Crann Manual.

Crann: A program for detecting adaptive evolution in protein-coding DNA sequences.

Crann was written by Chris Creevey while working in the lab of James McInerney at the National University of Ireland between 1999 and 2002.

AIM: To detect adaptive evolution in protein-coding genes.

The program Crann has been developed in order to provide fast heuristic methods of detecting adaptive evolution in protein-coding genes. It is important that the user

A short digression into population genetics is now necessary. A small population is usually characterized by frequent extinctions of some lineages and radiations of other lineages – a phenomenon we think of as random genetic drift. A larger population is a more stable entity, with smaller amounts of random genetic drift. In order for an advantageous mutation to become fixed in a population, it is necessary for it to overcome random genetic drift. Darwin summarized his thoughts on natural selecn ihoughts "NTj 50 0 -50 250 586 Tm

connected by a phylogenetic tree. This phylogeny can be divided into two parts, between-species (interspecific) and within-species Ats,

ycur Using our reconstructed phylogeny, we identify all substitutions that occur across the tree and determine ccur

Using a G-test (or Fisher's exact test (Sokal and Rohlf 1981), when numbers are small) we can compare the ratio of RI substitutions to RV substitutions, with the expectation that this ratio is the same as the ratio of SI to SV substitutions (McDonald and Kreitman 1991).

Installing and running Crann

Crann is ave7ablen

Crann in these operating systems, type the command "*./crann*" or "*crann*".

Input files.
Crann requires as input aligned homoligous sequences in fasta format. These sequences must all be contained in a single file. See the section   only on option 1 of the main menu for more details.
It is also possible to input a phylogeny for Crann to use in its execution. In this case the tree must be in phylip format without any branch lengths or distances included. See the section on option 7 of the general options menu for more details.

Output files.
Crann produces several output files, only one of which the user can specify the name. If646 Tm (to) Tj 50757a50 995.21 768 Tm (4 o) Tj 50757e

and Luo (1985) may also be used (see the general options menu). These distances are written to the following files; the Dn distances to 'Dn.dis', the Ds distances to 'Ds.dis' and the value

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In order to give the tree directionality, please define those sequences which form the
outgroup

Sequence numbers, and names as follows
No: 1 Name:  Human
No: 2 Name:  Mouse
No: 3 Name:  chimp
No: 4 Name:  gorilla
No: 5 Name:  dog
No: 6 Name:  cat
No: 7 Name:  cow
No: 8 Name:  horse
No: 9 Name:  sheep
No: 10 Name: goat
No: 11 Name: fox 8 Name:  horse
```

every reconstructed ancestral

This is the size of the section of the sequences that will be used to calculate the pair-wise

Once the user has selected the genetic code being used, Crann re-examines the sequences using the selected genetic code and displays a summary. This is the same type of summary as

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Would you like to compare all sequences in memory,(1) (default)
 Or would you like to hWou8t those sequences not to be included (2) ?

Please seou8t 1 or 2 (1..2)    [1]:
```

If the user confirms that they wish to seou8t sequences not to be

General options 0: Return to main menu.

This option is always the default when the user is at the general options page. Choosing this returns the user to the main menu.

Main Menu, option 8: About Crann.

Choosing this option prints a splash page to the screen with the details of the version and compilation date of the version of Crann being used.