

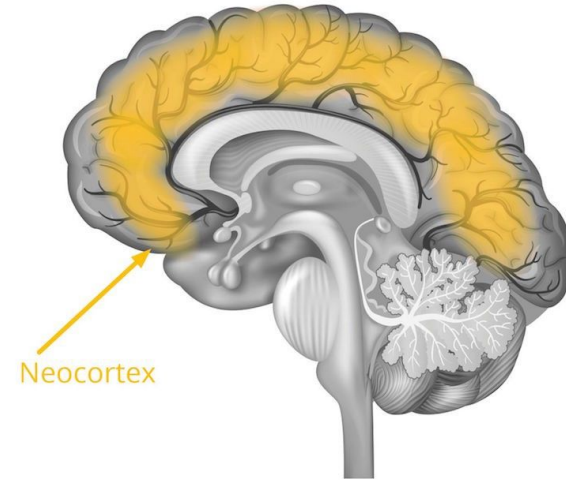


A Saturated Reconstruction of a Volume of Neocortex

Brian Soong

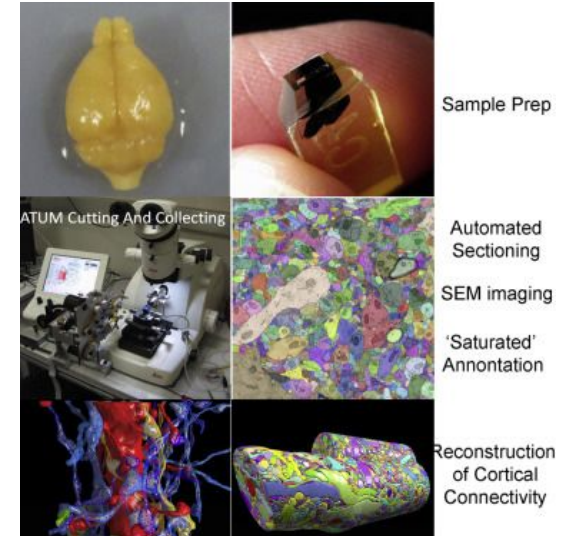
Opportunity

- The “precise relationships” of synaptic connections in brains are still widely unknown and undocumented, could be useful in studying developmental disorders
- Neuroscientists were just beginning to employ EM in neural tissue
- Are creating microscale connectomes worth it?
- The neocortex itself, involved in higher cognition, is desirable to research



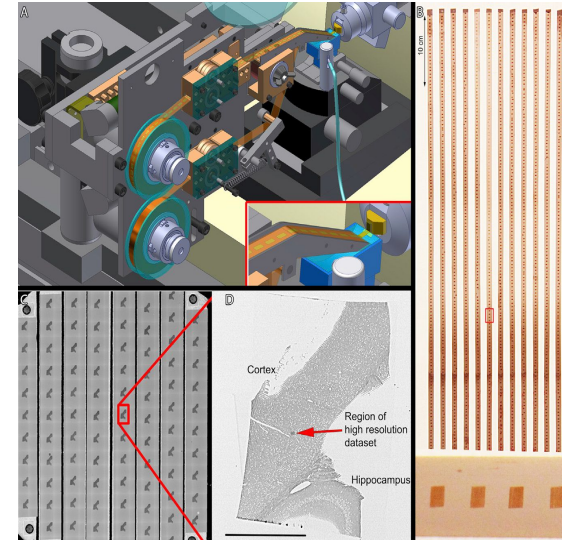
Challenge

- A full connectome of the mouse brain would be difficult and expensive
- Even at the small scale of $1500\text{ }\mu\text{m}^3$, hand annotation is arduous
- Not sure if any useful data exists — completely new territory
- Not only is imaging the tissue difficult, but so is finding substantive analysis



Action

- Using custom built machinery, the piece of brain was chopped into 2,250 slices at 29 nm thick
- Tracing of axons and dendrites proved extremely accurate (>99%), but also time consuming
- RhoANA, deep learning software, sped up image analysis greatly
- Analysis of synapses in relation to nearby dendritic spines and axons





Resolution

- A stepping stone for other neuroscientists
- All data and methods available publicly on openconnectome.org
- If future research can identify patterns in synaptic connectivity, then such intensive work doesn't need to take place
- The refutation of Peter's rule leaves unknown factors in synaptic development to be identified

124 lines (106 sloc) | 3.85 KB

```
1 % FindOrphans Make tables of objects that crosss shell 0 or 1 times
2 %{
3 COPYRIGHT 2013, 2014 Jeff W. Lichtman, Narayanan (Bobby) Kasthuri,
4     Daniel Berger, and Jose A. Conchello
5 %}
6 %{
7 CAVEAT EMPTOR:
8     This script was writen to be used once (read writen in haste). Thus,
9     it is neiter very flexible, nor well documented, nor easy to maintain.
10 %}
```



Feedback

- Very much an exploratory study with no prior functional studies to direct research
- Mapping the brain in relation to connectomics is analogous to how sequencing genes is related to genomics — no functional information required!
- Huge effort placed into making the data publicly accessible



Regardless, we recommend you to [update your browser](#).