Installing the Staden Package

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1 Introduction

On the accompanying tape you will find executables for one of SunOS 4.x, Sun Solaris 2.x, DEC Ultrix, DEC OSF/1 and Silicon Graphics SGI operating systems. Also there are sources for all the programs in the Staden package. Programs in the package are:

mep and xmep Motif exploration program.

nip and xnip Nucleotide interpretation program.

nipl Nucleotide interpretation program (library). Searches nucleotide libraries for patterns of motifs.

pip and xpip Protein interpretation program.

pipl Protein interpretation program (library). Searches protein libraries for patterns of motifs.

sip and xsip Similarity investigation program.

sipl Similarity investigation program (library). Compares a probe protein or nucleic acid sequence against a library of sequences.

sap and xsap The original sequence assembly program.

bap and xbap Our latest, most advanced sequence assembly program.

dap and xdap An obsolete assembly program, superceded by *bap*.

lip Library interface program.

rep Repeat examination program.

ted X windows utility for displaying and editing fluorescent sequencing machine traces.

splitp1, splitp2 and splitp3 Refer to help/SPLITP.MEM.

sethelp Builds online help files.

gip Gel input program.

convert Converts between *xdap* and *xbap* databases.

cop and cop-bap Checks completed *xdap* and *xbap* databases for editing errors.

trace2seq Extracts sequence from trace files.

getABISampleName Extracts sample names from ABI trace files.

makeSCF Converts existing trace files to the compact SCF format.

alfsplit Splits the Pharmacia A.L.F. gel file into multiple files, one for each sample.

frog Relabels lanes in ABI trace files.

+ numerous scripts (including *squirrel (v1.4)***)**

2 Requirements

You will need a tape drive to read the software off the distribution tape (QIC-150, TK50, or Exabyte). You will also need a large amount of disk storage to accommodate the whole package. For release version-1993.0, requirements were 31Mb (SunOS 4.x), 36Mb (Sun Solaris 2.x) 30Mb (DEC Ultrix) 37Mb (DEC OSF/1) and 27Mb (Silicon Graphics SGI.)

To compile the Staden package you will require:

- An ANSI C compiler.
- A FORTRAN-77 compiler.
- X11 (Release 4 or 5).
- GNU make (except with SunOS and Solaris 2.x.)

3 Installation

To install the package,

1. Create a directory for where you would like the software to be placed. You may have to be superuser to do this.

```
mkdir /home/Staden
```

2. Change to this directory.

```
cd /home/Staden
```

3. Place the tape into the tape unit.

4. Extract the software off the distribution tape (NOTE: the device name may be different on your machine):

```
tar xvf /dev/rst0
```

5. C shell users should set the environment variable **STADENROOT** to be the directory where the package is installed and source the file *staden.login* found there. This is best done by adding lines to their *.login* file:

```
setenv STADENROOT /home/Staden
source $STADENROOT/staden.login
```

   Users of the Bourne shell, sh, should similarly add lines their *.profile* file:

```
STADENROOT=/home/Staden
export STADENROOT
. $STADENROOT/staden.profile
```

   The startup routines set environment variables and modify the shell's search path so that it can find the programs in the Staden Package. When users next log on to the system, they will be able to use the programs.

4 Installation on Unsupported Platforms

Install the software as you would for a supported machine. You will need to remake all executables. The script *Staden_install* can be used to help recompile the package. A large number of assumptions have been made, and you may need to change the makefiles to suit your system.

The sources have been organised into subdirectories of the directory **src**. In **Misc** are routines common to many programs. They should be made first. In **staden** are all the programs of the Staden suite (*mep*, *nip*, *pip*, *sap*, *sip*, *dap*, *gip*, *vep*, *lip* and *rep*) with the exception of *bap*.

Code for our latest sequence assembly program *bap* is in directories **bap** and **bap/osp-bits**. Make the objects in **staden** first, then the ones in **bap/osp-bits**, and finally the ones in **bap**. In **ted** is the trace editing program.

5 Other Software Provided

Other software and scripts can be found in the **alf**, **abi**, **cop**, **getMCH**, **scf**, **frog** and **scripts** directories. Each directory contains documentation describing the programs contained.

Since release version-1993.0 we have distributed the *squirrel (v1.4)* package. Please read the disclaimer that accompanies this software. Additional sources and scripts can be found in **expGetSeq**, **vepe**, **newted** and **squirrel-1.4** directories.

Many scripts (including *squirrel*) and filters were developed at the MRC-LMB for **INTERNAL USE ONLY**. We are aware that people elsewhere will want to develop similar software. We include them in the Staden Package merely as **EXAMPLES** of what has been achieved elsewhere. **THESE SCRIPTS WILL NOT WORK ON YOUR SYSTEM WITHOUT MODIFICATION.**

6 When All Else Fails...

If you have any problems please contact the authors, Rodger Staden (*rs@mrc-lmba.cam.ac.uk)*, Simon Dear (*sd@mrc-lmba.cam.ac.uk)* and James Bonfield (*jkb@mrc-lmba.cam.ac.uk)*, by email or by writing to us at: MRC Laboratory of Molecular Biology, Hills Road, Cambridge, CB2 2QH, U.K. We also welcome general comments on the package.