@AbstractSeqPup is a biological sequence editor and analysis program for Macintosh computers. It includes links to network services and external analysis programs.Features include multiple sequence alignment editor single sequence editor window read and wr several sequence file formats consensus,reverse,complement,degap operations automatic preference saving internet send mail, read mail internet sequence analysis services and more **NOTICE**: This is an early, unfinished version of the program. Expect it to fail in various ways. This release is made available to those who wish to test and comment on its future development. This release will expire on a date indicated in the About dialog.SeqPup is being written by Don Gilbert using DCLAP, a C++ Class Application framework, and founded on the NCBI Toolkit, especially it's Vibrant user-interface section written by Jonathan Kans. DCLAP is based loosely on the MacApp extensible programming framework from Apple Computer.You can obtain updates of this release thru anonymous ftp to ftp.bio.indiana.edu, in folder /molbio/seqpup, as seqpup.hqx (mac), seqpup.zip (mswin), seqpup-sun-sparc.tar.Z (sunos), and perhaps other binaries. There may be additional distribution software, data or information in this /molbio/seqpup folder. See the Readme files in it for details. If you obtain SeqApp thru Internet Gopher (perhaps even using the prior version of SeqApp), you may have skipped much of the messy details of extracting archived Mac files. Most Mac internet gopher clients include automatic un-binhexing from the

archived state. And now SeqApp is in a self-extracting archive file inside of the binhex encoding, which you extract the final application and support files from by double-clicking on.If you obtain this release thru FTP file transfer, you have a binhex encoded archive file. Various Mac utility programs will un-binhex an archive file, including Stuffit and Compact Pro. These are widely available from Mac software archives, user groups, and computing support people. The file SeqApp.Help is a plain text file which may be read from your favorite wordprocessor or from the Edit program in the Apps folder. If you have problems getting SeqApp to launch, and cannot read this help from SeqApp, please read it with another application to help solve the problem.Comments, bug reports and suggestions for new features (see below) may be addressed via e-mail to SeqApp@Bio.Indiana.EduHistorySeqApp was started Sept. 1990 as MacApp sequence editor/analysis platform on which analysis programs from other authors, typically command line w/ weak user interfaces, could be easily incorporated into a useable Mac interface.@SeqApp HelpSeqApp provides a biological sequence editor and related functions, including links to network services and external analysis programs. **********

**** NOTICE **** **** This is an early, unfinished version of the **** program. Expect it to fail in various ways. **** This release made available to those who wish **** to test and comment on its future development. **** **********This program is being written by Don Gilbert. It has already gone thru several changes since its start in September 1990. I don't expect it to mature for another year or two, as my prime programming time is holidays and weekends.Comments, bug reports and suggestions for new features (see below) may be addressed via e-mail to SeqApp@Bio.Indiana.EduWith any bug reports, I would appreciate as much detail as is reasonable without putting you off from making the report. Include description of Mac hardware, system software version. Include copies of data if relevant.If you need to use land mail, send to

Don Gilbert Biocomputing Office, Biology Department
Indiana University, Bloomington, IN 47405 A Gopher-only program called GopherApp (silly name), which is a subset of SeqApp, can be found thru the ftp archive as /util/gopher/gopherapp.hqx, or thru Gopher as "IUBio Software+Data/GopherApp, Mac Gopher client".This SeqApp program is copyrighted 1992 by D.G. Gilbert. It is written with MPW Object Pascal using the MacApp extensible Macintosh programming framework from Apple Computer, which copyrights the MacApp portion.Any external applications that may distributed with SeqApp are copyrighted by their respective authors and subject to distribution provisions as described by those authors. At present this includes ClustalV, by Des Higgins (see :Help:ClustalV.doc), CAP2 by Xiaoqiu Huang (see :Help:CAP2.doc), and BBEdit by Rich Seigel.@InstallingIf you obtain SeqApp thru Internet Gopher (perhaps even using the prior version of SeqApp), you may have skipped much of the messy details of extracting archived Mac files. Most Mac internet gopher clients include automatic un-binhexing from the archived state. And now SeqApp is in a self-extracting archive file inside of the binhex encoding, which you extract the final application and support files from by double-clicking on.If you obtain this release thru FTP file transfer, you have a binhex encoded archive file. Various Mac utility programs will un-binhex an archive file, including Stuffit and Compact Pro. These are widely available from Mac software archives, user groups, and computing support people.

Move this distribution folder and its contents to a Mac of your choice (see below). The file SeqApp Prefs contains some information that will be copied to your System Folder:Preferences: folder when SeqApp first starts up.Launch SeqApp by (a) double clicking it, (b) double clicking a sequence document written by it, (c) [System7] drag a TEXT file with sequence data on top of the application icon or its alias.The files in the folders Tables and Apps should be kept where they are, named as they are, and the file SeqApp.Help should remain where it is for SeqApp to work properly (for now).Verion 1.9a no longer works with Mac SE, nor with System 6 (see Known Bugs below). The last release of SeqApp would work on Mac SE (& by inference Mac Plus, Mac Classic) models, as well as on Mac SE/30, Mac II, Mac IIci, Mac Quadra & other Mac II models. It should work properly under Mac systems 6 and 7, though it has some features only for sys 7.SeqApp will work best with System 7 (see Child tasks) and with a network connection plus MacTCP software (see Internet). It does not require these outside of their specific functions.Color macs will find colored nucleotides a boon for aligning, but color is not required.@ViewsThere are now four main types of views or displays in SeqApp:A multiple-sequence view which is the primary display when you open a sequence document; the single sequence editting view; various print views which result from an analysis, like the Restriction map; and dialog views where you control some function.Many of these views have dialog controls -- push buttons, check boxes, radio controls and edittable text items -- to let you fine-tune a view to fit your preference. Many of these views also will remember your last preferences.When a view has edittable text items, including the sequence entry views, most usual Mac undo/cut/copy/paste features will work, as will font, size and style controls. Two or more views of the same data are possible. Some of these are truly views of the same data -- changes made in one view are reflected in another. Other views are static pictures taken of the data at the time the analysis was performed -- later changes to the data do not affect that picture.@@Aligned multi-sequence viewThe main view into a sequence document is the multiple sequence editor window, which lists sequence names to the left and sequence bases as one line that can be scrolled thru. Bases can be colored (now only nucleic colorings) or black. Sequence can be editted here, especially to align them, and subranges and subgroupings can be selected for further operations or analysis. Entire sequence(s) can be cut/copied/pasted by selecting the left name(s). Mouse-down selects one. Shift-mouse down selects many in group,

Command-mouse down selects many unconnected. Double click name to open single sequence view. Select name, then grab and move up or down to relocate.Select the lock/unlock button at the view top to lock/unlock text editting in the sequence line. With lock on (no editting) you can use shift and command mouse to select a subrange of sequences to operate on.Bases can be slid to left and right, like beads on an abacus, when the edit lock is On (now default). Select a base or group of bases (over one or several sequences), using mouse, shift+mouse, option+mouse, command+mouse. Then grab selected bases with mouse (mouse up, then mouse down on selection), and slide to left or right. Indels "-" or spacing on ends "." will be added and squeezed out as needed to slide the bases. See also the "Degap" menu selection to remove all gaps thus entered from a sequence.@@Single sequence viewFor entering/editting a single sequence, this view displays one sequence with more info and control. Edit the name here (later other documentation). Bring out this view by double-clicking sequence name in align view, or choosing Edit from Sequence menu.@@Print viewsVarious analyses provide non-editable displays. These are usually save-able as PICT format for editting in your favorite MacDraw program, or print-able.@Data filesSeqApp uses plain TEXT type files for its primary sequence data. These files can be exchanged without modification with many other sequence analysis programs. SeqApp automatically determines the sequence format of a data file when openning it. You have an choice of several formats to save it as. As of this writing, the GenBank format is prefered (see bugs).The program looks in the folder "Tables" for text files containing various data. At present these files include "Codon.Table" and "REnzyme.Table".There is a "SeqApp Prefs" file which stores various user options like window positions, mail address, child tasks. This automatically generated by SeqApp. It goes in a System Folder:Preferences: folder. Various temporary files are created for child tasks, generally in the :Apps: folder. Currently you cannot run the Child Tasks portion of SeqApp from a locked file server because these temporary files need to be created where the child applications reside. Otherwise, SeqApp should operate from a locked fileserver properly, and can be launched by several users at once.@@Restriction Enzyme TableThe file called "REnzyme.Table" contains restriction enzyme data, as distributed in REBASE by R.Roberts. The format used is identical to that used by GCG software.

{ documentation ...}

Commercial sources of restriction enzymes are abbreviated as follows: A Amersham (12/91) B BRL (6/91) ... X New York Biolabs (4/91) Y P.C. Bio (9/91).. {< separates data};AatI 3 AGG'CCT 0 ! Eco147I,StuI >OUAatII 5 G_ACGT'C -4 ! >EJLMNOPRSUVXAccI 2 GT'mk_AC 2 ! >ABDEIJKLMNOPQRSUVXY;AccII 2 CG'CG 0 ! Bsp50I,BstUI,MvnI,ThaI >DEJKQVXY;AccIII 1 T'CCGG_A 4 ! BseAI,BsiMI,Bsp13I,BspEI,Kpn2I,MroI >DEJKQRVY;Acc65I 1 G'GTAC_C 4 ! Asp718I,KpnI >DFNY@@Codon TableThe file called "Codon.Table" in folder "Tables" is used for translation of nucleic to protein sequence, and for backtranslation. This file may be replaced with a table of your choice in the following format (this format is identical to that used by GCG software codon tables). { any documentation... }AmAcid Codon Number /1000 Fraction .. {< data separator}Gly GGG 1743.00 9.38 0.13Gly GGA 1290.00 6.94 0.09... { continue for 64 codons }@FeaturesThe following topics describe main features found in the SeqApp menus.@@File **New** will create an align view of sequence data. New Text will create a plain text document, which is the format of the sequence data files also. **Open** will open an exising file. The default choice will open a file of sequences into a new window. You can choose “Sequence, append”, or hold down the SHIFT key, to open a sequence file and append it to an existing alignment window.Other **Open** options include opening a plain text file, a file of phylogeny trees in Newick format (see Phylip documentation), or a Gopher document.**Save**, Save as, Save a copy in, all will save the current document to disk files. Revert will restore the open align view to the last version saved to disk.**Save selection**, Saves only highlighted sequences to a new disk file. Doesn’t affect save status of current full alignment document.**Print** setup, print will print the current view.**Help** brings up a view to page thru the help file.

Preferences will set some user preferences. @@Editing**Undo**, **cut**, **copy**, **paste**, **clear**, **select all** -- these standard mac commands will operate on text as well as on sequences in (hopefully) intuitive, usual ways.**Find**, Find same, Find "selection" will search for strings in text.**Replace**, replace same will replace target strings (not yet enabled).@@Text stylingIn most of the edittable text windows (single sequence editor, plain text windows, mail, and such) you can specify text styles, fonts, sizes. These styles are not currently saved.@@Sequence manipulations**New sequence** -- append a new, blank sequence to the sequence document.**Edit** -- open single sequence editting view for selected items.**Reverse**, **Complement**, **Rev-complement** -- Reverse, complement or reverse+complement a sequence. Works on one or more sequences, and the selected subrange.**Rna-Dna,Dna-Rna** -- Convert dna to rna (t->u) and vice versa. Works on one or more sequences, and the selected subrange.**Degap** -- remove alignment gaps “~”. Works on one or more sequences, and the selected subrange. Gaps of “-” are locked and not affected by Degap. Works on one or more sequences, and the selected subrange.**Lock Indel & Unlock Indel** -- Convert from unlocked gaps “~”, to locked gaps “-”. Unlocked gaps will disappear and appear as needed as you slide bases left and right. Locked gaps are not affected by sliding nor by Degap. Works on one or more sequences, and the selected subrange.**Consensus** -- generate a consensus sequence of the selected sequences.**Translate** -- translate to/from amino acid. Relies on Codon.Table data.**Pretty print** -- a prettier view of a single or aligned sequences. Use these views to print your sequences. Printing from the editing display will not be supported fully, and may not print all of your sequence(s).**Restriction map** -- Restriction enzyme cut points of selected sequence. Also protein translation options.**Dotty plot** -- provide a dot plot comparison of two sequences.

Nucleic, amino codes -- These provide both reminders of the base codes, and a way to select colors to assocate with each code (new in v 1.9a). See below for some discussion of the two “aa-color” documents that now ship with SeqApp. Don Gilbert (gilbertd@sunflower.bio.indiana.edu) wrote:> If someone will suggest what colors should be associated with> what amino acids for an editor display I will put it into> a coming release of seqapp. At some point I'll make it> user-definable, but give me a starting selection.From ahouse@hydra.rose.brandeis.edu Fri May 28 19:06:00 1993Received: from hydra.rose.brandeis.edu (hydra.cc.brandeis.edu) by sunflower.bio.indiana.edu (4.1/9.7jsm) id AA20246; Fri, 28 May 93 19:05:58 ESTReceived: by hydra.rose.brandeis.edu (5.57/Ultrix3.0-C) id AA03670; Fri, 28 May 93 20:09:01 -0400Message-Id: <9305290009.AA03670@hydra.rose.brandeis.edu>Date: Fri, 28 May 1993 20:07:26 -0500To: SeqApp@bio.indiana.eduFrom: ahouse@hydra.rose.brandeis.edu (Jeremy John Ahouse)Subject: implemented aa colors for pre-rel seqAppCc: plc@med.unc.edu (Philip L. Carl), ahouse@hydra.rose.brandeis.eduX-Attachments: :Science:559:nuc acid colors.mod:Status: R

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Don Gilbert (& Phil Carl),        I have implemented Phil Carl's(*) modest proposal.Some of the suggestions were not possible, so I made changes.        Jeremy AhousePhil's suggestion is interspersed with my additions:Well, I have (as they say) a modest suggestion.  I suppose what peopleare really seeking are 20 colors for 20 amino acids.  I have a preliminaryproposal based on classifying the amino acids into chemical groups andfinding what seems to me to be easy pneumonics for each group.  ThusI would propose:Red for acidic amino acids; Glu, Asp (since red is a common danger signal and acids are dangerous(well maybe not amino acids, but it's a start))hue:        65500
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saturation: 65000brightness: 50000Blue for basic amino acids; Lys, Arg, His(blue and basic both start with "b")hue: 44000saturation: 65000brightness: 50000White for hydroxyl amino acids; Ser, Thr (as in whitewater) (this was not possible so I chose a cool "whitewater" color)hue: 33000saturation: 65000brightness: 50000Green for amide amino acids; Asn and Gln (since glutamine and asparagine rhyme with green)hue: 22000saturation: 65000brightness: 50000Yellow for sulphur amino acids; Cys, Met(this one's obvious)hue: 12000saturation: 65000brightness: 60000Black for hydrophobic amino acids; Ala, Val, Leu, Ile(Black is the opposite of white and so if white is for hydrophilichydroxyl amino acids black is a natural for hydrophobic ones)hue: 00000saturation: 00000brightness: 00000Orange for aromatic amino acids; Tyr, Phe, Trp (since "orange" sounds a little like "aromatic" and oranges are aromatic (if that suits you better))hue: 7000saturation: 65000brightness: 60000Purple for proline; Pro(since both have "prl" in them)hue: 51000saturation: 65000brightness: 60000Grey for glycine; Gly(since both start with "g" and grey is sort of blah-like glycine)hue: 00000saturation: 00000brightness: 30000*Phil CarlAssoc. DirectorProgram in Molecular Biology and BiotechnologyUniversity of North Carolina, Chapel Hill==========From Heikki.Lehvaslaiho@cc.helsinki.fi Mon Jun 7 07:49:07 1993Received: from kruuna.helsinki.fi by sunflower.bio.indiana.edu (4.1/9.7jsm) id AA23282; Mon, 7 Jun 93 07:49:04 ESTReceived: from [128.214.99.33] (MeikkuMac1.pc.Helsinki.FI) by kruuna.helsinki.fi with SMTP id AA10914

(5.65c8/IDA-1.4.4 for <SeqApp@Bio.Indiana.Edu>); Mon, 7 Jun 1993 15:49:08 +0300Message-Id: <199306071249.AA10914@kruuna.helsinki.fi>Date: Mon, 7 Jun 1993 15:50:09 +0200To: SeqApp@Bio.Indiana.EduFrom: Heikki.Lehvaslaiho@Helsinki.FI (Heikki Lehvaslaiho)X-Sender: lehvasla@kruuna.helsinki.fiSubject: aa colorsX-Attachments: :Tuma:36142:GDE aa-colors:Status: RHi,I am including a file with amino acid color codes that are used in StevenSmith's GDE. This scheme was not mentioned in the Usernet discussion, butI've grown accustomed to it. At least, it is no worse that any other of themyriad possible coloring choices.If you haven't got other schemes in files yet, drop me a note and I'll seewhat I can do. GDE

```
aa-colors:                          2 4 - b i t               M a cCOLOR
AA      R       G       B       R       G
B-------------------------------------------------------------------Magenta
AGPST   255     000     255     65535   0       65535Black           BDENQZ  000
000     000Red             C       225     000     000     57600   0       0Blue
FWY     000     000     255     0       65535   65535Light blue      HKR     000
192     192     0       49344   49344Green           ILMV    000     192     000     0
49344   0Gray            JOUX    145     145     145     37265   37265   37265
      -HeikkiHeikki Lehv{slaiho
<Heikki.Lehvaslaiho@Helsinki.FI>Bitnet:lehvasla@finuh.bitnetX.400:
/G=Heikki/S=Lehvaslaiho/O=Helsinki/ADMD=fumail/C=fi/Meilahti Medical Departments,
P.O.BOX 21 (Haartmaninkatu 3)SF-00014 University of Helsinki, FINLANDPhone: +358-0-434
6408         FAX: +358-0-434 6491
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@@InternetThe Internet features of SeqApp let you interchange ideas and data with people and biocomputing services around the world. If your Mac is connected already to the Internet, you probably are familiar with electronic mail and some of its uses. SeqApp includes a selection of network access features in the developing area of networked biocomputing. You will find access to me, at least to get comments and bug reports to me, very easy. There is a feature to send and receive e-mail, as well as mail links to customized e-mail services. These include searching for sequence similarity via

BLAST and FastA programs on the Genbank/Intelligenetics computers, fetching sequences, data and software from Genbank and EMBL.There is now an feature called Gopher, which gives you access to a wide range of information services now developing on the Internet. Gopher is something like Telnet or FTP (file transfer), but also different. It includes some of the keyword searching features of WAIS (Wide Area Information Services). There are currently several biology gopher services found around the globe. These include fast and up-to-date keyword searches of GenBank, EMBL, PIR and other important biology databanks.**NOTE**: Several people write to me asking for help configuring SeqApp for email use. This is often site-specific, and I can't help too much. Especially if your site doesn't support POP mail, then please just ignore the POP mail reading feature of SeqApp. It is not required for sending mail nor other features, and it is only poorly developed. You are in general much better off using some other mail reading service than what is in SeqApp. I may even remove the POP portion from SeqApp (does anyone use it regularly now? would you really miss it?).If you have problems in general with SeqApp network functions, make sure that other MacTCP-based applications work on your computer before reporting the problem to me. You may need to work with computer support people at your site to iron out general problems with MacTCP applications (including NCSA Telnet, TurboGopher, Fetch, Eudora e-mail, and various commercial TCP applications).@@@Mail PreferencesThe mail prefs dialog asks for your return e-mail address, your preferred SMTP mail host, and your POP mail address and password. These addresses may be similar. Return e-mail address: This is where another person should send mail so it will reach you.

Example: Bob.Jones@Bio.Indiana.Edu or: bjones@sunflower.bio.indiana.edu SMTP Mail host: This is the internet address of the computer thru which SeqApp will send out mail to the rest of the world.

Example: Sunflower.Bio.Indiana.Edu

@@@Send MailSend an electronic mail message. You must enter an address to send to, and have entered your return address in the mail preferences dialog.**NOTE**: Network status information is displayed in the top line of the current Gopher window. If a network connection seems to be frozen, or if a file you are fetching seems too big, you can frequently halt the transfer with a COMMAND-PERIOD keypress combination, as is standard for other Mac applications.As of release 1.8a, the Gopher client is stable and usable.

@Mail-based Search and FetchVarious network resources provide biocomputing services thru e-mail. These include retreiving sequence entries from the various databanks (GenBank, EMBL, PIR), fetching help documents, and searching for sequences in the databanks that match your query sequences.

@BugsVersion 1.9a involved major amounts of rewriting of the underlying program code, without as many improvements as I would have liked. This major rewrite was prompted by the move from Apple's extensible macintosh application framework, MacApp version 2 to version 3. The move was needed because MacApp 2 is essentially obsolete. New general application features are found in MacApp version 3, a few of which you may notice. Also, this is preliminary to translating the code from the Object Pascal language into the C++ language. The future of MacApp is to move to a computer-make independent application framework called Bedrock, which may be available in 1994 for Mac, Windows, and possibly Unix systems. It is my hope to move SeqApp onto this, but I make no promises or predictions at this time.There are still several known bugs, and probably some unknown bugs lurking in this release. A prime rule in using this software is to be aware of its incomplete nature, and **save early and often**. While the move to MacApp 3 fixed some bugs inherent in MacApp 2, it also generated some new bugs where my code didn't jive with the changes and I couldn't find the incompatibility in time to release this update. Some of these new known bugs that remain in this release of SeqApp are listed below.If SeqApp freezes or fails under System 7, you may be able to abort it without rebooting your machine or hurting other active programs. Try this magic key sequence: command-option-escape keys, pressed togetherwhich should force SeqApp or whatever application is frontmost to quit.Please also send in detailed descriptions of bugs you find. If the bug seems to be erratic, as many are, try to find some circumstances which will cause it to appear repeatable and explain these to me. Your reports will help improve this program for you and others. E-mail bug reports to SeqApp@Bio.Indiana.Edu

@HistorySeqApp was started Sept. 1990 as MacApp sequence editor/analysis platform on which analysis programs from other authors, typically command line w/ weak user interfaces, could be easily incorporated into a useable Mac interface.March 1994, version -1. First public release of SeqPup, the platform-independent version derived from the earlier Macintosh SeqApp. SeqPup will eventually include most or all of SeqApp's features, and new features will be added. 20 June 93, version 1.9a162 -- a minor update, with these bug fixes since last release: -- fixed base number index in align view to correctly index the bases. Also fixed base number index scrolling link to sequence scrolling. -- fixed paste of align sequence into blank window to correctly update full width of display.12+ June 93, version 1.9a157+ -- a semi-major update, and time extension release with various enhancements and corrections. These include -- lock/unlock indels (alignment gaps). Useful when sliding bases around during hand alignment, to keep alignment fixed in some sections. -- color amino (and nucleic) acids of your choice. -- added support for more sequence file formats: MSF, PAUP, PIR. SeqApp now relies on the current Readseq code for sequence reading & writing. -- save selection option to save subset of bases to file. -- addition the useful contig assembly program CAP, written by Xiaoqiu Huang. -- major revision of preference saving method (less buggy, I hope) -- major revision of the underlying application framework, due to moving from MacApp 2 to MacApp 3. -- fixed a bug that caused loss of data when alignment with a selection was saved to disk.5 Oct 92, version 1.8a152+ -- a semi-major update with various enhancements and corrections. These include - corrections to the main alignment display, - improvements to the help system, - major changes to the sequence print-out options, -- including addition of a dotplot display (curtesy of DottyPlot), -- a phylogeny tree display (curtesy of TreeDraw Deck & J. Felsenstein's DrawTree), -- improved Pretty Print, which now has a single sequence form and a better aligned sequence form, -- improved Restriction map display, - addition and updating of several e-mail service links, -- including Blast Search and Genbank Fetch via NCBI,-- BLOCKS, Genmark, and Pythia services,- updated Internet gopher client (equal to GopherApp),- editable Child Tasks dialogs- addition of links to Phylip applications as Child Tasks- addition of Phylip interleaved format as sequence output option11 June 92, version 1.6a35 is primarily a bug fix release. Several of the disasterous bugs have been squashed. This version now works on the Mac SE model, except for sendmail. No new features have been added.

7Jun92, v. 1.5a?? -- fixed several of the causes of mysterious bombs (mostly uninitialized handles), link b/n multiseq and 1-seq views is better now, folded in GopherApp updates, death date moved to Jan 93, 25Mar92, v1.5a32 (or later). First release to general public. Includes Internet Gopher client. Also released subset as GopherApp for non-biologists.4Mar92, v 1.4a38 -- added base sliding in align view. Bases now slide something like beads on an abucus. Select a section with mouse, then grab section and shift left or right. Gaps are inserted/removed as needed. For use as contig aligner, still needs equivalent of GCG GelOverlap to automatically find contig/fragment overlaps.Also added "Degap" menu item, to remove "." and "-". Fixed several small bugs including Align pretty print which again should display.2Mar92, v 1.4a19 -- fixed several annoying bugs, see SeqApp.Help, section on bugs for their resolution. These include Complement/Reverse/Dna2Rna/ Translation which should work now in align view; Consensus menu item; entering sequence in align window now doesn't freeze after 30+ bases; pearson/fasta format reading; ...10Feb92, v 1.4a6 -- fix for Mac System 6; add Internet service dialogs for Univ. Houston gene-server, Geneid @ BU, Grail @ ORNL; correct About Clustalv attribution.5Feb92, v 1.4a4 -- limited release to network resource managers, clustalv authors, testers.Vers 1.4, Dec91 - Feb92. Dropped multi-sequence picker window, made multi-align window the primary view (no need for both; extra confusion for users). added pretty print, restriction map, sequence conversions. Generalized "call clustal" to Hypercard-like, System 7 aware menu for calling external tasks. Fleshed out internet e-mail objects, added help objects, window menu, nucleic/amino help windows. Many major/minor revisions to all aspects to clean out bugs. Preliminary release to a limited set of testers (1.4a?)Vers. 1.3, Sept - Dec91. Modified clustalv for use as external app (commandline file, background task, ...). Added basic Internet e-mail routines call clustal routine (preliminary child task) Many major/minor revisions to all aspects to clean out bugs. Jun91-Aug91: overwork at other tasks kept SeqApp on back burner.Mar91-Jun91: not much work on SeqApp, fleshed out TCP methods (UTCP, USMTP, UPOP).Feb 1991, vers 1.2? made available to Indiana University biologists and NCBI biocomputists.Vers. 1.1, Oct 1990, multiple sequence picker and multiple sequence alignement window, including colored bases, added to deal with alignment and common multi-sequence file formats.Version 1, Sep 1990. Single sequence edit window + TextEdit window, from MacApp skeleton/example source + readseq.

NOTE: The Tasks menu requires Macintosh System 7 to operate.@@Example Child task: BBEditA simple child application is BBEdit, which is a useful plain text editor that surpasses the 32,000 character limit for text files which encumbers the current SeqApp.A suggested SeqApp configuration to run BBEdit is as follows: Choose Add Child Task from Tasks menu. Provide the App name as the full path and name to the BBEditprogram, e.g., :Apps:BBEdit Provide a description of the program, e.g., A simple text editor. Provide a menu name, e.g., Text edit... Name the input files relative to where SeqApp is located. This should usually be in the same folder as the application. There is no command file for BBEdit. Erase the default command name.

Provide an input sequence file name, e.g., :Apps:Edit-tmp.seq

Specify the minimum number of selected sequences that the child task requires, e.g., 0 for Edit Name the child task output files relative to where SeqApp is, and whether they should be opened as sequence or text files. Only one output file from Edit is edited input file, e.g., :Apps:Edit-tmp.seqWhen the new child app is configured, click the Okay button. The configuration is saved in SeqApp Preferences, and installed in the Tasks menu. To run this newly configured task, select sequences from the Alignment editor, then select the task from the Task menu.Select Remove Child Task menu item to remove a task. @@Example Child task: ClustalV

ClustalV is a multiple sequence alignment program written by Des Higgens and colleagues.A suggested SeqApp configuration to run ClustalV is as follows:

Choose Add Child Task from Tasks menu. Provide the App name as the full path and name to the ClustalV program, e.g., :Apps:ClustalV

Provide a description of the program, e.g., A multiple sequence alignment application. Provide a menu name, e.g.,

Multiple align... Name the input files relative to where SeqApp is located. This should usually be in the same folder as the application. Provide the correct command file name, e.g., :Apps:ClustalV.commands Enter the command line text, with file names relative to where the child task is located, e.g., -infile=Clustal-tmp.inseq -output=pir -align -maxn=30 (the -infile, -output, and -align command switches are discussed below. -maxn is a temporary addition by this author to specify max # species) This command file name is currently hard-coded into the ClustalV program (as modified by the author); the command-line inputs that drive the program are taken from a file called "clustalv.commands" in the same folder as ClustalV. Provide an input sequence file name, e.g.,

:Apps:Clustal-tmp.inseq Specify the sequence file format, e.g.,

NBRF Specify the minimum number of selected sequences that the child task requires, e.g., 2 for ClustalV Name the child task output files relative to where SeqApp is, and whether they should be openned as sequence or text files. One output file from ClustalV is the aligned sequences, in pir format. ClustalV automatically names it as "infile-prefix".pir, e.g., :Apps:Clustal-tmp.pir

A second output file from ClustalV is a dendrogram. ClustalV names this as "infile-prefix".dnd, e.g., :Apps:Clustal-tmp.dnd When the new child app is configured, click the Okay button. The configuration is saved in SeqApp Preferences, and installed in the Tasks menu. To run this newly configured

task, select sequences from the Alignment editor, then select the task from the Task menu.Select Remove Child Task menu item to remove a task. @@Example Child task: CAP contig alignmentThis program will automatically align gel fragments by sliding the sequences to find best matching regions. Gaps are not introduced within a sequence.A suggested SeqApp configuration to run CAP is as follows: Choose Add Child Task from Tasks menu. Provide the App name as the full path and name to the CAP program, e.g., :Apps:CAP2 Provide a description of the program, e.g., A gel contig assembly application.

Provide a menu name, e.g., Contig align... Name the input files relative to where SeqApp is located. This should usually be in the same folder as the application. Provide the correct command file name, e.g.,

:Apps:CAP2.commands Enter the command line text, which for CAP includes input and output sequence files, and two numbers: minimum # bases to overlap, and percent matches, e.g., CAP2-tmp.inseq CAP2-tmp.outseq 20 85 You can run CAP interactively and find out more about it, or see CAP2.doc for help. The command file name is hard-coded into the CAP2 program. The command-line inputs that drive the program are taken from a file called "CAP2.commands" in the same folder as CAP2. Provide an input sequence file name, e.g.,

:Apps:CAP2-tmp.inseq Specify the sequence file format. This must be pearson/fasta. e.g., Pearson/Fasta Specify the minimum number of selected sequences that the child task requires, e.g., 2 for CAP

Name the child task output files relative to where SeqApp is, and whether they should be opened as sequence or text files. One output file from FragAlign is the aligned sequences. The command line option tells FragAlign the name of the output file, e.g., :Apps:CAP2-tmp.outseq

When the new child app is configured, click the Okay button. The configuration is saved in SeqApp Preferences, and installed in the Tasks menu. To run this newly configured task, select sequences from the Alignment editor, then select the task from the Task menu.Select Remove Child Task menu item to remove a task.