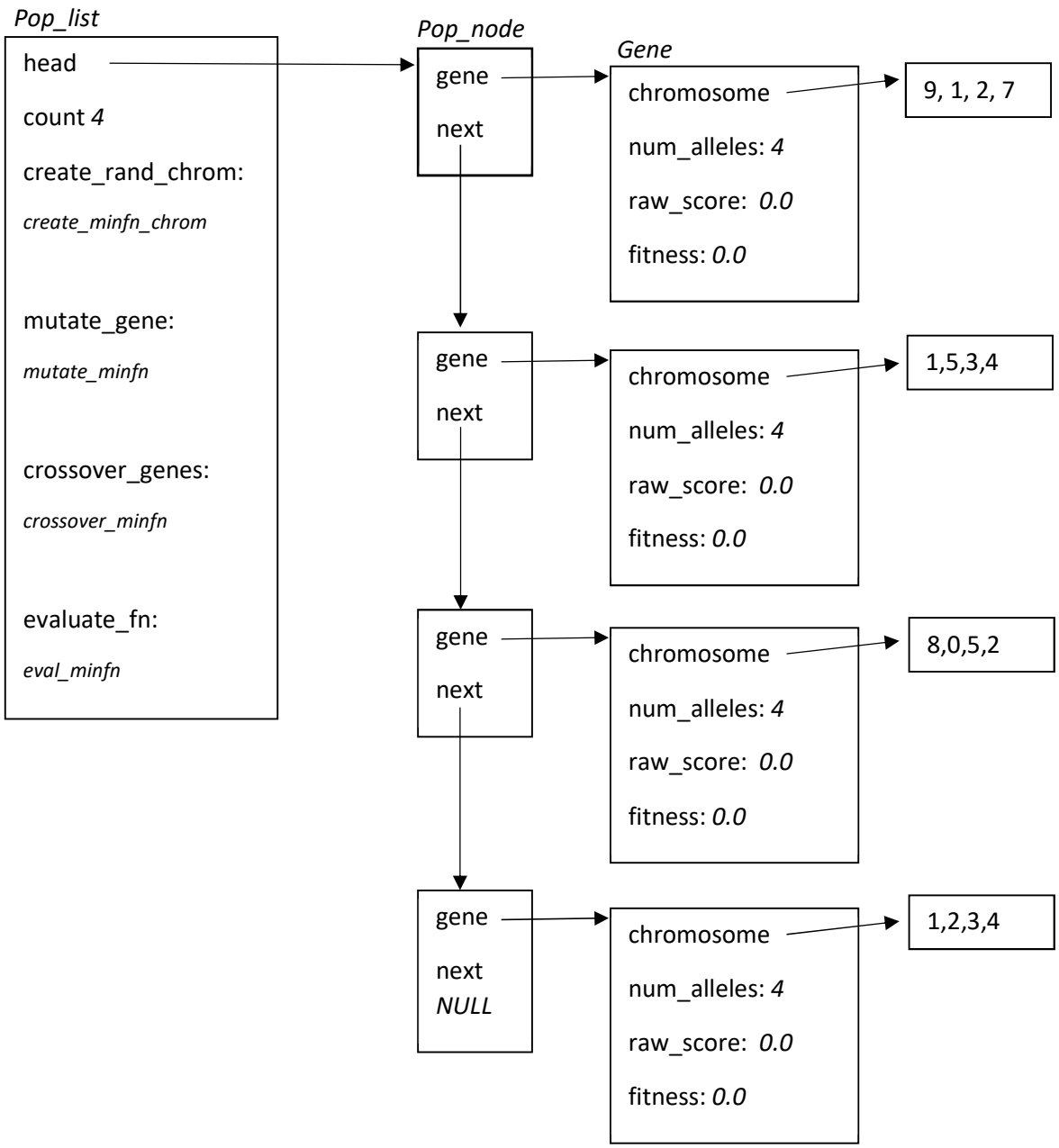
A small (very small!) population of minfn genes:



InVTable

0	1	3	4	2	40
1	…	…	…	…	…
…	…	…	…	…	…
49	…	…	…	…	…

The invector of (1,3,4,2,40) means the minfn equation is: 1a + 3b + 4c + 2d = 40. As described in the minfn specification document, the raw score calculation would be: abs(1a + 3b + 4c + 2d - 40).

Taking the first gene (9,1,2,7), the raw score would be: abs(1 * 9 + 3 * 1 + 4 * 2 + 2 * 7 – 40) = 6.

Similarly, the raw score for gene (1,5,3,4) is 4, for (8,0,5,2) is 8 and for (1,2,3,4) is 13. As described in the GAPrimer, fitness is initially calculated as 1/(rawScore + 1), giving initial fitness values of 0.143 for gene (9,1,2,7), 0.200 for (1,5,3,4), 0.111 for (8,0,5,2) and 0.071 for (1,2,3,4). The total of the initial fitness values in the population is therefore 0.143 + 0.200 + 0.111 + 0.071 = 0.525

Normalising the fitness scores is just dividing them by the total population fitness, giving 0.143/0.525 = 0.272 for gene (9,1,2,7), 0.381 for (1,5,3,4), 0.211 for (8,0,6,2) and 0.136 for (1,2,3,4). The population is then sorted, with the gene with highest fitness score at the head of the population list. A simple sort such as Bubble Sort would suffice. Instead of re-ørdering the Pop_nodes in the list, it is simpler to just swap which Gene the gene member of a Pop_node points to.

Once the population is sorted, a new population of 'child' genes is created, as described in the GAPrimer – this is a new list of Pop_nodes containing only child genes. Once the new population list is created, the old list is deleted and the Pop_list head member set to point to the new list.