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Biomech Planar Motion Analysis System Quick Reference Guide

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This Guide is intended to assist users through the series of programs collectively known as the Biomech Planar Motion Analysis System. This system consists of stand-alone programs that can run under DOS or Windows. Windows programs are provided for the execution of the DOS programs in a Windows environment. These programs have been tested to operate with Windows versions 98, ME, 2000, XP and NT.

It is assumed that you have already digitized a sequence of motion pictures using the Ariel Performance Analysis System (APAS) and that you may have also recorded ground reaction forces with Kistler's *BioWare* system. If you used the *Simi* or another motion analysis system you will need to convert your data files to the format used by the Biomech system. This can be done by the *Conv2DG.exe* program that can be accessed from the *Imager* program (*Imager98.exe*). If you have already converted your digitized data, skip the following section and start at the section labelled: Starting the Biomech Planar Motion Analysis System.

Conventions

Throughout this guide the following conventions are used to identify certain types of items. A **boldface** and **sans serif** typeface is used to indicate a button on a Windows form. For example, an exit button is typed as, **Exit**. The underlined character, in this case the, x, identifies the hotkey. To use a hotkey in Windows, press the **Alt** button and x together to cause the exit button to be "depressed." Menus or items in menus are in a **sans serif** font but are not in boldface. For example, the file menu will appear as File. To identify a submenu or an item within a menu a vertical line (|) is used to separate the menu from the submenu or item. For example, File|Save, indicates that the Save is an item of the File menu. Names or phrases in *italics* are either file or program names or the names of listboxes. For example, the main Biomech program is called, *Bmwin98.exe*.

Transferring Files from the APAS Computer

To use the Biomech software you must put your data files in subdirectory on your data processing computer. Two files should have been created by the APAS, *trial.CF* (Common File) and *trial.#T* (where # can be 1 through 9). These files must be written onto a floppy diskette and then transferred to your data processing computer. For example, if your files are in the default APAS data directory, perform the following commands from the DOS command prompt to copy your files to your diskette.

```
D:
CD \pasdata
COPY trial.* A:
```

where, *trial*, is the name that you gave your digitized “sequence.”

To run the Biomech software you will need to create a “control file” also called a model file. This file will have the same filename as your data file but has the file extension, .CFB. It will contain information about how to construct your linked-segment model and what data processing is to be performed. A copy of this file should always be included with your data files. Trial names should follow DOS 8.3 file naming conventions. That is they should be only 8 characters long, contain no blanks or periods (.) and only contain letters and numbers (characters such as \$, @, (,), {, }, _, ` , ' , & , - , ! and # are also permitted); directory names follow Windows conventions.

Remove the diskette and insert it into your data processing computer. From the DOS prompt, you must create a data directory for your files. Create a subdirectory with the same name as your data file. E.g., from the command line enter:

```
CD \data\walking
MD trial
```

Next, copy your data files to this directory. Enter, for example:

```
COPY A:trial.* c:\data\walking\trial
```

Starting the Biomech Planar Motion Analysis System

The following pages are arranged in the order that the various programs must be executed.

Kinematic analyses must be performed before any kinetic analyses. That is, the kinematics program must be run first, then either the *Energy*, *Force* or *Momentum* programs. The *Powers* program can only be executed if the *Force* program has already been run. The *Graph* program can be used to display data from any of the programs but users will probably want to use *Excel* or *Quattro Pro* to produce graphical output. A separate manual is available to describe how the *Graph* program works (i.e., Graph User’s Manual).

To start the system, open the Biomech Motion Analysis folder from the Windows desktop and click on the *Biomech for Windows (Bmwin98.exe)* icon. Use this program to run the system and open the various programs necessary to process and analyze the various data files. It is assumed that you have put the required data files (APAS .1T and .CF files and *BioWare* .DAT file) in a subdirectory of a directory called DATA (e.g., c:\data\trial). Use the directory listbox (File|Open directory) to locate your data directory and have the *Data files* listbox display your data files. You are now ready to start data processing.

Using the Biomech for Windows System

Image Scaling and Refining

Click the **I**mager button to start the *Imager98* program. Once it is running click **o**nce on your .1T (or .2T, ...) file then click on the **V**iew, **E**dit & **C**onvert button. This will open your data file for editing and saving in a format suitable for Biomech (but not APAS). You can fix any digitizing errors and add event codes at the appropriate frames. To save the changes press **W** and enter the number **-5**. This will renumber your data from **-5** so that 6 frames precede the first analyzable frame. These frames will be discarded after digital filtering and double differentiating has been done to the data.

The data can now be “refined”, that is, scaled to metric units and straightened, in case the camera was not aligned orthogonally to the plane of motion. Click the **D**ata menu item then select **S**cale/Refine data (Cinedata). After the program has completed execution you can click the **Y**es button to view the refined data. Complete the refining process by clicking the **E**xit button.

Customizing a Control File (.CFB)

To customize your control file (.CFB) press the **.CFB E**ditor button. This program will copy various details from your digitized data file (.DG) to your control file. Click the **C**hoose **M**odel button. From the dialog box, go to the Biomech directory and open the file, *Default.CFB*. Alternately, you may choose a file that you know is similar to the data file you are analysing; this file could be a previous trial from the same subject or a trial from another subject that is part of the same project or has the same number of markers as the current trial.

Next, click on the data file (.DG) that you have just converted, to copy information from it to the new control file. Press the **S**ave **M**odel button to save newly created control file to disk. To check the model, click the **S**how **F**igure button. Press the **I**dentify **S**egments button to determine if the markers correspond to the segment end-points correctly. Close this window and click the **D**iagnos**t**ics button. If there are errors attempt to correct them with the editor. You may need to ask for assistance from an experienced user at this point.

To custom the file for your subject, click the **S**ubject and **T**rial **P**arameters button and then enter the subject's body mass in the appropriate box. Make sure that the frame rate is set for the correct speed (30 or 60 for APAS or 80 for *Simi*). The subject height may also be entered but is not essential for the analysis. Click **O**K to record the changes. The subject's sex can also be set using the drop-down list on the home page.

Next, click the **S**how **S**egments button and enter the subject's segment lengths (in centimetres) in the appropriate columns. The values in the other columns are probably correct and do not need editing.

Lastly, click the **S**how **C**ycle and the **S**how **E**vents buttons and identify the duration of the motion sequence. In general, you should digitize extra data before and after the motion period you are interested in examining. In the *Movement Cycle* window you should indicate the frame number that is the start of the movement and then the frame that ends the movement. The number of frames during the movement will be calculated automatically. Close these windows with the **O**K buttons.

You should now resave the model. The control file (model) should now reflect the subject's physical dimensions and the digitized trial's characteristics. The control file also contains standardized information on how to analyze the data. For more information about what is contained in the control file examine the Biomech User's Manual. The **M**anual button will open this file with Acrobat Reader.

To custom filter each marker coordinate it is suggested that you perform a Fourier analysis or Noise analysis of your data. Click the **S**how **C**utoffs button and then click either the **N**oise or **F**ourier buttons. The Noise analysis tends to cause greater smoothing of the data than the Fourier analysis. We recommend the Noise analysis cutoffs. Once either of these programs have been run,

you may click the **Read Suggested Cutoffs** button. (You may have to close this window and reopen it to enable the **Read Suggested Cutoffs** button.) The recommended cutoff frequencies for each marker coordinate will be displayed. Close this window and save the model (**Save Model** button) to keep these suggested cutoff frequencies.

Kinematics

After returning to the *Biomech for Windows* program click the **Refresh File Lists** button. Click on control file (model) in the *Models (.CFB)* listbox. To run a check on the validity of the control file select the **Programs|Error Check** item. This program checks for whether the control file correctly characterizes the data file. It also checks the segment lengths at each frame with the measured segment lengths. If there are no problems you may now compute the kinematics. If problems occur seek help from an experienced user.

Press the **Programs|Kinematics** item. Press the **Yes** button to view the calculated kinematics. You can also view the smoothed data by clicking the **Animate|Filtered data (.KM)**.

Energies and Momentums

After the Kinematics program has completed execution it is now possible to compute the mechanical energies of each segment, limb and even the total body, if all body segments were digitized. This is realized by the *Energy* program, which can also perform a work analysis on the movement cycle. Similarly the linear and angular momenta of each segment and the total body may be computed by the *Momentum* program. To run either or both of these programs click the items, **Programs|Work-Energy** or **Programs|Momentum**.

If no external forces were recorded **and** the body, limb or segments of interest were not in contact with the environment (i.e., airborne motions or free-swinging limbs), the program, *Force.exe* can also be executed. This program will perform an inverse dynamics analysis of the joints connecting the various segments. Just click the item, **Programs|Force (Inverse Dynamics)**. If your subject did experience ground reaction forces then you will have to synchronize these forces with the kinematics data. This process is outlined in the following section.

The results from these programs may be viewed by clicking on the associated files in the listbox labelled *Output files*. The filenames are ENERGY.OUT, MOMENTUM.OUT and FORCE.OUT.

Inverse Dynamics and BioProc2

BioProc2

To perform inverse dynamics with motions that involve contacting the environment (usually the ground) force data from transducers or usually force platforms must be collected. The Kistler *BioWare* program, the APAS *Analog* module and the *Simi* system can record and store these data. The Biomech system provides a means of converting the data collected by these programs to a format suitable for analysis. The stand-alone program *BioProc2* can read various analog data sources and in many cases can detect the presence of force platform data. It can then save the data with a format (.RF) that is compatible with the Biomech system.

First, copy your data file (we will assume a *Bioware* .DAT file or an APAS .ANA file) to the same computer as your digitized movement data. Start the *BioProc2* program and open the file. Press the **Graph** button to view your data and if it is suitable save the data in .RF format. Use the menu item **Save|Reduced Forces Format (.RF)**. The filename must have the same filename as your digitized data (i.e., *trial.RF*) and must be saved in the same directory as your digitized data.

You will need to determine the frame numbers corresponding with ipsilateral foot-strike (IFS). This can be done by viewing your .DG file with the *Imager* program.

Start **Biomech for Windows**, click on your data file, then select the item **Model|Add forces to model**. Note, if this option is “greyed” it is because the .RF file is not named correctly or does not exist in the data directory. After the program starts, answer the prompts appropriately. The first question asks for the frame number immediately before ipsilateral foot-strike (IFS). The next question depends upon which way the force platform was oriented. This is usually answered, **4**, if a Kistler force platform was used and the subject moved from left to right. The next question selects which plane of motion is being analysed. It is usually answered with a **1**, to indicate the sagittal plane. The last question asks where the force platform is located with respect to the origin (0,0) of the digitized motion data (in centimetres, X then Y). Ideally, the answer is, **0,0**, meaning that the origin of the digitized motion is the same as the force platform centre. The locations of the centres of pressure of the ground reactions forces are usually referenced to the centre of the force platform by the software supplied by the manufacturer (e.g., Kistler’s *BioWare*).

Forces and Moments of Force

To ensure that the data are synchronized appropriately select the **Refined data (.CN)** item from the **Animate** menu. The ground reaction forces should appear under the foot and synchronized with foot-strike and toe-off. If they do not, ask an experienced user for assistance. Once the force platform data have been synchronized with the motion data, inverse dynamics analysis may proceed. To perform inverse dynamics, click the item **Programs|Force (Inverse Dynamics)**. The results appear in the file, **FORCES.OUT**, in the *Output files* listbox.

If your data are from a walking trial, you may now view the “support moment” graphically by selecting the **.GRA, SUPPORT.GRA**, from the listbox that appears after pressing the **Select Type of Graph** button. Next press the **Create Graph(s)** button. After the program has completed execution click the **Refresh File Lists** button and click on the file, **SUPPORT.PLT** in the *Graphs* listbox.

Power Analyses and Graphing

Powers

Power analyses of the forces and moments of force can only be undertaken after an inverse dynamics analysis. In general, only the powers produced by the net moments of force created at each joint are analyzed. The *Powers.exe* program can also compute the instantaneous powers of each segment and the powers transferred by the joint forces and moments, but these are rarely used in biomechanical investigations. Once inverse dynamics are computed, the item Programs|Powers will be enabled. Click it to start the power analyses. The results are stored in the file, POWERS.OUT.

Graphing

There are a number of different ways graphing your data. If a single lower extremity is analysed the usual graph consists of the angular velocities, net moment of force and their associated powers (also called the moment powers) for the ankle, knee and hip joints. To create these graphs select one of the following .GRA files from the listbox displayed by pressing the **Select Type of Graph** button: SLOWWALK.GR, WALK.GRA, JOG.GRA, RUN.GRA or SPRINT.GRA. Each .GRA file uses different ordinate scaling to suitably display your graphs. You can also click the **Edit .GRA file** button to modify one of these files. Consult the *Graph Users' Manual* before attempting this option. Only experienced users should try to modify these files.

Lastly, to produce printed versions of these graphs you will need to have a suitable printer selected as your default Windows printer. The software, *PrintGLW* (or *PrintGLD* for DOS), are available for this purpose. After single-clicking on the graph (.PLT file) that you want to have printed. Select the item, Graph|Print graph... then choose one of the displayed items. For example, if your printer is a Lexmark laser printer you could select *Laserjet 4/5/6 & Lexmark (2)*. The graph will be sent to the printer and spooled for printing. Before printing more graphs, check that it printed correctly. If the printer is incorrectly selected, the printed output will contain pages of incomprehensible text.

To embed a graph into a PowerPoint presentation or Word document you will need to register the .PLT filetype with Windows. The graph's format is called *Hewlett-Packard Graphics Language* or HPGL. It is a standard graphics format which is also part of the PGL specification. To register this file type, which can have extensions, .PLT, .PGL, .HGL or .HPGL among others, you will need the files (PLT.REG and HPGLIM32.FLT). These are available from our FTP site (<ftp://137.122.122.66/f/ftp/pub/microsoft/powerpoint/>). The file HPGL.TXT explains how to register this filetype. Only experienced Windows users should attempt this upgrade. WordPerfect users do not need to register HPGL files.

If you do not want coloured figures to embed in your text documents select the option, Graph|Options|Black on White (for WP or Word), then recreate the graph, **Create Graph(s)**. The graph will appear to be blue on black if previewed with *PrintGLW*, but will embed in your document as black on white. You can then resize to fit your document, as desired. Use the coloured versions of the graphs for Word Perfect *Presentations* or *PowerPoint*.