
Ariel Dynamics, Inc.

FILTER MODULE

Revision 1.0



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ARIEL FILTER PROGRAM

INTRODUCTION

The **ARIEL FILTER** software is used to remove small random digitizing errors or "noise" from the transformed image sequence. In addition, because the motion of each point is determined by a continuous smooth function, the **ARIEL FILTER** software is able to compute point velocities and point accelerations for each frame in the image sequence. Smoothing is always performed following transformation and prior to the presentation phase.

It is not necessary to understand the technical basis for smoothing in order to run the **ARIEL FILTER** software and as such this section may be skipped. The Technical Aspects of Transformation and Smoothing section presents the mathematical basis for the smoothing algorithms used by the **ARIEL FILTER** software for those desiring a more technical discussion of smoothing theory.

The digitizing process involves measuring the location of each body joint. As with any type of measurement, there is no correct value, only an estimate to some known level of accuracy. Therefore, each measurement consists of two parts: the actual or true value, plus an error value due to the inability to perform exact measurements. If there is only a single measurement, it is impossible to separate the error value from the true value. However, if repeated measurements are made, statistical theory allows the estimation and removal of the error, provided the error is of a random nature.

Digitized joint locations are a type of repeated measurement. For a number of consecutive frames or time intervals, the location of each joint is measured. These measurements consist of the true joint location plus a random digitizing error due to the inability to position the stylus or cursor to the exact joint location.

Two obvious questions are "What is Optional Smoothing?" and "How does one determine the best smoothing values for a given joint?" The **ARIEL FILTER** software has been designed to allow visual determination of optimal smoothing by viewing smoothed curves, as well as power spectrum curves, on the graphic display. Often, there is very little difference between the raw

displacement curves and the smoothed curves since digitizing errors tend to be small. It is necessary to highlight the differences in these curves in order to tell how well a given smoothing value approximates true joint motion.

One method would be to greatly enlarge each curve to allow small variations to be easily viewed. The **FILTER** module allows for this feature, but there is a better way.

In addition to the displacement curves, the **FILTER** module can display velocity and acceleration curves for each component. Since the derivative of a curve is the slope or rate of change of the values for that curve, taking successive derivatives has the effect of emphasizing or highlighting the variations or "noise" in the data. Thus, by viewing the acceleration curves, the extent of random error remaining in the data can more easily be determined. Smoothing values can then be adjusted accordingly.

WHAT'S NEW IN FILTER 1.0

A few of the new features you will see in **FILTER** version 1.0

1. **Smooth Data Curves.** Data curves are displayed for each of the X, Y, and Z components.
2. **Power Spectrum Curves.** Simultaneous display of Power Spectrum curve for each of the X, Y and Z components.
3. **APAS Tool Bar.** A toolbar has been added to allow the user to activate individual APAS modules from within the main programs.
4. **Sliding Adjustment Bars.** Sliding adjustment bars have been added to allow independent smoothing adjustments with real-time results.

SYSTEM REQUIREMENTS

The following table provides the basic guidelines for minimum and recommended hardware to provide the best possible performance. The software requires a minimum of Microsoft Windows 95/98 and APAS-2000 Revision 1.0 or later.

Component	Minimum	Recommended
Pentium Computer	Pentium 233	Pentium II 333 MHz or higher
Video Display	S-VGA (256 Colors)	High Color Display (65,000 colors or more)
RAM	32 MB	64 MB or more

TO START THE FILTER PROGRAM

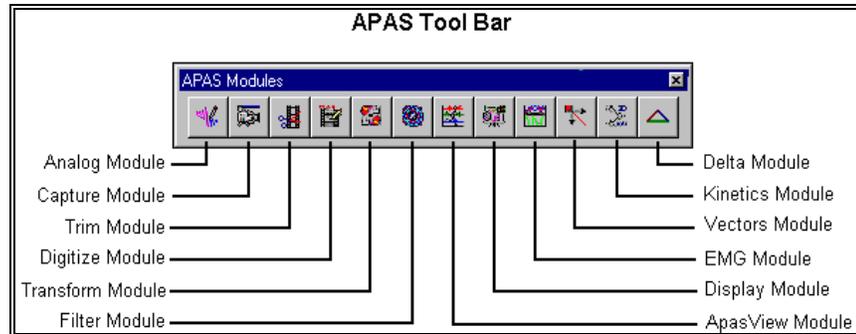
1. Double-click the **FILTER** icon located in the **APAS System** window group. The main FILTER window will appear.

SCREEN LAYOUT

Prior to performing the **FILTERING** process, you should take the time to familiarize yourself with the format and contents of the various screens listed below:

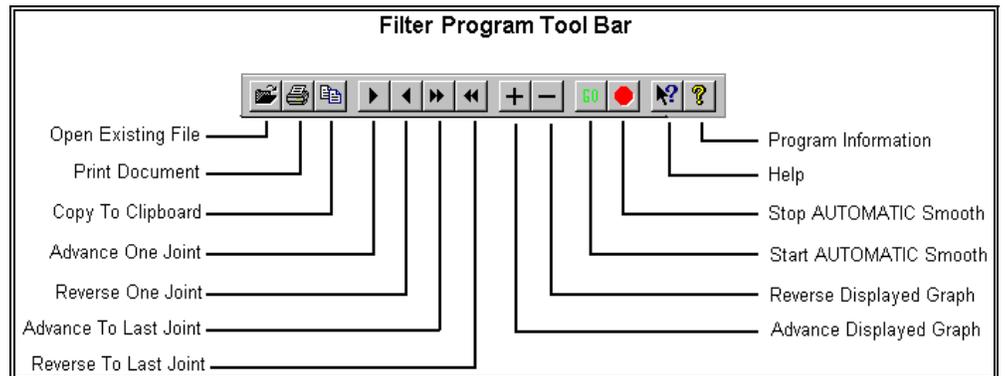
THE APAS TOOL BAR

You can activate any of the APAS software modules from within the current program by selecting the icons located on the APAS tool bar. The tool bar is toggled on/off using the APAS Toolbar command in the VIEW menu. A check mark in the left column of the menu indicates that the toolbar is currently active. The toolbar can be re-located anywhere in the main program window by dragging it with the mouse. Clicking the appropriate icon can activate the following program modules. Icons are pictorial representations of programs, commands or functions.



THE TOOL BAR

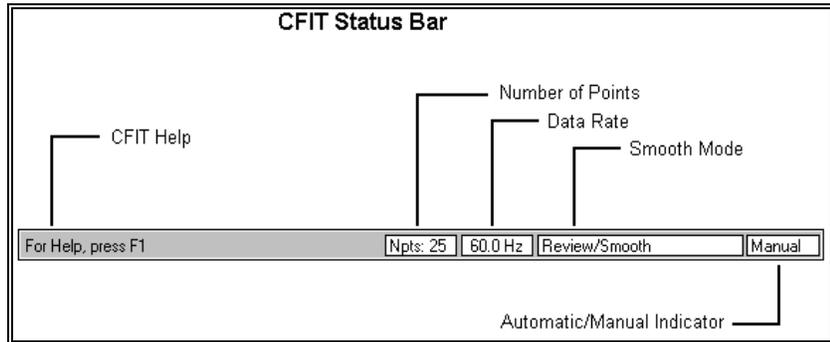
You can activate many functions by selecting the icons located on the **FILTER** program tool bar. The tool bar is located near the top of the window. Icons are pictorial representations of commands or functions. You can access the following commands by clicking the appropriate icon.



THE STATUS BAR

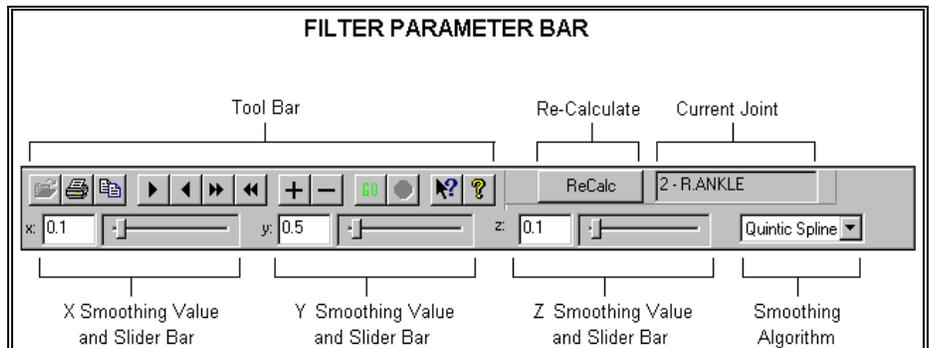
The status bar provides useful information about the current status of the file during the Smoothing process. The status bar is located at the bottom of the **FILTER** window. The far-left side of the status bar is divided into four separate fields. The left field displays the total number of points in the selected sequence. The DATA RATE field indicates the data frequency. The third field

indicates the SMOOTH MODE. The right field indicates whether the sequence is being smoothed Manually or Automatically.



THE FILTER PARAMETERS BAR

You can activate most smoothing functions by selecting the desired option located on the **FILTER** Parameters bar.



Smoothing Values - The data curves show the smoothed and raw values for each of the coordinate components, X, Y, and Z for all frames in this sequence. The **FILTER** module automatically selects the default smoothing algorithm as well as the default smoothing values. The degree of smoothing for each coordinate joint is controlled by the smoothing values.

The smoothing value for the spline algorithms is the average error allowance for each point on the curve in user units. Thus, if the units for this sequence are centimeters, the default smoothing value allows the smoothed curves to vary from the raw curves by an average of one centimeter for each point along the curves. The smoothing value for the digital filter algorithm represents the "cut-off" frequency.

To change the degree of smoothing for one or more of the coordinate curves, new smoothing values must be entered. Smaller values allow less error and thus fit the raw data more closely. Larger values allow more error and thus produce smoother curves. New values are entered by either selecting the

desired X, Y and/or Z data field and typing the desired value, or by adjusting the slider bar in the left and right directions.

When all changes have been entered, the Re-Calc button is selected to display the new curves showing the results of the new smoothing values. Since smoothing is a repetitive process, this procedure may be repeated several times for each joint.

Smoothing Algorithm - Smoothing algorithm is selected when the algorithm or computational method used to smooth the data values is to be changed. The current algorithm is displayed in the Algorithm field. After selecting the desired algorithm, the Re-Calc button must be selected to graph the data curves with the new algorithm.

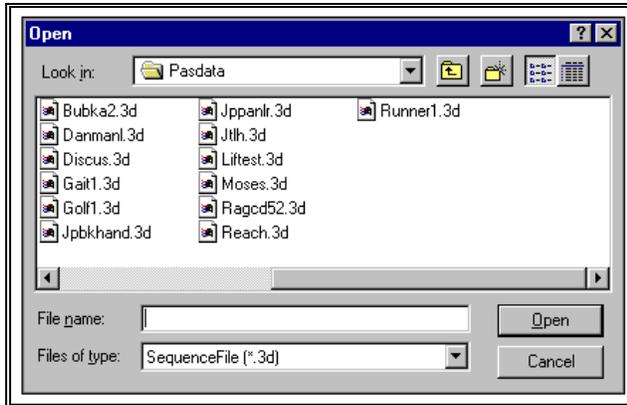
Re-Calculate - The Re-Calc button is selected when the current joint curves are to be re-smoothed using the algorithm and smoothing values that appear in the Parameters bar. The new curves will be displayed showing the results of the new parameters.

Current Joint - The Joint data field lists the current joint for smoothing. This option can also be used to smooth a joint out of the normal consecutive sequence of joints. For example, the Joint data field could be used to return to a previously smoothed joint to check smoothing or to re-smooth that data and then to proceed to the next joint to be smoothed. Another application might be to smooth a specific joint or joints while skipping other joints. This would be the case if one wished to perform a partial analysis, perhaps only considering the motion of certain body joints or segments and ignoring others. In most cases, it is recommended that all body joints be smoothed. Otherwise, certain joint and segment velocities and accelerations would be missing when subsequent analysis functions such as viewing, graphing and printing were performed.

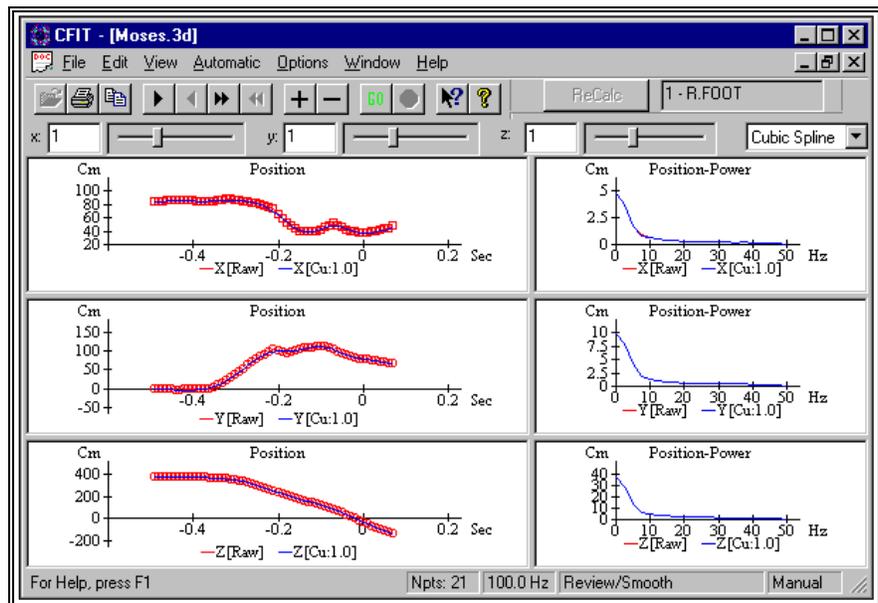
SMOOTHING A SEQUENCE FILE (MANUAL)

Prior to performing the smoothing procedure, make certain that the desired sequence has been completely digitized and transformed. It is possible to re-smooth a sequence at any time, as the original un-smoothed data is always retained along with the current smoothed data values.

1. Choose the **OPEN** command from the **FILE** menu. The **OPEN File** Dialog box will appear.



The OPEN File Dialog box looks for a particular type of file (files that have the extension of ***.3D**). This file is automatically created when a Sequence file is transformed using either the ARIEL TRANSFORMATION software module. The OPEN File Dialog box can be used to specify the Drive, Directory, and Name of the sequence file to be retrieved. Select the sequence name to be smoothed and then select **OPEN** to proceed. When the desired sequence is opened, three smoothed data curves and corresponding power spectrum curves will appear on the graphic display. The smoothing values and algorithm for the first joint will be determined by the default settings.



2. Select the desired **algorithm** from the Parameters bar at the top of the **FILTER** window.
3. Specify the **X, Y** and **Z** smoothing values in the corresponding data fields from the Parameters bar at the top of the **FILTER** window. The slider bars can also be used to adjust the smoothing values and display the results in real-time.
4. Select the **ReCalc** button in the Parameters bar to smooth the data curve using the specified algorithm and smoothing values.

5. Select **VIEW, GRAPH FWD** to toggle between position, velocity, acceleration and 3rd derivative for viewing the desired "smoothed" curve.
6. Repeat steps 2 through 5 until the desired smoothing algorithm and values are achieved.
7. Select **VIEW, NEXT JOINT** to advance to the next sequential joint in the sequence.
8. Repeat steps 2 through 6 for each of joint in the selected sequence.
9. Select **OPTIONS, SUMMARY** to display a list of smoothed points, and the algorithms and smoothing values used.
10. Select **FILE, EXIT** to exit the **FILTER** program.

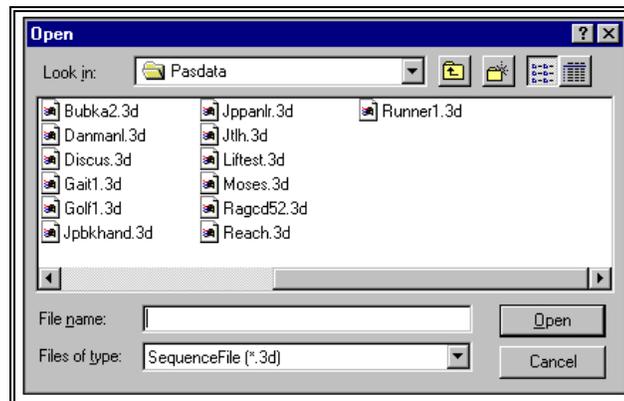
SMOOTHING A SEQUENCE FILE (AUTOMATIC)

This mode smoothes all the remaining joints in this sequence with the current default smoothing algorithm and values. It is the equivalent of selecting the NEXT JOINT command once for each joint after the current one. Automatic smoothing is used when completing the smoothing process as rapidly as possible and without additional human interaction is the concern and not obtaining optimal smoothing for each joint.

The curves for each joint will still be displayed as smoothing is performed, however, re-smoothing of joints is not allowed during the automatic process. At the end of the process, individual joints may be re-smoothed if desired.

Typically, the first joint is smoothed manually and the default smoothing algorithm and values are then adjusted accordingly before selecting the Automatic option. In general, the best smoothing is performed manually rather than in automatic mode.

1. Choose the **OPEN** command from the **FILE** menu. The **OPEN File** Dialog box will appear.



The OPEN File Dialog box looks for a particular type of file (files that have the extension of **(*.**3D**)**). This file is automatically created when a Sequence file is transformed using the

TRANSFORMATION software module. The OPEN File Dialog box can be used to specify the Drive, Directory, and Name of the sequence file to be retrieved. Select the sequence name to be smoothed and then select **OPEN** to proceed. When the desired sequence is opened, three smoothed data curves and corresponding power spectrum curves will appear on the graphic display. The smoothing values and algorithm for the first joint will be determined by the default settings.

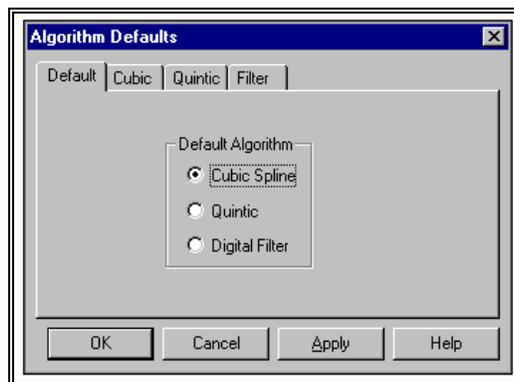
2. Select **OPTIONS, ALGORITHM** to set the Default Algorithm and Default Smoothing values for the specified algorithm. These parameters are best determined by manually smoothing the first joint.
3. Select **AUTOMATIC, BEGIN** (or the **GO** icon in the Toolbar) to begin the automatic smoothing function.
4. Select **OPTIONS, SUMMARY** to display a list of smoothed points, and the algorithms and smoothing values used.
5. Select **FILE, EXIT** to exit the **FILTER** program.

OPTIONS

The **ARIEL FILTER** software contains many options designed to enhance the smoothing process. Selecting the **OPTIONS** menu accesses these options. Available options allow for selecting the default algorithm and smoothing values, changing the smoothing mode and providing a summary of smoothing values used for the current sequence.

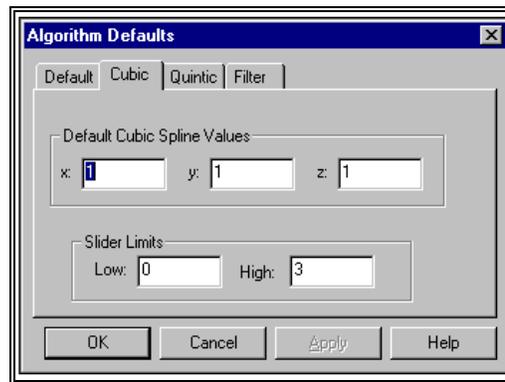
SMOOTHING ALGORITHMS

The **Algorithm** command is selected from the **OPTIONS** menu when the algorithm or computational method used to smooth the data values is to be changed. When this command is selected, the Algorithm Defaults menu will be displayed listing the smoothing algorithm that is currently set as the default algorithm.



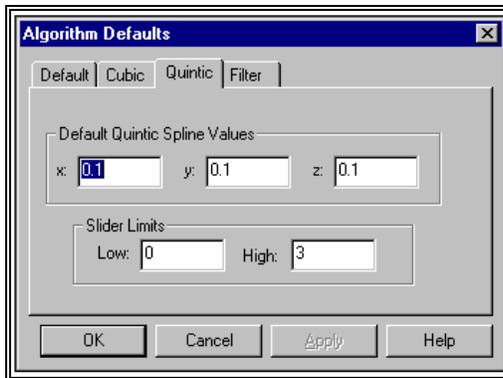
CUBIC SPLINE ALGORITHM

The **Cubic Spline** algorithm is based on traditional spline function theory and has been enhanced to allow approximate fitting rather than the traditional exact fitting to the data points. The "closeness-of-fit" can be adjusted using the smoothing values. Smaller smoothing values result in a closer fit to the original data while larger values result in smoother curves. A cubic spline is constructed of piecewise third-order Polynomials that pass through a set of control points. When this algorithm is utilized, the user should be aware that the second derivative (acceleration curve) of each Polynomial is forced to zero at the end points regardless of the actual data. The Cubic and Quintic splines are the most sophisticated of the smoothing algorithms and give the best results in approximating complex data curves. Select the Cubic tab to enter the Default smoothing values and slider limits for the Cubic Spline algorithm.



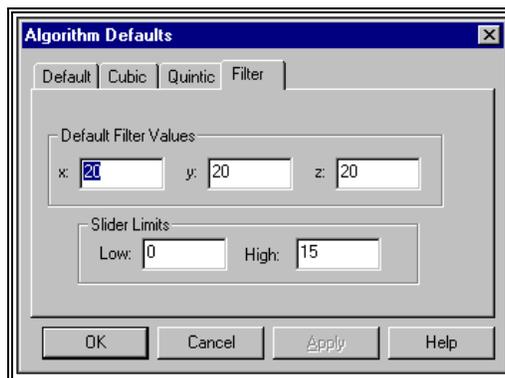
QUINTIC SPLINE ALGORITHM

The **Quintic Spline** algorithm, like the Cubic Spline, is based on traditional spline function theory and has been enhanced to allow approximate fitting rather than the traditional exact fitting to the data points. The "closeness-of-fit" can be adjusted using the smoothing values. Smaller smoothing values result in a closer fit to the original data while larger values result in smoother curves. A Quintic spline is constructed of piecewise fifth-order Polynomials that pass through a set of control points. Quintic spline smoothing proves extremely useful for cyclical type motion such as pedaling a bicycle. The Cubic and Quintic splines are the most sophisticated of the smoothing algorithms and give the best results in approximating complex data curves. Select the Quintic tab to enter the Default smoothing values and slider limits for the Quintic Spline algorithm.



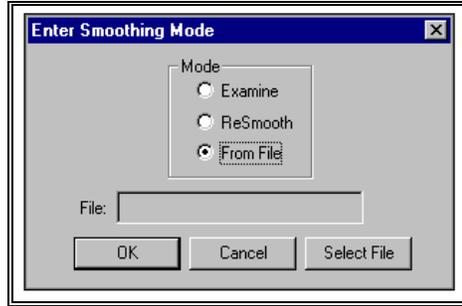
DIGITAL FILTER ALGORITHM

The **Digital Filter**, algorithm smooths the data points by removing or attenuating "noise" above the selected cutoff frequency while retaining the lower frequency data. Larger values produce a closer fit while smaller values produce smoother curves. This is just the opposite of spline smoothing. Select the Filter tab to enter the Default smoothing values and slider limits for the Digital Filter algorithm.



MODE

The **Mode** command is selected from the **OPTIONS** menu when the smoothing mode used to smooth the data values is to be changed. When this command is selected, the Enter Smoothing Mode menu will be displayed listing the smoothing mode that is currently selected.



EXAMINE MODE

The **Examine Mode** is selected when all un-smoothed joints are to be smoothed using the current default smoothing values, but only the current smoothing values for joints already smoothed are to be displayed. This is the default mode for smoothing, as it allows the user to return to previous joints to inspect smoothing without inadvertently changing the smoothing values. Previously smoothed joints may be re-smoothed by specifying new X, Y and/or Z values and selecting the ReCalc button.

RESMOOTH MODE

The **Resmooth Mode** is selected when every joint is to be smoothed with the current default XYZ smoothing values. Joints that have been previously smoothed will be re-smoothed with these default values. This mode should be used when a previously smoothed sequence is to be re-smoothed.

FROM FILE MODE

The **File Mode** is selected when the smoothing values from the corresponding joint in a previously smoothed sequence is to be used as the default smoothing values for the current sequence. Corresponding joints are matched by joint ordinal (i.e. 1st, 2nd, 3rd, etc.) not by joint name. This option is frequently used when smoothing a number of sequences of the same activity that were digitized by the same person and is also frequently used in conjunction with the automatic mode. When this option is selected, an additional menu will be displayed for selecting a previously smoothed sequence.

SUMMARY

The **Summary** option can be selected from the **OPTIONS** menu to present a table summary of the smoothing performed on the current sequence. This table shows, for each joint, if smoothing has been performed and the smoothing values and algorithm used. The summary option is helpful for quickly checking that smoothing has been completed for all the joints in the sequence. This is useful if joints have not been smoothed in the normal consecutive sequence, as when the Next Joint option is used.

Joint	Algorithm	X	Y	Z
R.FOOT	Quintic	1.000	0.100	0.500
R.ANKLE	Cubic	0.500	0.500	0.500
R.KNEE	Cubic	0.500	0.500	0.500
R.HIP	Cubic	0.500	0.500	0.500
L.HIP	Cubic	0.500	0.500	0.500
L.KNEE	Cubic	0.500	0.500	0.500
L.ANKLE	Cubic	0.500	0.500	0.500
L.FOOT	Cubic	0.500	0.500	0.500
L.HAND	Cubic	0.500	0.500	0.500
L.WRIST	Cubic	0.500	0.500	0.500

OK

TYPICAL SMOOTHING PROCESS

Set the display to Acceleration curve. With each curve type other than position, it will be observed that there is no raw curve, but rather a last curve. This is because the only measured or raw data values are joint displacements. The other curve types are all computed from smoothed displacement curves. By comparing the current curves to the last curves, the effect of changes in the smoothing values can be observed and used to hone in on the best values to use. This is the recommended procedure for obtaining optimal smoothing values for each joint.

While viewing the acceleration curves, try selecting a very low smoothing value for each of the coordinate curves, like a value of 0.3. This causes the smoothed displacement curves to fit very closely to the raw displacement curves; so closely that they actually fit noise as well as data.

The effect on the acceleration curves show large and almost random fluctuations; an impossibility for human motion. Now try smoothing again with an intermediate smoothing value, such as 1.0, for each curve. The acceleration curves become quite smooth; a reasonable approximation of true human motion. Now if a large value such as 5.0 is used for each curve, the acceleration curves are virtually flat. True variations in the data have been removed as well as noise.

This exercise illustrates the goal of proper smoothing to remove random fluctuations from the acceleration curves while leaving as much of the true variation as possible. The smoothing process may start with higher smoothing values and work down, or with lower smoothing values and work up until the acceleration curves show maximum smooth variation without random variation.

NOTE: Different smoothing values may be used for each of the coordinate curves. Also there is no exact best smoothing value since this is a process of approximation. Once satisfactory fitting is achieved, additional manipulations with very small changes in smoothing values will be of little benefit.

Once a joint has been properly smoothed, select the Next Joint function to advance to the next sequential joint. The smoothed values for the current joint will be saved and the raw values for the next joint will be accessed and smoothed using the default smoothing values. Continue this process until all the joints in the sequence have been smoothed. At this point, one may either

Exit from the **FILTER** module or select another sequence for smoothing using the Open command on the File menu.

TECHNICAL ASPECTS OF SMOOTHING

Digitized data contains random error or "noise" due to the inability to exactly locate the position of body joints. Although this error is small, it introduces noticeable effects when derivatives of joint displacements are taken to calculate velocity and acceleration. The error or "noise" has a frequency on the order of the frequency of the digitized video frames, typically 30 to 200 Hz. Human motion exhibits significantly lower frequencies, typically 5 to 15 Hz or less. Since the frequency of the noise is well above that found in true joint motion, this error term can be removed or attenuated by the application of appropriate mathematical smoothing or filtering processes.

Historically, different types or classes of functions have been used to smooth raw biomechanical data. Early work employed polynomial regression and finite difference methods. These functions, although easily applied, did not model complex patterns of human motion very well. More recent studies such as Zernicke and others (5) and McLaughlin and others (2) indicate that cubic spline functions are better suited for close approximation of human movement patterns. The APAS employs two features that improve the quality of smoothing over previously reported applications of this method.

The first feature is the provision for interactive smoothing with visual feedback. Since this smoothing method is one of approximation, repeated smoothing attempts are usually necessary to obtain optimal results. Each time smoothing is performed; the Ariel system provides visual graphic comparisons of the raw data, the current attempt at smoothing, and the previous smoothing attempt. Smoothing values can then be changed, if desired, and the smoothing process repeated until the best values are obtained.

The second feature is the allowance for variation in "closeness of fit" in specific regions of a single joint motion curve. Biomechanical data may occasionally contain brief intervals of high frequency activity, such as when some type of impact occurs in an otherwise smooth sequence of motion. By increasing the "closeness of fit" in these regions only, the smoothing module can retain true high frequency motion while removing high frequency noise from the rest of the data.

Specifically, the cubic spline smoothing method computes a smooth displacement curve for each joint that minimizes the second derivative (acceleration curve) while deviating from the raw data points by no more than a specified amount. Stated mathematically, if a set of N measurements are made at times $t[-]i[-]$, $i=1,N$ designated as:

$$y[-]i[-] = y(t[-]i[-])$$

then the cubic spline algorithm finds the curve $f[-]0[-](t)$ from all curves $f(t)$ such that:

$$\int_{t[-]1[-]}^{t[-]N[-]} f''(t) dt$$

is minimized by $f[-]0[-](t)$, subject to the constraint:

$$N$$

$$\sum_{i=1}^n w_i [f(t_i) - y_i] Q$$

The term w_i is a weighting factor for the allowed error or deviation at each point and Q is the total allowed deviation. When $Q = 0$, an exact fit to the data is obtained. The values for w_i and Q are interrelated. If w_i is the error in point y_i , then each term in the sum is the number of standard deviations between the raw and fitted values. In this case, the confidence interval for Q becomes:

$$M - (2M)^{1/2} Q M + (2m)^{1/2} M = N + 1$$

The minimizing function can be found using the calculus of variations. Details as to the derivation can be found elsewhere (4). The solution is a series of cubic curves, called splines, one for each interval in the range $[t_1, \dots, t_N]$. This solution can be expressed as:

$$f(t) = a_i + b_i(t-t_i) + c_i(t-t_i)^2 + d_i(t-t_i)^3 \quad (5)$$

such that $f(t)$ and $f'(t)$ are all continuous. The smoothing algorithm calculates the coefficients a_i , b_i , c_i , and d_i given t_i and $y(t_i)$ and smoothing values w_i and Q . By choosing $Q = N$, different degrees of smoothing can be obtained by varying w_i . Calculation of velocity, acceleration and third derivative at the observation times is accomplished by taking the appropriate derivatives of equation (5) as follows:

$$\text{Velocity} \quad V(t_i) = b_i \quad (6A)$$

$$\text{Acceleration} \quad A(t_i) = 2c_i \quad (6B)$$

$$\text{3rd derivative} \quad D3(t_i) = 6d_i \quad (6C)$$

The smoothing algorithm is applied independently to each coordinate dimension (X, Y, and Z) of each joint in an analysis sequence. As mentioned previously, the process is interactive with the operator repeatedly smoothing while varying the allowed error or "closeness of fit" w_i until the desired degree of smoothing is obtained. Standard smoothing sets the value w_i the same for all data points. The "Impact" and "Relax" options allow individual w_i values to be increased or decreased to accommodate intervals on the data curve with unusual variations. Finally, the "Error-values" option uses w_i values that are proportional to error values measured in the digitizing module for individual joints.

References

1. Abdel-Aziz, Y.I., & Karara, H.M. "Direct linear transformation from comparator coordinates into object space coordinates in close-range photogrammetry." In ASP Symposium on Close-Range photogrammetry. Falls Church, Va.: American Society of Photogrammetry, 1971.
2. McLaughlin, T.; Dillman, C.J., & Lardner, T.J. "Biomechanical analysis with cubic spline functions." Research Quarterly, 48:569-582, 1977.
3. Shapiro, R. "Direct linear transformation method for three-dimensional cinematography." Research Quarterly, 49:197-205, 1978.

4. Reinsch, C.H., "Smoothing by spline functions." Numerische Mathematik, 10:177-184, 1967.
5. Zernicke, R.F., Caldwell, G., & Roberts, E.M., "Fitting bio-mechanical data with cubic spline functions." Research Quarterly, 47:9-19, 1976.

FILTER QUICK REFERENCE

1. Select **FILE, OPEN** (or the **OPEN** icon in the Toolbar) to Open desired Sequence.
2. Select desired sequence from displayed *.3D files.

AUTOMATIC SMOOTHING

- 1.* Select **OPTIONS, ALGORITHM** to set the Default Algorithm and Default Smoothing values for the specified algorithm.
2. Select **AUTOMATIC, BEGIN** (or the **GO** icon in the Toolbar) to begin the automatic smoothing function.
3. Select **OPTIONS, SUMMARY** to display a list of smoothed points, and the algorithms and smoothing values used.
4. Select **FILE, EXIT** to exit the **FILTER** program.

MANUAL SMOOTHING

1. Select the desired **algorithm** from the Parameters bar at the top of the **FILTER** window.
2. Specify the **X, Y** and **Z** smoothing values in the corresponding data fields at the top of the **FILTER** window. The slider bars can also be used to change the smoothing values with the results displayed immediately.
3. Select the **ReCalc** button to smooth the data curve using the specified algorithm and smoothing values.
4. Select **VIEW, GRAPH FWD** to toggle between position, velocity, acceleration and 3rd derivative for viewing the desired "smoothed" curve.
5. Select **VIEW, NEXT JOINT** to advance to the next sequential joint in the sequence.
6. Repeat steps 1 through 5 for each of joint in the selected sequence.
7. Select **OPTIONS, SUMMARY** to display a list of smoothed points, and the algorithms and smoothing values used.
8. Select **FILE, EXIT** to exit the **FILTER** program.

EDIT / RE-SMOOTH SPECIFIC JOINT

1. Select **VIEW, SELECT JOINT** to select the desired joint.
2. Specify the desired Algorithm and X, Y and Z smoothing values.
3. Select the **ReCalc** button to smooth the data curve using the specified algorithm and smoothing values.

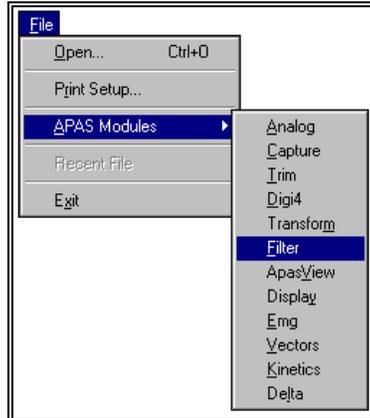
4. Repeat steps 1 through 4 for each joint to be re-smoothed.
5. Select **OPTIONS, SUMMARY** to display a list of smoothed points, and the algorithms and smoothing values used.
6. Select **FILE** and **EXIT** to exit the **Ariel FILTER** program.

* These are only required to be selected once. The program will remember the current settings unless changed by the user.

FILTER MENUS

Listed below are the various menus for the **FILTER** program. Select the desired menu to see a description of the available commands for each menu.

FILE COMMAND MENU



Open

Selected to open an existing sequence file for smoothing or re-smoothing.

Print Setup

Selected to adjust the printer settings prior to issuing the PRINT command.

APAS Modules

Selected to open additional APAS modules while keeping the current program open. When this command is selected, the user will be presented with a list of APAS modules.

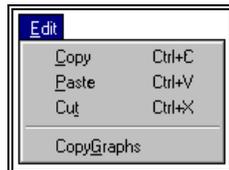
Recent File

Provides a list of the most recent sequences accessed by the FILTER program. These sequences can be recalled by selecting the desired sequence using the mouse.

Exit

Selected to EXIT the FILTER program.

EDIT COMMAND MENU



Copy

Select the COPY command to make a COPY of the selected item and temporarily copy it to the Windows Clipboard. The items are placed in the clipboard so that it can be Pasted into another area of the same application or into another Windows application. To avoid losing this item, you should Paste it before performing any additional editing..

Paste

Select the PASTE command to insert a copy of the item currently in the Windows clipboard. This item could have been cut or copied from almost any Windows application.

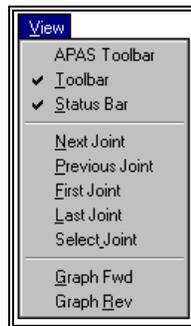
Cut

Select the CUT command to remove the selected item and temporarily copy it to the Windows Clipboard. The items are placed in the clipboard so that it can be Pasted into another area of the same application or into another Windows application. To avoid losing this item, you should Paste it before performing any additional editing.

CopyGraphs

Select the CopyGraphs command to copy all of the displayed graphs to the Windows clipboard. The graphs can then be copied into Windows compatible programs using the Paste command.

VIEW COMMAND MENU



APAS Toolbar

Selected to toggle on/off the APAS toolbar. When this option is active, the APAS toolbar will be displayed and allow the user to select additional APAS modules while keeping the current program open. The toolbar can be positioned to the desired position by dragging it with the mouse. The check mark to the left indicates that the APAS Toolbar will be visible.

Toolbar

Selected to alternately either display or hide the Toolbar located at the top of the FILTER window. The check mark to the left indicates that the Toolbar will be visible.

Status Bar

Selected to alternately display the status bar located at the bottom of the FILTER window. The check mark indicates that the Status Bar will be visible.

Next Joint

Selected to advance to the next sequential joint in the sequence for smoothing.

Previous Joint

Selected to reverse to the previous sequential joint in the sequence for smoothing.

First Joint

Selected to reverse to the first joint in the sequence for smoothing.

Last Joint

Selected to advance to the last joint in the sequence for smoothing.

Select Joint

Selected to smooth a joint out of the normal consecutive sequence of joints accessed using the Next Joint command. When this command is selected, the desired joint can be selected from a menu of available sequence joints.

Graph Fwd

The Graph Forward command is selected to toggle forward through the position (P), velocity (V), acceleration (A) and 3rd derivative (D3) curves.

Graph Rev

The Graph Reverse command is selected to toggle backward through the position (P), velocity (V), acceleration (A) and 3rd derivative (D3) curves.

AUTOMATIC COMMAND MENU



Begin

Selected to smooth all the remaining joints in the current sequence with the default smoothing algorithm and X, Y, and Z values.

Stop

Selected to Stop the Automatic Smoothing process prior to completion.

OPTIONS COMMAND MENU



Algorithm

Algorithm is selected when the algorithm or computational method used to smooth the data values is to be changed. When this option is selected, the Algorithm menu will be displayed listing the default smoothing algorithms that may be selected as well as the default values for each of the specified algorithms.

Mode

Mode is selected to enter the smoothing Mode for the current file. When this option is selected, the Smoothing Mode menu will be displayed listing the available modes; Examine, Resmooth, and File.

Summary

Summary is selected to present a table summary of the smoothing performed for the current sequence. This table shows, for each joint, if smoothing has been performed and the smoothing values and algorithm utilized.

WINDOW COMMAND MENU



Cascade

Selected to arrange all programs that are window sized in an overlapping CASCADE. This will not arrange a program that has been minimized to an icon.

Tile

Selected to re-size the program windows to fit side-by-side on the screen. Since Windows will include all programs that are window-sized in the tile setup, it is best to minimize all programs that are not currently being used so it will not take up space on the screen.

Arrange Icons

Selected to automatically ARRANGE ICONS in a straight row. The user has no control over where the icons are placed.

HELP COMMAND MENU



Index

Selected to provide an INDEX of Help related topics.

Using Help

Selected to provide instructions on using the Help Windows.

About CFIT

Provides program information, version number and copyright for the FILTER program.

