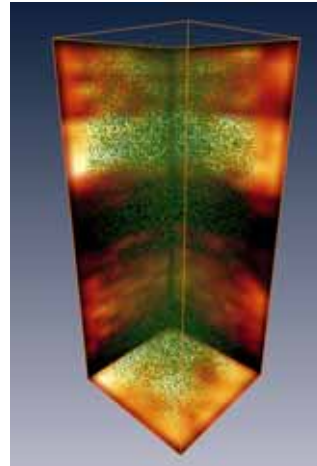
- Input: 3D confocal images containing stained somata (cell bodies)
- Problem: detect somata, resolve overlap
- Method:
 - 1) Binary segmentation
 - 2) Morphology-based splitting of clusters
 - 3) Volume model-based splitting of clusters



Oberlaender et al. (2009): Automated three-dimensional detection and counting of neuron somata. *J Neurosci Methods*, 180(1):147–160

3D neuron distribution (2)

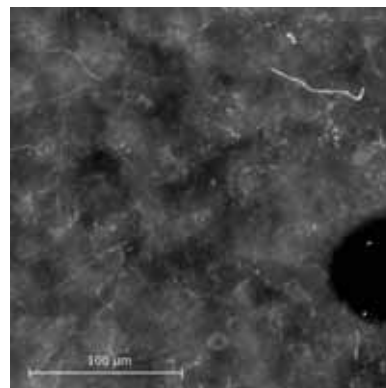
- Volume containing cortical column
- 2 x 2 x 40 confocal sections
- ~18k neurons in cortical column
- Density varies w.r.t. cortical depth



H.S. Meyer et al (2010): *Number and laminar distribution of neurons in a thalamocortical projection column of rat vibrissal cortex. Cereb Cortex. 20:2277-2286*

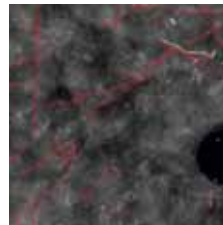
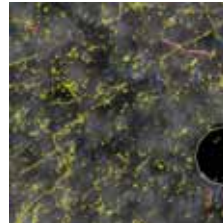
Morphology reconstruction

- Input: stack of transmitted light brightfield images (~35 sections)
- Problem: trace axons and dendrites, align stack, combine sections
- Complications: thin foreground structures, uneven dye penetration, stained background, large data (~20 GB/section)
- Approach:
 - 1) Automatic section tracing
 - 2) Interactive intra-section post-processing
 - 3) Automatic alignment
 - 4) Interactive inter-section post-processing (final quality control)
 - 5) Optional semantic labeling



Morphology reconstruction: “inverse tracing”

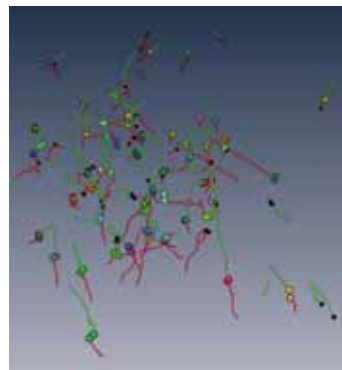
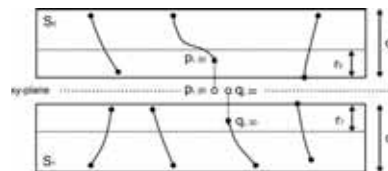
- Staining problems and sectioning may cause skipping of branches
- Ensure completeness
- Very conservative automatic tracing, accepting over-segmentation
- Manually remove false positives using dedicated tool (Amira filament editor)



V.J. Dercksen et al (2012): *Interactive visualization—a key prerequisite for reconstruction of anatomically realistic neural networks*. In: Visualization in Medicine and Life Sciences II. Springer-Verlag. In press.

Morphology reconstruction: section alignment

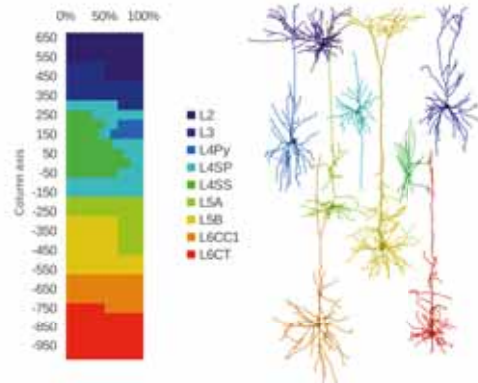
- Input: thin sections containing traced fragments
- Problem: alignment
- Point matching of near-boundary points
- Detection of maximal clique in distance compatibility graph
- Scaling and rigid alignment



V.J. Dercksen et al (2009): *Automatic alignment of stacks of filament data*. Proc IEEE International Symposium on Biomedical Imaging: From Nano to Macro (ISBI), 971-974.

Morphology reconstruction: dendritic cell types

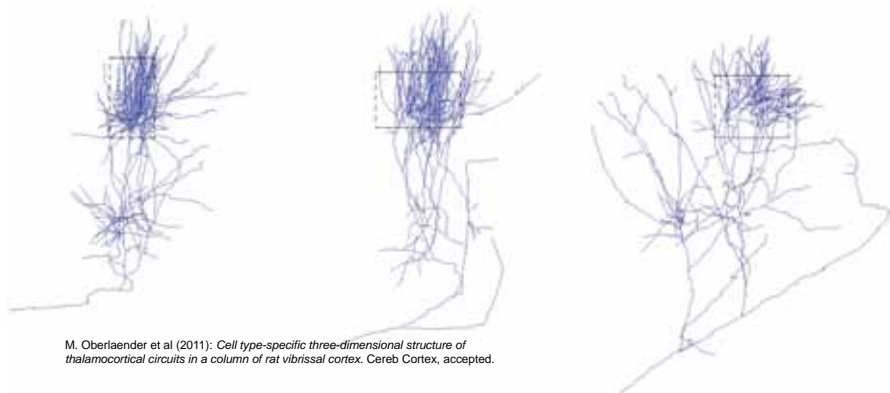
- ~100 dendritic reconstructions
- Classification:
9 excitatory cell types
- Relative frequency
w.r.t cortical depth
(Cortical depth recorded
during dye injection)



M. Oberlaender et al (2011): *Cell type-specific three-dimensional structure of thalamocortical circuits in a column of rat vibrissa cortex*. Cereb Cortex, accepted.

Morphology reconstruction: axons

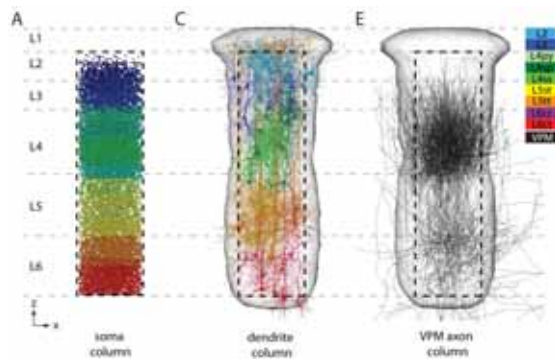
- Axons: Long-ranging, thin, complex
- VPM axons project into column
- Convey input from whiskers



M. Oberlaender et al (2011): *Cell type-specific three-dimensional structure of thalamocortical circuits in a column of rat vibrissa cortex*. Cereb Cortex, accepted.

Cortical column assembly

- Place somata according to given neuron density
- Place dendrites by duplicating morphologies, satisfying cell type frequency



M. Oberlaender et al (2011): Cell type-specific three-dimensional structure of thalamocortical circuits in a column of rat vibrissal cortex. Cereb Cortex, accepted.

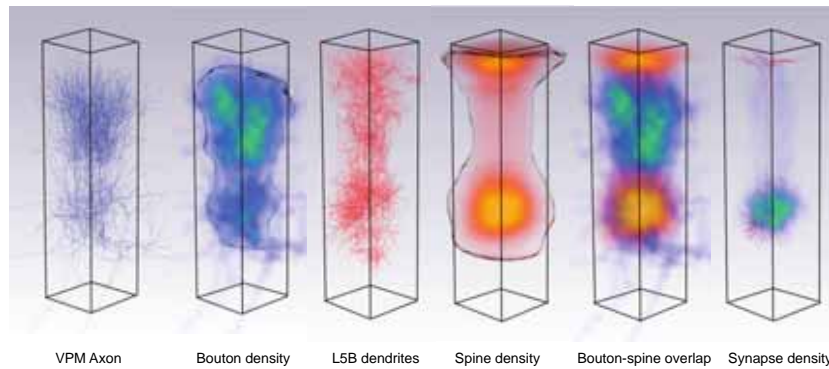
Synaptic connectivity

- Number of synapses estimated from structural overlap (Peters' rule)
- Synapse estimate in $50^3 \mu\text{m}^3$ grid cells
 - # boutons = axon length * bouton density
 - # spines = dendrite length * spine density
 - # synapses: $c_{i,j}(x, y, z) = f(x, y, z) * s_i(x, y, z) * \frac{b_j(x, y, z)}{S(x, y, z)}$

$c_{i,j}$ = # synapses of post-synaptic neuron i with pre-synaptic type j
 b_j = # boutons of pre-synaptic type j
 s_i = # spines of cell i
 S = total # spines
 f = optional factor for inhibitory cell compensation

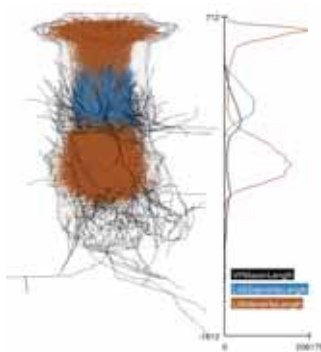
- Synapse position input for simulation
- Realization of pre-synaptic cell for each synapse is generated before simulation (depending on convergence/divergence parameters)

Synaptic connectivity: VPM-L5B example



Visual analysis of anatomical network properties

- Current work: Interactive exploration of neural network properties
- Collect evidence to validate model, support hypotheses
- Produce images for publication
- Tool: query-based selection and evaluation for visual and quantitative analysis



Example:

```

selection VPMaxon = axon where CellTypeIs('VPMaxon')
selection L5Bdendrites = dendrite where CellTypeIs('L5B')
selection L4SSdendrites = dendrite where CellTypeIs('L4SS')
profile VPMaxonLength = length(VPMaxon, Z, 25)
profile L4SSdendriteLength = length(L4SSdendrites, Z, 25)
profile L5BdendriteLength = length(L5Bdendrites, Z, 25)

selection allDendrites = dendrite
profile L5Bsynapses =
  synapses(VPMaxon, L5Bdendrites, allDendrites, XYZ, 50)
profile L4SSsynapses =
  synapses(VPMaxon, L4SSdendrites, allDendrites, XYZ,
  50)
    
```

Simulation of signal flow (Stefan Lang)

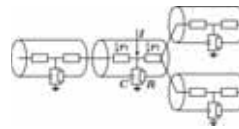
- Membrane potential (V)
- Hodgkin-Huxley equations describe V in response to input/output current through membrane channels and synapses

$$C \frac{dV}{dt} = -(\sum I_i + I_{\text{leak}}), \quad I_i = \frac{V - E_i}{R_i(V, I)}$$

- Cable equations describe V change through compartments

$$\frac{r_m}{r_l} \frac{\partial^2 V}{\partial x^2} = c_m r_m \frac{\partial V}{\partial t} + V$$

- Coupled PDEs of reaction-diffusion type
- Finite Volume scheme
- t-dependent eqs implicitly discretized by Crank–Nicholson or Backward–Euler schemes
- Simulation software NeuroDUNE www.neurodune.org



Simulation parameters

- Anatomical parameters
 - Number of neurons
 - Morphology
 - Spine, bouton densities
 - Number of synapses
 - Synapse positions on dendrites
 - ...
- Physiological parameters
 - Electrical parameters
ion channel conductances, reversal potentials, resting potential, etc.
 - Convergence/divergence
 - Pre-/post-synaptic neuron pairing
 - Input signal (#spikes)
 - Input synchrony
 - Synaptic efficacy
 - ...

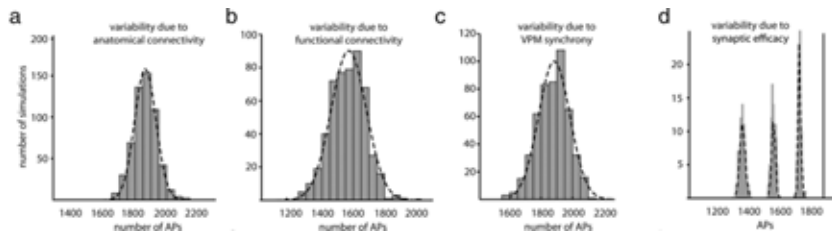
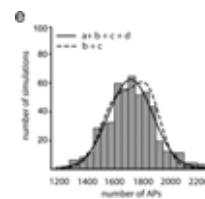
Simulation parameters

- Anatomical parameters
 - Number of neurons → Anatomical data
 - Morphology → Anatomical data
 - Spine, bouton densities → Values reported in literature
 - Number of synapses → Anatomical data
 - Synapse positions on dendrites → Parameter study
 - ...
- Physiological parameters
 - Electrical parameters (ion channel conductances, reversal potentials, resting potential, etc.) → Values reported in literature
 - Convergence/divergence → Values reported in literature
 - Pre-/post-synaptic neuron pairing → Parameter study
 - Input signal (# spikes) → Measured in vivo
 - Input synchrony → Parameter study
 - Synaptic efficacy → Parameter study
 - ...

S. Lang et al (2011): *Simulation of signal flow in 3D reconstructions of an anatomically realistic neural network in rat vibrissa cortex*. Neural Netw. 24:998-1011.

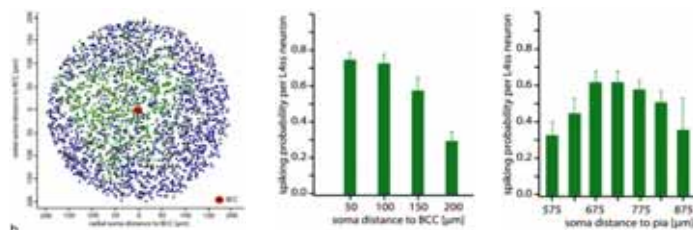
Simulation: parameter sensitivity study

- Model: VPM (285) → L4 spiny stellates (2770)
- Monte Carlo: 507 runs per trial
- Dependent parameter: number of L4SS spikes
- 4 independent parameters were varied:
 - Anatomical connectivity (synapse positions)
 - Functional connectivity (pre- and post-synaptic neuron pairs)
 - VPM input spike timing (synchrony)
 - Synaptic efficacy (% spikes that elicit post-synaptic signal)
- Functional connectivity and input synchrony explain most variance



Simulation: example result

- Location-specific spiking response
- Spiking response decreases
 - with distance to barrel column center (BCC)
 - towards layer boundaries (L3, L5)
- This behavior has been reported for L2/3 cells in literature



Future challenges

- Tools for explorative analysis of simulation results
- Anatomic modeling of larger brain volumes (currently: barrel field, ± 25 columns)
- Utilization (also) of electron-tomographic images: particularly automatic segmentation of TB sized data
- Gradual, step-wise improvement of understanding: anatomy – physiology – function

Acknowledgement to collaborators



Vincent J Dercksen
ZIB, Berlin



Marcel Oberländer
MPI Florida, Jupiter, FL



Bert Sakmann
MPI Florida, Jupiter, FL



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IWR, Heidelberg

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