BioDesign Software Release Notes
Version 2.2

These notes summarize the changes made to BIOGRAF, POLYGRAF, and NMRgraf in version 2.2. The notes are divided into four sections. The first section describes new hardware supported. Section II outlines the use of the Dreiding-II force field which is now the default parameter set. The third section itemizes the major enhancements to the program, and Section IV contains notes about the operation of the programs and the capabilities of certain computers and workstations. In addition, this release includes fixes for many bugs reported since the 2.1 release.

If you have difficulties with the installation of this release or questions about it, BioDesign Customer Support can provide assistance. Our Customer Support Hotline is 818-793-3756 (FAX: 818-793-8098).

I. New Hardware Supported

The 2.2 release now supports the IBM RISC System/6000 platforms and the Stardent Titan P3 processor. The table in Section IV lists the operating systems used to build the 2.2 release on each of the platforms.

II. Dreiding-II Force Field

A paper describing the Dreiding-II force field has been accepted for publication in *J. Phys. Chem.* and is currently in press.[1] The abstract of the paper is presented in Appendix L of the *BIOGRAF Reference Manual*. Dreiding-II represents a significant advance in the quality of the Dreiding force field. The concepts of the Dreiding force field have been extended to a wider range of element types (B, Ga, Ge, As, Se, In, Sn, Sb, Te, I) and additional rules have been devised to improve the generality and accuracy of the force field. Dreiding-II is now used as the default parameter set.

The purpose of this section is to provide an overview for using Dreiding-II for mechanics and dynamics calculations. It is not intended to provide the detailed account of the development of Dreiding-II which is covered in the Dreiding paper. With this in mind there are several items that need to be addressed: Dreiding-II atom types, hydrogen-bond parameters, and parameter file size.

The atom types in Dreiding-II are the same as those in Dreiding-I with two significant exceptions. The first is for the new atom types added to Dreiding-II that do not exist in Dreiding-I. Obviously if these atom types are used in a Dreiding-II calculation, then it will be difficult to go back to Dreiding-I. The second exception is for the atom types of hetero-atoms with implicit hydrogens. Dreiding-II does not contain unique atom types of this sort; however, to facilitate the transfer from Dreiding-I, the Dreiding-II parameter set contains "place holder" atom types that have names identical to the corresponding atom types in Dreiding-I. The "place holder" atom types behave exactly like non-implicit hydrogen atom types when run in Dreiding-II. For example, a molecule created

[1] S. L. Mayo, B. D. Olafson and W. A. Goddard III, *J. Phys. Chem.*, (in press).

ANALYZE

Several new functions have been added to the ANALYZE menu.

VOLUMES (BIOGRAF and POLYGRAF only): A VOLUMES option is now available for measuring and displaying molecular volumes and surface areas. Common, residual, inverse, or unified volumes for several molecules may also be computed and displayed. The free volume (unoccupied space) may be determined for periodic systems. This can be helpful in predicting physical properties of polymers such as rigidity, gas permeability, and weight. Included vs excluded volumes may be computed and displayed, a feature which can be useful in receptor site mapping. VOLUMES is described in Section 6.6 of the *BIOGRAF Reference Manual* and in Section 3.3 of the *POLYGRAF Reference Manual.*

PROTEIN (BIOGRAF and NMRgraf only): A PROTEIN analysis feature has also been added which checks proteins for irregular structural features including D-amino acids, *cis*-peptides, and non-Ramachandran phi and psi angles. The dihedral angle values for disulfide linkages can also be determined. This option is described in Section 6.7 of the *BIOGRAF Reference Manual.*

POLYMER (POLYGRAF only): A POLYMER analysis feature has been added which allows the user to measure end-to-end distance, radius of gyration, cell volume, and density for selected structures. This is done using the SIZE option. Bar plots showing the distribution of states for every unique torsion angle may also be made using the STATES option. See POLYMER in Section 3.1 of the *POLYGRAF Reference Manual.*

TRAJECT: The TRAJECT function allows the user to make two-dimensional or three-dimensional plots from data in trajectory files. Color-coding of an additional variable may also be used in conjunction with the 2-D or 3-D plots. Data from any trajectory variable (time, energy terms, geometric measurements such as distances, angles, and dihedrals) can be plotted against any other, or against data from an outside database (via the MERGE function; see PLOT below). The user may select any point on the plot and have the values for that point displayed. The structure associated with a selected point may also be displayed and saved for further analysis. The TRAJECT functions are described in Section 6.8 of the *BIOGRAF Reference Manual.*

PLOT (BIOGRAF and POLYGRAF only): A new PLOT option has been added which allows the user to display a plot, change its appearance, or merge its data with the data from another plot file. The merge function also allows simple arithmetic operations to be performed on data common to both files. As with the TRAJECT option, the plots can be 2-D or 3-D, and include a color-coded variable if desired. Plot files which can be used include those generated using conformational search, trajectory analysis, and polymer analysis. However, any plot file, including those from an outside database, can be used, provided it meets the format requirements. Contour plots may also be created from conformational search data. PLOT is described in Section 6.9 of the *BIOGRAF Reference Manual.*

Plot File Format: A new plot file format is now used in place of the potential energy surface (*pes*) file format. Plot files can be generated from conformational search, trajectory analysis, and polymer analysis data. The extension used for plot files is *plot.*

ENERGY

Monte Carlo Search: A new Monte Carlo search feature has been added which generates random conformations of molecules by applying random rotations to a molecule's rotatable bonds. It differs from the SEARCH option accessed under ENERGY in that *all* the rotatable bonds are varied (instead of selected dihedrals). It also allows torsions contained within rings to be searched and uses bump checking to reject conformations with atoms that are too close together. See M CARLO in Section 12.13 of the *BIOGRAF Reference Manual.*

Enhanced Conformational Search: The SEARCH function has been improved so that the dihedral angles being examined during a sequential search may now be constrained to a specified value during subsequent energy minimizations. The ability to fix the dihedrals during minimization provides improved speed and yields a more accurate portrayal of the impact of the conformational change. A DRAW ON/OFF switch has also been added so that the user can turn off the display of the conformations generated during the search and thus speed up the process. See CNSTRN ON/OFF Section 12.8.10 and DRAW ON/OFF, Section 12.8.3 of the *BIOGRAF Reference Manual.*

Search Plots: The potential energy surface for sequential searches varying one or two dihedral angles can now be saved as plot files. These plot files can then be read in and displayed as plots of the dihedral angles and the total energy. Plots of two dihedral angles are displayed as contour plots. Note that one can use these features to generate and display Ramachandran plots. This is done using READ PLOT (which has replaced READ PES) on the SEARCH menu. See READ PLOT in Section 12.8.12 of the *BIOGRAF Reference Manual.*

Restart Dynamics: A new option has been added to all the DYNAMICS menus which allows the user to add information to the end of an existing trajectory file and to restart dynamics calculations using the last set of velocities as starting velocities (rather than having the starting velocities be assigned randomly). This is equivalent to a continuous run. See APPND TRJ in Section 12.6.1 of the *BIOGRAF Reference Manual.*

Using Extracted Velocities: The velocities for an extracted conformation may now be assigned as starting velocities for the next dynamics run (instead of using randomly assigned velocities). This is done via a new USE VEL option which has been added to all the DYNAMICS menus (except impulse dynamics). See USE VEL in Section 12.6.1 of the *BIOGRAF Reference Manual.*

Constrained Minimization Menu Changes: The POINTS option on the CON MIN menu has been renamed. It is now called NINCRMNT (number of increments); it still functions as before. The E CONVRGE option which was used to set the convergence criterion has been replaced with the MIN VAR option. MIN VAR brings up a new menu which in addition to allowing the user to set the convergence criterion also allows changes in other minimization variables, such as the update frequency and the minimization algorithm. See NINCRMNT, Section 12.7.6 and MIN VAR, Section 12.7.7 in the *BIOGRAF Reference Manual.*

Trajectory File Format Updated: An LDUMMY variable must be included for periodic trajectories; it is reserved for future use and must be set to false. A new parameter (S2RDOT) describing the velocities for cell coordinates has also been added. See Section D.5 of the *BIOGRAF Reference Manual.*

Number of Bonds, Angles, and Torsions Allowed Increased: The maximum number of bonds, angles, and torsions allowed has been increased from 15,000 to 45,000. This will allow more complex simulations.

MATCH

Centroids Matching (BIOGRAF and POLYGRAF only): A CENTROIDS option has been added which does a least squares fit on the geometric centers of mass (centroids) of selected groups of atoms from two structures, thus expanding the matching capabilities beyond those already available for pairs of atoms (PAIRS) and lists of atoms (GROUPS). See CENTROIDS, Section 15.3 of the *BIOGRAF Reference Manual.*

BUILD

Expanded Carbohydrate Library: The Carbohydrate fragment library has been modified and expanded to include a more useful set of monosaccharides. A total of 52 fragments are now available. See Appendix B.6 of the *BIOGRAF Reference Manual.*

Nucleotide Library Renamed: The BIOGRAF library of nucleotide fragments for building single, double and triple strands is now more appropriately called the BioDesign library of nucleotide fragments, as it is available with all BioDesign software products that use the RNA-DNA builder (not just BIOGRAF). "BioDesign" therefore replaces "biograf" as the option which appears on the menu when using READ LIB to read this library in. See READ LIB, Section 19.6.2 in the *BIOGRAF Reference Manual.*

Trim Function Expanded (POLYGRAF only): The TRIM function available under the Periodic Builder now provides two additional functions. Previously, one could delete all atoms which extended outside the unit cell. Now, one may also move extended fragments back inside the unit cell or move whole molecules into the unit cell. These functions are useful in visualizing periodic systems. See TRIM, Section 1.3.4 in the *POLYGRAF Reference Manual*

MISCELLANEOUS

CMND: A new command mode toggle (CMND) has been added to the box in the lower left corner of the display. This allows the user quick and easy access to command mode at any time. Previously, the only access was via the CMND MODE toggle on the UTILITIES menu. See Section 1.9 of the *BIOGRAF Reference Manual.*

SRTN: A new Super Return toggle (SRTN) has also been added to the box in the lower left corner of the display, providing quick and easy access to the entry-level menu. Toggling SRTN immediately returns you to the entry-level menu no matter where you are in the Functions menu tree. See Section 1.7.1 of the *BIOGRAF Reference Manual.*

RIBBONS (BIOGRAF and POLYGRAF only): A RIBBONS option is now available on Silicon Graphics IRIS 4D workstations and IBM RISC System 6000 workstations which is useful in identifying helices and displaying the general folding pattern for proteins, peptides, and polymers. The user may specify the ribbon width, color, and number of threads used. RIBBONS is accessed under the GROUP menu. See Section 3.14 of the *BIOGRAF Reference Manual.*

Vector Width on Titan: Titan users may now specify the width of vectors used to draw lines when rendering structures in VECTOR mode. As with the IRIS and RS6000, this is done using the VEC WIDTH option. See Section 3.10 of the *BIOGRAF Reference Manual.*

Macro and User Files: In addition to data files, macro files and additional user files are now also included with BioDesign software. The macro files contain sample macros which illustrate how to write macros, demonstrate various feature of the program, or extend its capabilities. The user files contain sample subroutines which demonstrate various aspects of the user programming interface or enhance the utility of the program. See Appendix C.2 and C.3 of the *BIOGRAF Reference Manual.*

Auxiliary Programs: Three auxiliary programs are now included with the program which allow users to examine the information in trajectory files and to transfer trajectory files from one kind of computer to another. These are the *rdtrj*, *wrtrj*, and *shtrj* programs. See Appendix N of the *BIOGRAF Reference Manual.*

DOCUMENTATION

RS6000 Updates: The documentation has been updated throughout to incorporate support for the IBM RISC System/6000.

Updating the Nonbond and Hydrogen Bond Lists: The documentation has been modified to state that the nonbond and hydrogen bond lists are automatically updated on a regular basis during *batch* energy calculations (and not during interactive runs). The documentation also points out that during interactive minimizations, these lists are only updated once each time the MINIMIZE toggle is picked, and suggests that it is wise initially to use several short minimization runs so that these lists are updated frequently. Longer runs may be used once the energy change is small and the structure is closer to a local minimum. See NBLIST and HBLIST, Sections 12.5.8 and 12.5.9 in the *BIOGRAF Reference Manual.*

Dynamics Time Step: The default time step on the dynamics variables menu was listed incorrectly as 0.002 picoseconds. This has been corrected to read 0.001 picoseconds. See TIME STEP in Section 12.10.3 of the *BIOGRAF Reference Manual.*

Batch Instructions (BIOGRAF and POLYGRAF only): Instructions on how to set up batch calculations have been expanded and clarified, and differences between running batch on the UNIX and VMS operating systems have been more clearly described. See BATCH, Section 12.14 in the *BIOGRAF Reference Manual.*

Appendix C Renamed: Appendix C has been renamed "Supplementary Files" and in addition to data files, it includes a brief description of the macro files and user files now supplied with the program.

Macro Action Variables: Several of the special "action variables" described in the Appendix on macros have not yet been implemented. The descriptions for these variables have been removed from the documentation. See Appendix K.2.1 of the *BIOGRAF Reference Manual.*

Dreiding Report Replaced with Abstract of Paper: The report on the Dreiding Force Field presented in Appendix L has been replaced with the abstract of the paper on the same subject. See Appendix L of the *BIOGRAF Reference Manual.*

E&S Startup Info Now in Installation Guide: Information on starting up Evans and Sutherland systems previously described in Appendix N of the *BIOGRAF Reference Manual* now appears in Appendix B of the *BioDesign Installation Guide*. Appendix N now describes the auxiliary programs which are shipped with the program (*rdtrj*, *shtrj*, and *wrtrj*).

Installation Guide Renamed, Updated: The *BIOGRAF and POLYGRAF Installation Guide and COMSTRUCT Users Guide* has been renamed the *BioDesign Installation Guide*. It now includes installation instructions for NMRgraf in addition to BIOGRAF and POLYGRAF, and has a new section describing installation on the RS6000. Other changes include the addition of installation verification instructions for all UNIX machines, changes in recommended swap area and disk space to accommodate the new program, and information describing startup on Evans and Sutherland systems.

COMSTRUCT: COMSTRUCT now uses the Dreiding-II force field as the default. See the *BioDesign Installation Guide*, Appendix A.

Programmer's Manual Renamed: The *BIOGRAF and POLYGRAF Programmer's Manual* has been renamed the *BioDesign Programmer's Manual*.

IV. Notes

Operating Systems: BioDesign tracks operating system changes and tests the compatibility of its products with them. However, we only build our products against one version of an operating system at a time. Below is a table summarizing the operating systems used to build the 2.2 release. Detailed system hardware and software requirements may be found in the *BioDesign Installation Guide*.

System	Operating System Used to Build
Alliant FX	4.0.0
DEC VAX	4.7
IBM RISC System/6000	3.1 (with mpp 3001 update)
Silicon Graphics IRIS	3.2.1
Stardent Titan P2	2.2
Stardent Titan P3	3.0.1 RevA*B*
Sun Microsystems Sun-4 and SPARCstation	4.0.1

Installation on the Titan and RS6000: Before running the *verify* procedure, the user must first be in X windows. To start X windows on the Titan, type ***xstart***; on the RS6000, type ***xinit***.

Known Problems with IBM RS6000 Release:

- Window resizing is not supported in this release. However, the initial program window size can be set by changing the parameters XSIZE and YSIZE in the Defaults file. See Section D.9 of the *BIOGRAF Reference Manual.*
- Side-by-side stereo is not supported in this release.
- Occasionally buffering problems cause the display to be temporarily out of synchronization with the current state of the program. This can be fixed by toggling V220 in the box at the lower left of the display.
- Occasionally the red border around the display which indicates atom picking may not appear. This is related to the buffering problem described above.
- The auto scan animation of trajectory files slows down with continued use.