COMPUTATIONAL NEUROSCIENCE

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Contents

Contents									-			
Preface									2			
1	Intr	0										3
	1.1	Types of Models										3
	1.2	Receptive fields										3

Preface

What follows are my notes on computational neuroscience, acquired mostly through self-study. The major sources that have been consulted are as follows.

- ► Computational Neuroscience, an online course on Coursera by the University of Washington.
- ▶ Neuronal Dynamics, a freely available online textbook.
- ► Lecture notes on Computational Neuroscience by Todd Troyer.

As these are the fruits of quite unguided explorations through the vast terrains of computational neuroscience, it's astronomically unlikely that these are void of errors. I take full responsibility for all mistakes within. But in exchange, I urge you, the reader, to do me a couple of favours. First, read everything (these notes *and* everything else that you will ever read) with a hint of healthy scepticism - all the authors are, just like you and I, humans. And second, let me know of the errors you find here - be they "hard errors" (i.e. something scientifically incorrect), or "soft errors" (i.e., something that isn't, strictly speaking, incorrect, but could be presented better). Computational biology is a joy of a ride - I hope you have as much fun reading these notes as I have had in preparing these.

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Chapter 1

Intro

1.1 Types of Models

- ▶ Descriptive \rightarrow *what?*
- ▶ Mechanistic \rightarrow *how?*
- ▶ Interpretive \rightarrow *why?*

1.2 Receptive fields

- ▶ Patterns of activation of a receptor
- ▶ Retinal ganglion cells have a centre-surround pattern of activation
- ► Cells in the V1 or V2 cortex have more complex patterns of activation e.g. oriented bars or more complex features
- ► Each layer builds on top of the previous ones to represent more and more complex patterns
- ➤ Our task:
 - o Describe the receptive fields at each layer (what biology is doing)
 - Explain the *mechanism* by which the higher-order receptive fields arise out of the lower-order fields (*how* low-level "instructions" give rise to "complex" biology)
 - o *Interpret* the computational advantages and disadvantages of the obtained models over other possible models (*why* biology chose this model over others)