Erik Garrison thesis corrections

Chapter 2
- Section 2.1: Provide, and refer to, an illustrative example of a very simple variation graph, showing explicitly the paths, nodes, edges, as constructed in one or two ways based e.g. on a minimal alignment of reads from a diploid genome or short sequences.
- Section 2.4.3: Clarify the description of the GCSA2 structure and its construction.
- Fig. 2.3 right: Explain precisely what is represented in each of the columns of the table, how these data relate to Fig 2.3 left, and explain by referring to the element in the table how the blue and red arrow represent one step of the backward and forward search algorithm respectively.
- Fig. 2.4: Explain this figure properly and in full (what the various elements represent and what it helps explain), ideally in the caption.
- Section 2.5; Describe explicitly the DP algorithms referred to as 'Viterbi' (pp. 70, 72, 73) (and if possible justify the use of this name by showing that it is mathematically analogous to the Viterbi or other max-sum algorithm as used in the graphical model/HMM literature).
- Fig. 2.6: Explain this figure properly and in full, ideally in the caption.
- Fig. 2.7: Improve the explanation in the caption, and possibly edit the figure for clarity. What black rectangles etc.
- Figs. 2.9, 2.10: Explain in the captions what do the colours represent.

Chapter 3
- Throughout, resolve the terminolgy for Cactus, e.g. assembly/alignment/graph.
- Fig. 3.11: Explain fully what this figure shows; what is meant by 'dotplot'.
- Fig. 3.19: Expand the caption to describe what this figure shows.