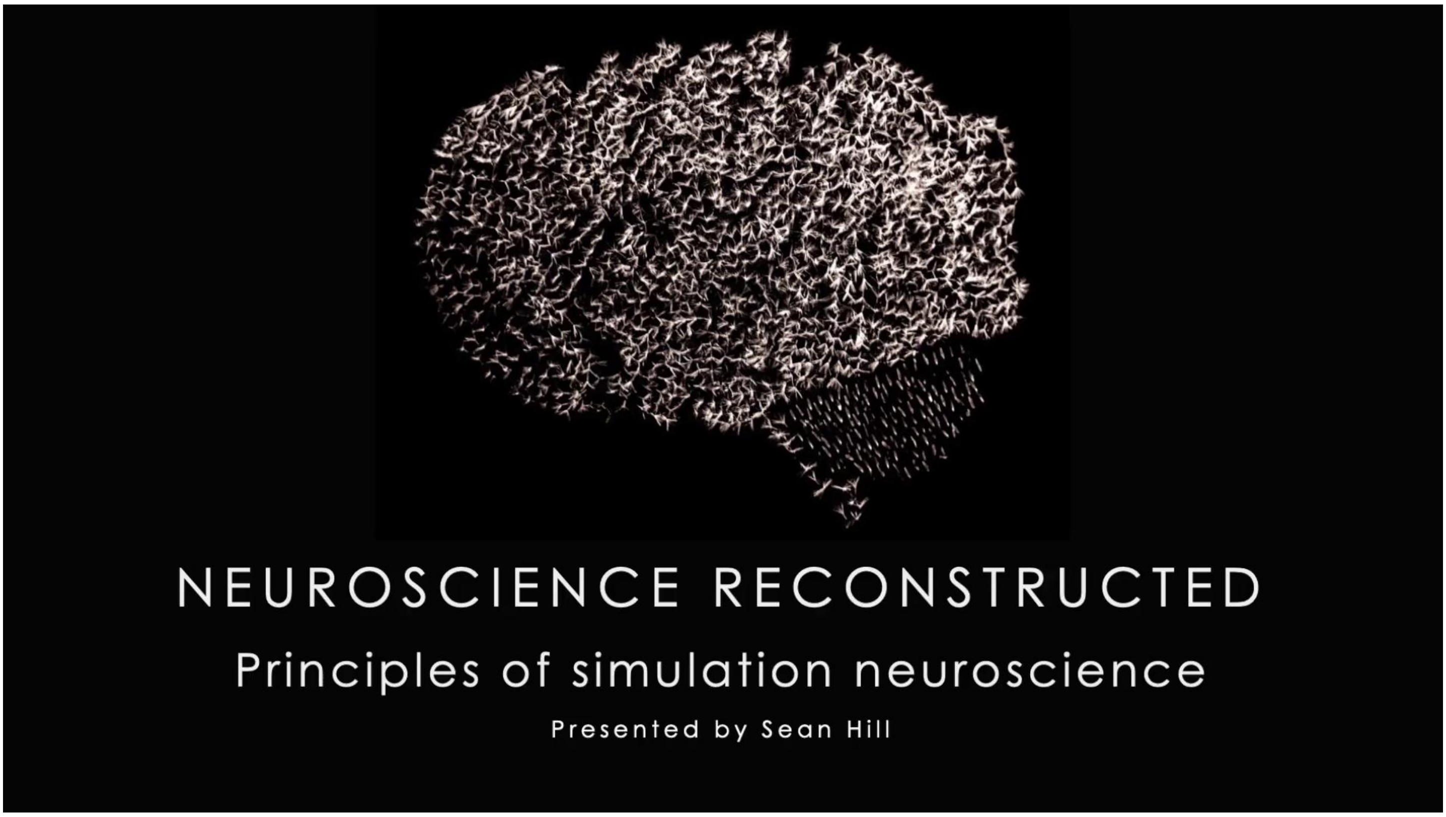

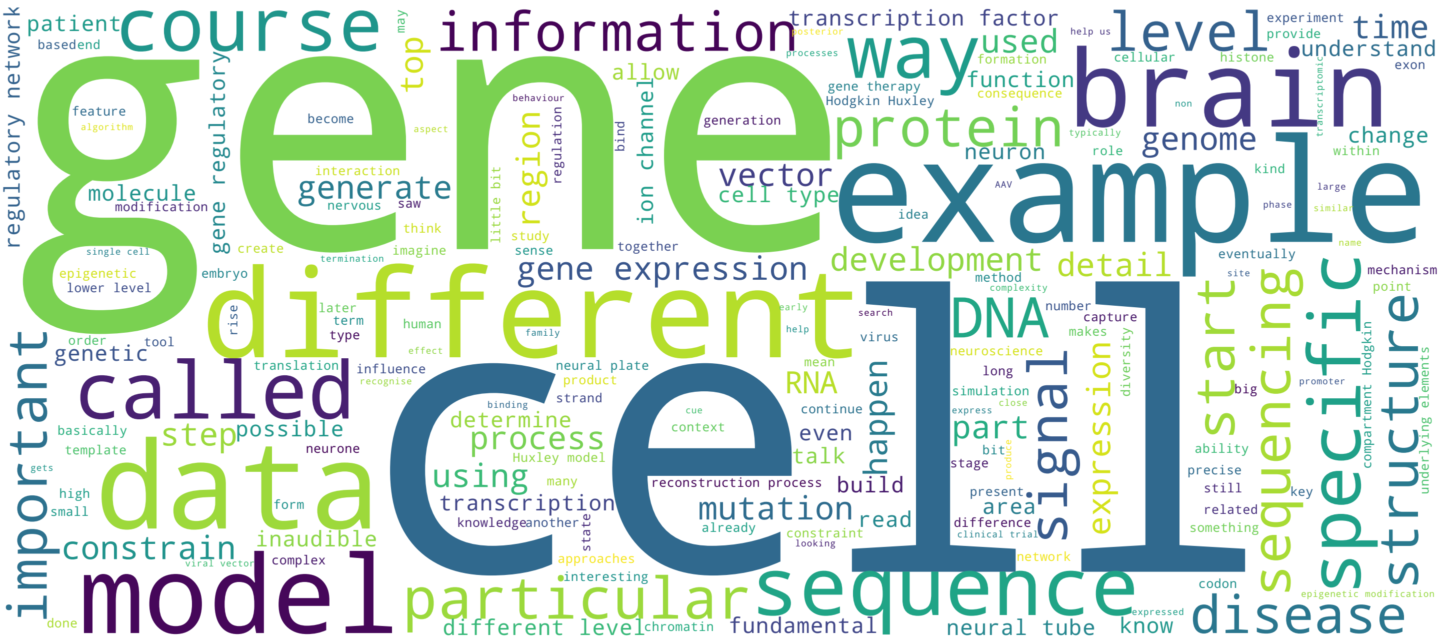

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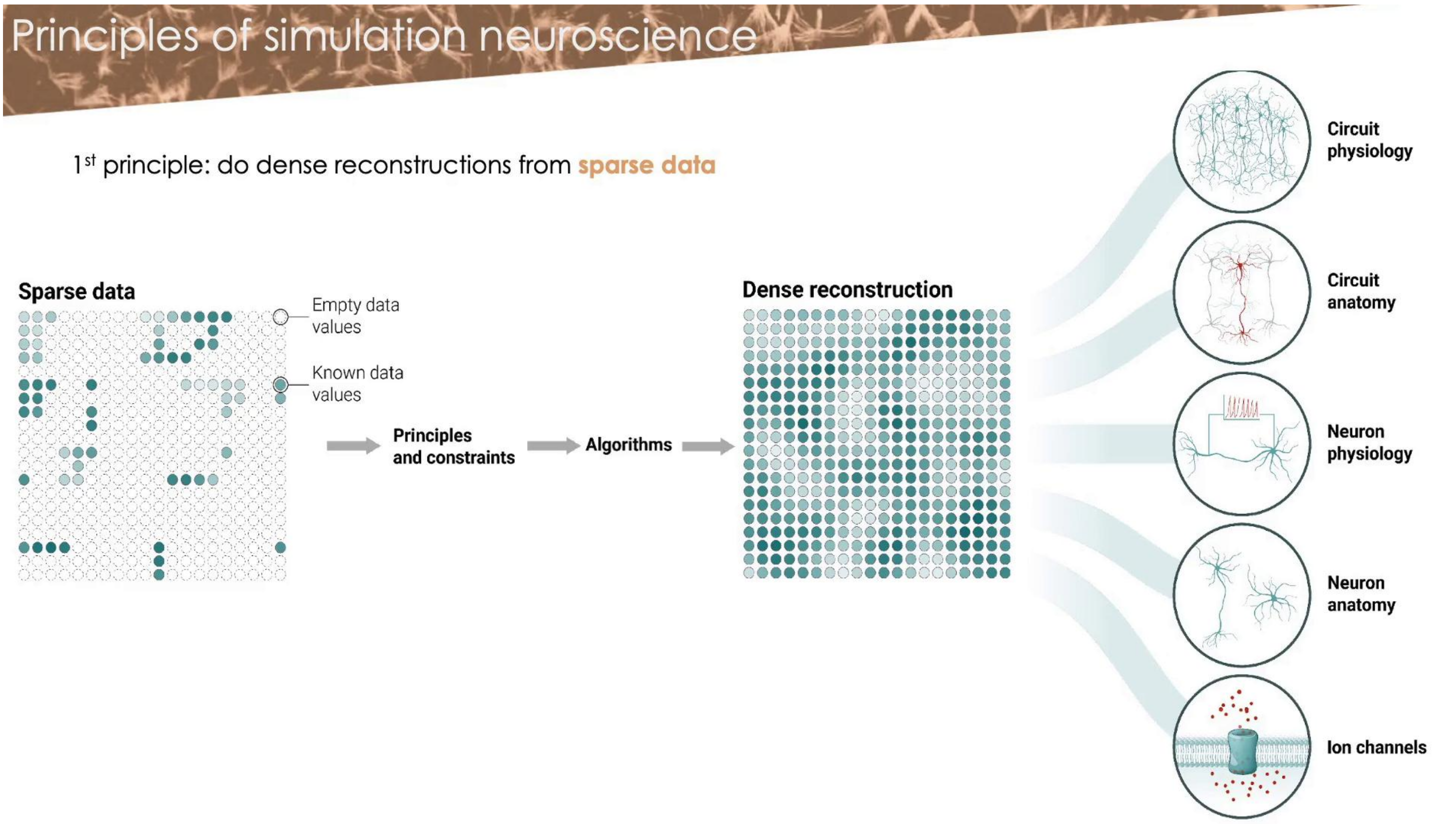


In simulation neuroscience, one of the core principles is that we want to reconstruct or build these dense reconstructions, dense biological reconstructions from sparse measurements, but using biological principles and constraints. We recognise that we will not be able to measure all of the little dots here. But we do have anchoring points and we do have constraints on many elements that we can formulate in the context of algorithms in our reconstruction process. In doing so, we can actually assemble knowing properties, for example, biological constraints on ion channels, using, for example, the three dimensional morphology of the neurons to constrain, of course, the potential connectivity, the circuit anatomy, using the neurone physiology to constrain the distribution of the ion channels. All of these knowledge, all of this biological knowledge, can help us constrain the reconstruction process so that we build something that uses known biological measures but ultimately respects the biophysical limits on the circuitry that we're modelling.

Notes

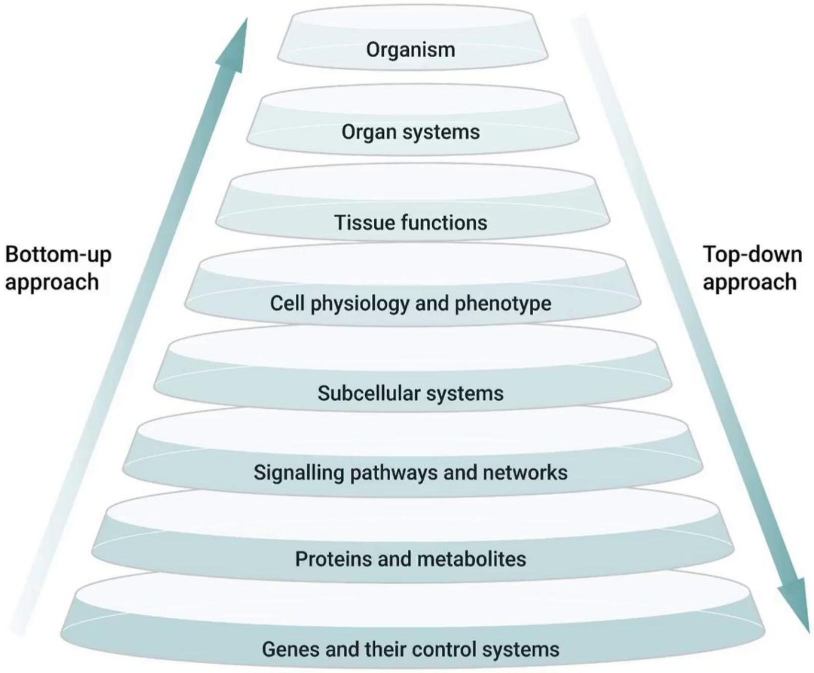
Summary

0m 05s

Principles of simulation neuroscience

2nd principle: reconstruct **bottom-up**

- **Bottom-up approach:** integrates data and knowledge from lower levels to explain phenomena observed on higher levels
- **Top-down approach**: uses known phenomenon from higher levels to deduce how components of lower levels should behave

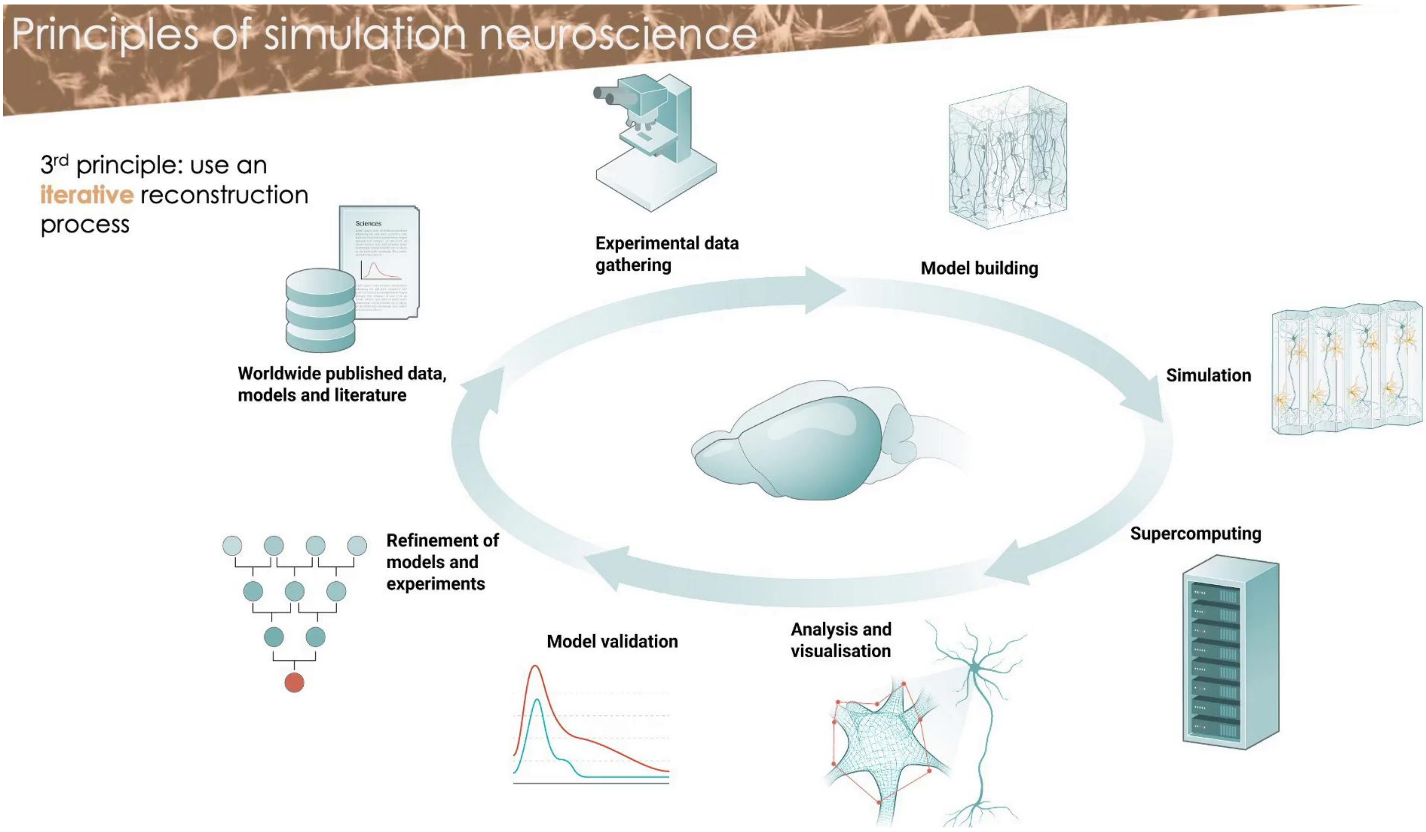


Another element of this is to really integrate data and knowledge from lower levels and build larger and larger systems basically, as a consequence of those underlying elements. For example, building a microcircuit from its building blocks and from its component neurons and synapses and so on to see the emergent function of the circuit. Another approach called the top down approach starts with high level phenomena and makes a hypothesis as to how the underlying elements contribute to that and creates a top-down model of the system, eliminating a lot of the lower level detail which may be considered extraneous. Of course, it's really a combination of these two approaches that can ultimately give you a rich understanding and ability to navigate the complexity of the brain.

Notes

Summary

1m 28s



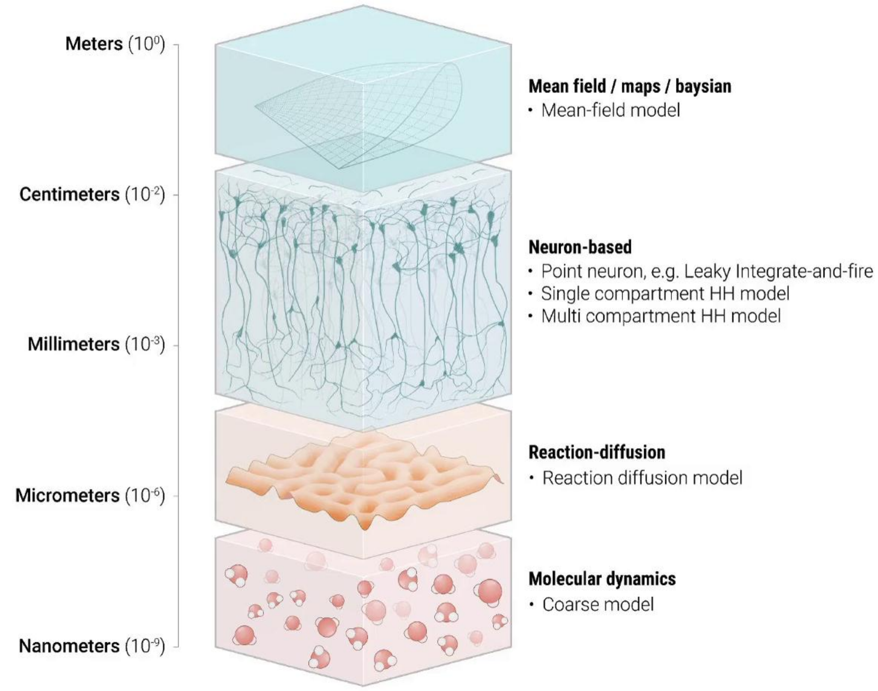
Another principle is really using an iterative reconstruction process. Starting, for example, from data, available models, available literature, available data from the laboratory, gathering new data, using that to build models, run simulations. Then through the super computing, the once you've run the simulations, to also analyse and visualise the data coming out of those simulations, validate the models against other data that you did not use to build them. Then, of course, there's always differences between the model and reality. You need to use those differences in a way to gain insight about how do you continue to refine the models by integrating additional data from the literature or going and pursuing new experiments to fill in gaps in specific measures that are needed to constrain the model. This cycle continues.

Notes

Summary

2m 34s

What can we model?



What can we model? We can model all different levels. Anything that we can capture and describe mathematically from the molecular dynamics to reaction diffusion models, to neurons, and these can take different levels of detail. For example, neurons could be modelled as point neurons, single compartment Hodgkin–Huxley model, multi compartment Hodgkin–Huxley models, or if you go up to a more coarse grain scale, mean field models, and we'll talk a bit about that.

Notes

Summary

3m 41s

Reductionism & abstraction

Modeling is a trade-off between **generality, realism and precision**.

The level of detail of a model depends on:

- The biological question the model aims to answer
- The level of the biological data the model is based on
- The smallest amount of detail the model needs to accurately reproduce biological features
- Which biological features can be quantified experimentally

The reason you choose different levels of detail is it's a trade off between the generality, how accurately you're able to capture and recreate system behaviour, and as well as the precision, how precise do you want to be? It really has to do with the question that you want to answer. The level of the data that you have to constrain the model, and the smallest amount of detail that the model needs to accurately reproduce the biological features. In which of those features can then you actually quantify experimentally to constrain your models?

Notes

Summary

4m 09s