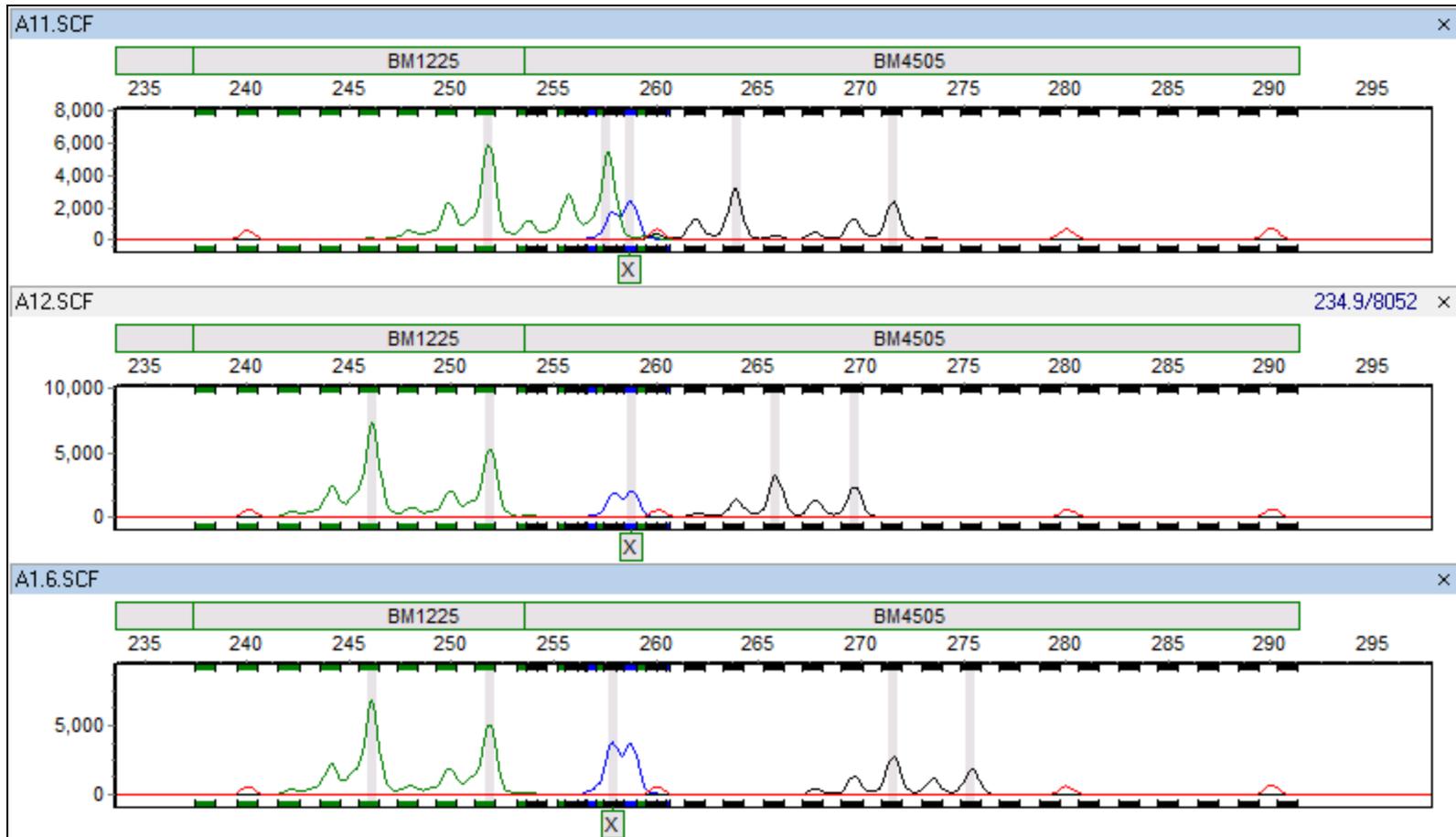
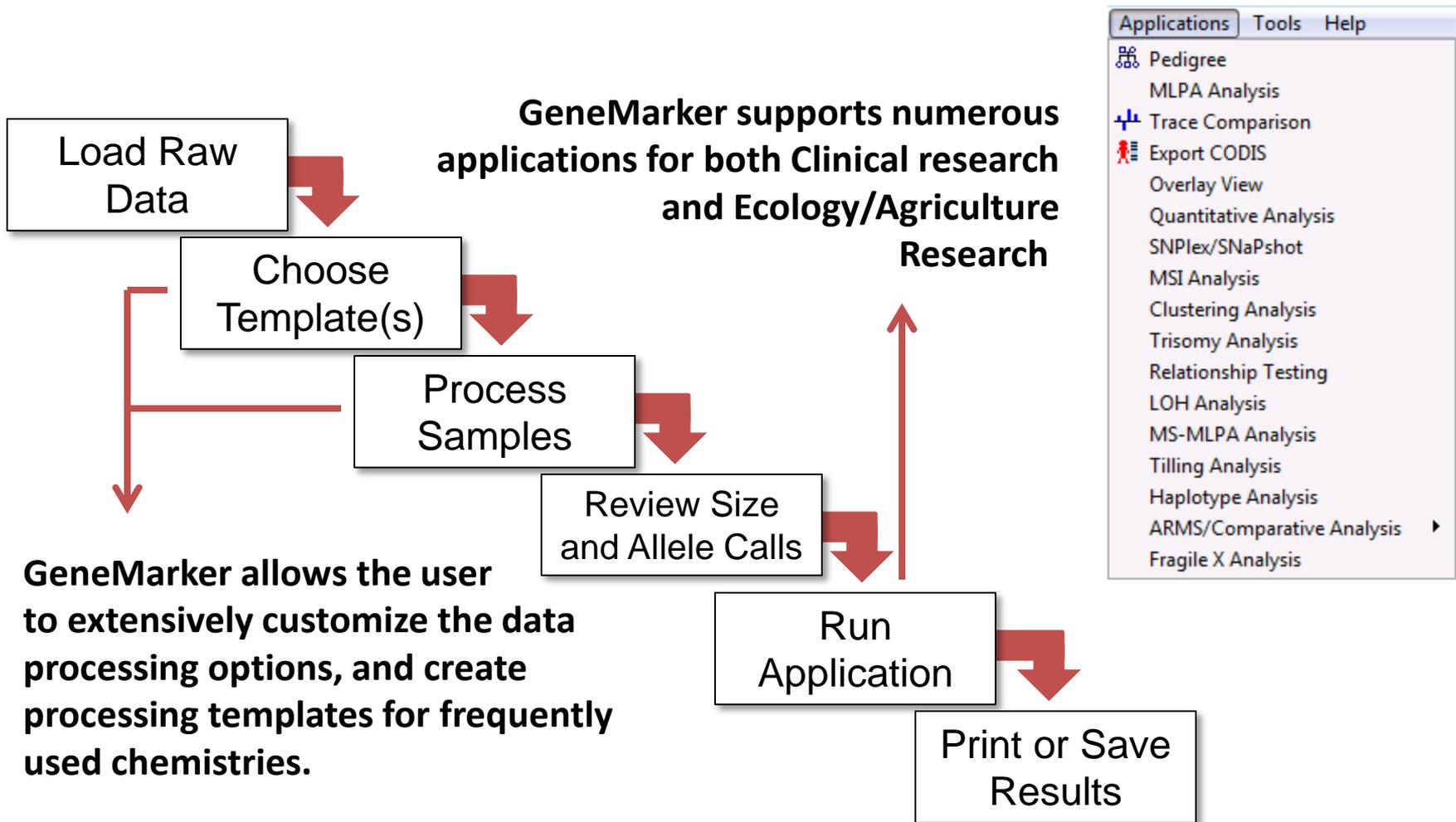


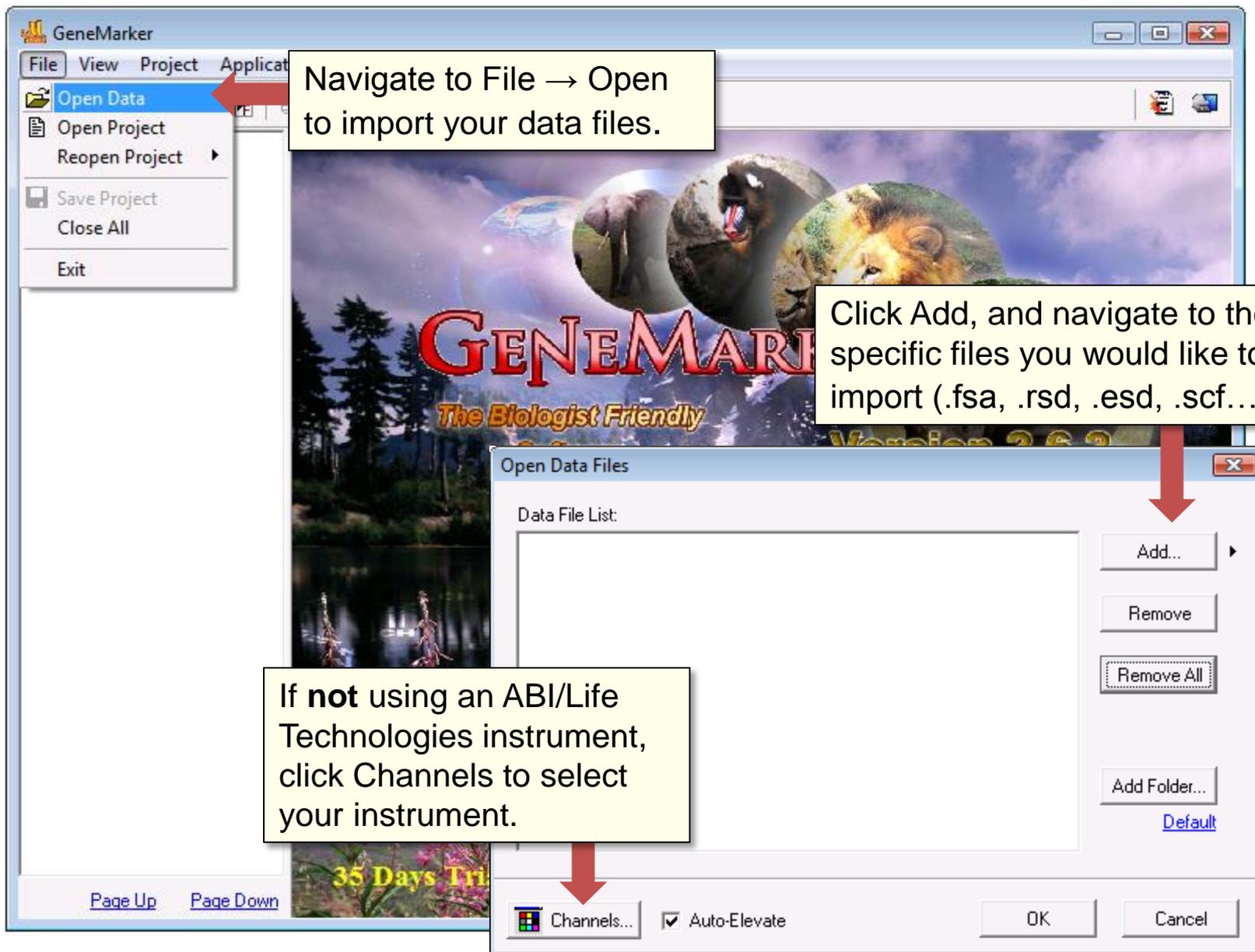
GeneMarker[®] Quickstart Guide

The Biologist Friendly Software



GeneMarker Workflow





The screenshot displays the GeneMarker software interface with a file list on the left and three stacked chromatogram traces on the right. The traces are labeled '052_B04.SCF', '052_B04.SG1', and '052_H03.SG1'. The x-axis for the top two traces ranges from 0 to 5,000, while the bottom trace ranges from 0 to 2,000. The y-axis represents signal intensity. A toolbar at the top contains various icons, including a dye-color icon. Three callout boxes provide instructions: one for toggling a synthetic gel image, one for zooming in and out, and one for opening/closing files. A red arrow points to the dye-color icon, and another red arrow points to the synthetic gel image icon. A blue dashed box highlights a region in the bottom trace, with a red arrow pointing to it.

GeneMarker - Untitled

File View Project Applications Tools Help

Click the dye-color icon to display individual dye colors.

Toggle a synthetic gel image on and off.

Double-click a sample file to open/close it

To zoom in on a trace, use your mouse to draw a box from **Left to Right**. To zoom back out, draw a box from **Right to Left**.

052_B04.SCF

052_B04.SG1

052_H03.SG1

Page Up Page Down

The screenshot shows the GeneMarker software interface. The main window is titled "GeneMarker - Untitled" and has a menu bar with "File", "View", "Project", "Applications", "Tools", and "Help". A red arrow points to the "Run" button (a green triangle) in the top toolbar. A callout box explains: "To process your samples, (size and allele calling), click the green triangle icon, or navigate to Project → Run." The left sidebar shows a file tree with "Raw Data" containing various sample files like "052_B04.SCF", "052_BO", "052_HO", etc. The "Run Wizard" dialog box is open, titled "Template Selection". It contains a list of templates: "_Trisomy", "AFLP", "FragileX", "LOH", "Microsatellite_Dinucleoti", "MLPA", and "MCI". The "Template Name" field is set to "_Trisomy". Other fields include "Panel" (Trisomy_Panel), "Size Standard" (GS500), "Standard Color" (Red), and "Analysis Type" (Fragment (Animal)). There are "Save" and "Delete" buttons, and "Back" and "Next" navigation buttons. A red arrow points to the "Save" button. A callout box explains: "Or select a pre-saved template". Another callout box explains: "Select your panel, your size standard, standard color, and analysis type." A third callout box at the bottom explains: "Input a new template name a click Save to create a new template." The background shows a genomic track with a scale from 0 to 5,000.

GeneMarker - Untitled

File View Project Applications Tools Help

Raw Data

052_B04.SCF 2,000 3,000 4,000 5,000

052_BO

052_HO

061_BO

061_BO

062_CO

062_CO

063_DO

063_DO

064_EO

064_EO

065_FO

065_FO

066_GO

066_GO

067_HO

067_HO

068_AO

068_AO

069_BO

069_BO

Run Wizard

Template Selection

Set the template of the project

Select an existing template or create one

_Trisomy

AFLP

FragileX

LOH

Microsatellite_Dinucleoti

MLPA

MCI

Template Name: _Trisomy

Panel: Trisomy_Panel

Size Standard: GS500

Standard Color: Red

Analysis Type: Fragment (Animal)

Save Delete

1326.8/2136

Page Up Page Down

500 0

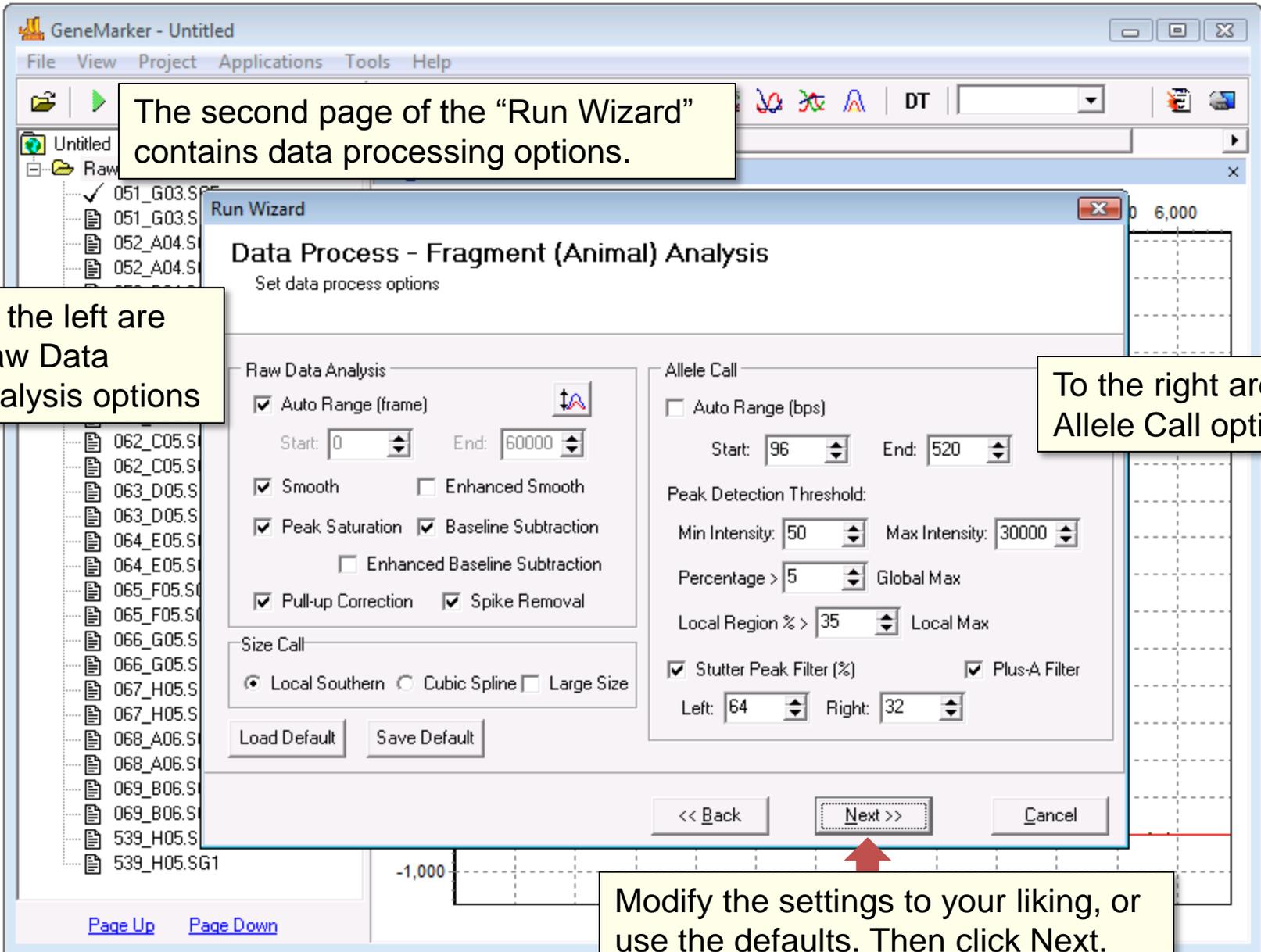
<< Back Next >> Cancel

To process your samples, (size and allele calling), click the green triangle icon, or navigate to Project → Run.

Or select a pre-saved template

Select your panel, your size standard, standard color, and analysis type.

Input a new template name a click Save to create a new template.



The second page of the “Run Wizard” contains data processing options.

To the left are Raw Data analysis options

To the right are Allele Call options

Modify the settings to your liking, or use the defaults. Then click Next.

The last page of the Run Wizard sometimes contains additional settings, depending on which analysis type you have selected.

Again, make any changes or use the defaults and then click OK.

The screenshot shows the GeneMarker software interface. The main window displays a list of files under 'Raw Data' and a plot area. Overlaid on this is the 'Run Wizard' dialog box, specifically the 'Additional Settings - Fragment (Animal) Analysis' page. The dialog box contains the following settings:

- Allelic Ladder: NONE
- Allele Evaluation Peak Score:
 - Reject < 1.00
 - Check 7.00
 - < Pass
- AFLP -- Unconfidence at Rightside: Score < 30

At the bottom of the dialog box, there are three buttons: '<< Back', 'Ok', and 'Cancel'. A red arrow points to the 'Ok' button.

The screenshot displays the GeneMarker software interface. On the left is a file tree under 'Allele Call' listing various sample files. The main window shows two DNA electropherogram plots for '051_G03.SCF' and '051_G03.SG1'. Each plot has three peaks labeled with marker names (D21S1437, D21S11, D13S628) and their corresponding allele sizes (e.g., 115, 127, 238, 242, 247, 327, 331). A 'Report' window is open on the right, showing a table of results. A red arrow points to the save icon in the report window's toolbar.

The report table contains all the allele calls that were made.

Click the save icon to save the report table as a text or excel file.

Green icons mean a peak passed all analysis parameters. Red or yellow peaks were in the "check range" of at least one parameter.

Green icons here show that size calling was successful.

Sample	Marker	Allele#	Allele#
051_G03.SCF	D21S1437	115	127
051_G03.SG1	D21S1437	115	127
051_G03.SG1	D21S11	238	242
051_G03.SG1	D13S628	327	331
051_G03.SG1	D13S634	401	
051_G03.SG1	D18S535	479	491
052_A04.SCF	D21S1437	127	131
052_A04.SCF	D21S11	257	260
052_A04.SCF	D13S628	327	
052_B04.SCF	D21S11	257	260
052_B04.SCF	D13S628	327	
052_B04.SCF	D13S634	401	411

Click the size calibration icon to see a size calibration chart for each sample.

The screenshot shows the GeneMarker software interface. The main window displays a list of samples with columns for 'No.', 'Sample Name', and 'Score'. The 'Calibration Charts' window is open, showing a grid of charts for various samples. The top chart is a 'Expected Size - GS500' chart with peaks at 50, 100, 150, 200, 250, 300, 350, 400, 450, and 500. Below it is a larger chart for '052_A04.SCF' with peaks at 35, 50, 75, 100, 130, 150, 200, 250, 300, 340, 400, 450, and 490. The bottom section contains a 3x3 grid of smaller charts for samples: 052_A04.SCF, 052_B04.SCF, 062_C05.SCF, 063_D05.SCF, 064_E05.SCF, 066_G05.SCF, 068_A06.SCF, 069_B06.SCF, and 051_G03.SCF. Each of these charts plots 'Size (bps)' on the y-axis (0 to 400) against 'Frame' on the x-axis (2,000 to 8,000). A red arrow points from the text box to the size calibration icon in the software's toolbar.

No.	Sample Name	Score
1	052_A04.SCF	92
2	052_B04.SCF	92
3	062_C05.SCF	92
4	063_D05.SCF	92
5	064_E05.SCF	92
6	066_G05.SCF	92
7	068_A06.SCF	92
8	069_B06.SCF	92
9	051_G03.SCF	91
10	052_H03.SCF	91
11	061_B05.SCF	91
12	065_F05.SCF	91
13	067_H05.SCF	91
14	819_A06.SCF	91
15	819_B06.SCF	91
16	820_C06.SCF	91
17	821_E06.SCF	91
18	845_A05.SCF	91
19	847_C05.SCF	91
20	848_D05.SCF	91
21	849_E05.SCF	91
22	852_F05.SCF	91
23	993_F05.SCF	91
24	539_H05.SCF	90
25	846_B05.SCF	90
26	820_D06.SCF	87
27	853_G05.SCF	87

Click the chart/table icon to display a peak table below the electropherogram.

Right-click to add a new peak, or modify an existing peak.

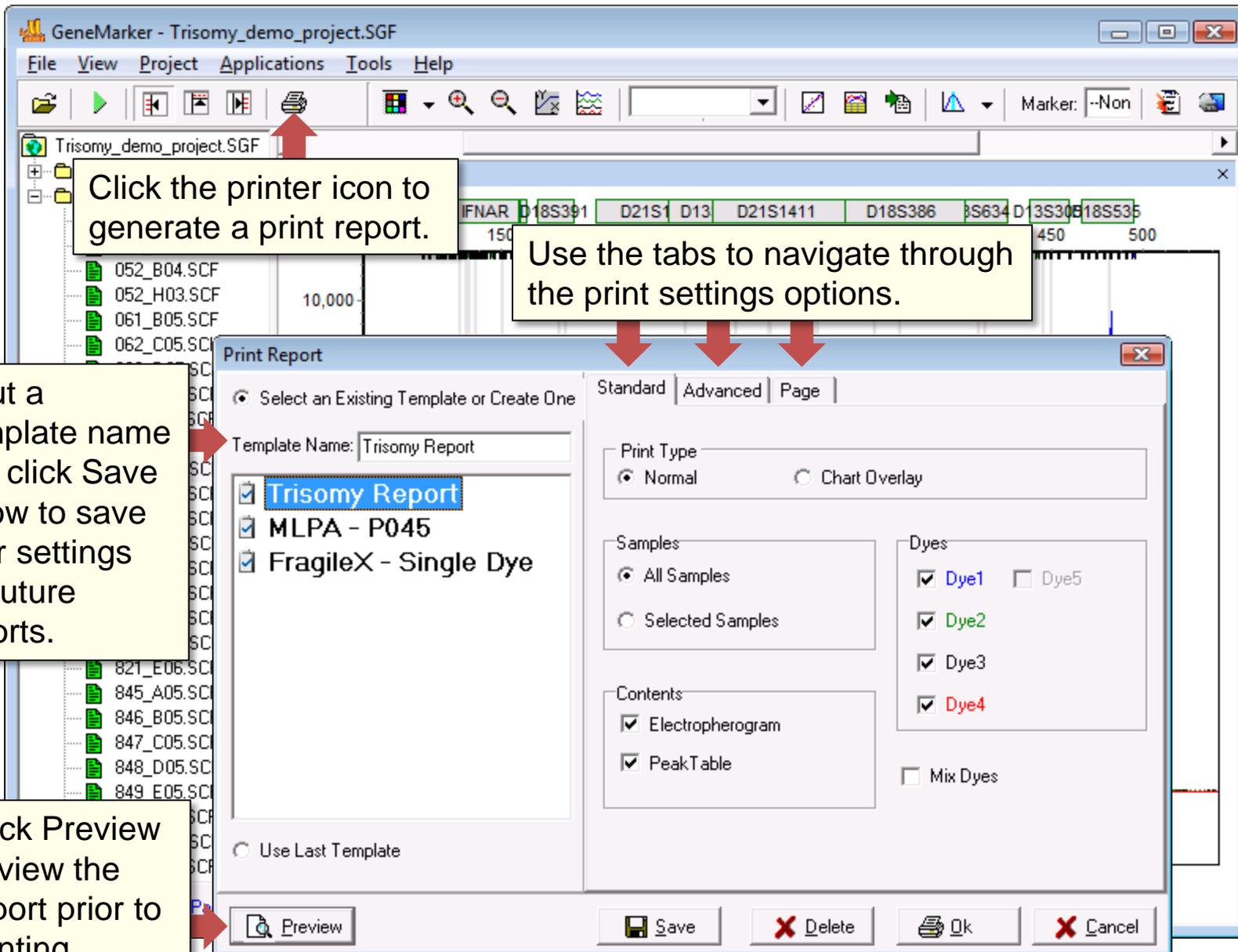
No.	Dye	Size	Height	Area	Marker	Allele	Differ		Sample Comments
1	Blue	131.2	4255	31243	D21S1437	131	0.00	Pass	500.0
2	Blue	250.8	2416	18691	D21S11	251	0.20	Pass	357.3
3	Blue	297.4	4442	37521	D13S628	297	0.00	Pass	500.0
4	Blue	322.8	3916	38814	D13S628	323	0.10	Pass	409.0
5	Blue	410.5	5945	72083	D13S634	411	0.10	Pass	442.6
6	Blue	414.4	5499	65984	D13S634	415	0.20	Pass	422.2
7	Blue	482.4	9751	151893	D18S535	483	0.30	Check	421.2 [<SAT (Repaired)>]

Among other things, this table displays why a peak was flagged.

The screenshot shows the GeneMarker interface with the 'Applications' menu open. The 'Trisomy Analysis' option is highlighted. A text box explains that after reviewing size and allele calls, users can navigate to various embedded applications. Below the menu, a chromatogram displays peaks for several markers. At the bottom, a table provides detailed data for each peak.

After reviewing your size and allele calls, navigate to one of several embedded applications.

No.	Dye	Size	Height	Area	Marker	Allele	Difference	Quality	Score	Allele Comments	Sample Comments
1	Blue	131.2	4255	31243	D21S1437	131	0.00	Pass	500.0		
2	Blue	250.8	2416	18691	D21S11	251	0.20	Pass	357.3		
3	Blue	297.4	4442	37521	D13S628	297	0.00	Pass	500.0		
4	Blue	322.8	3916	38814	D13S628	323	0.10	Pass	409.0		
5	Blue	410.5	5945	72083	D13S634	411	0.10	Pass	442.6		
6	Blue	414.4	5499	65984	D13S634	415	0.20	Pass	422.2		
7	Blue	482.4	9751	151893	D18S535	483	0.30	Check	421.2	[<SAT (Repaired)>]	
1	Green	128.1	3134	19533	D18S1002	128	0.00	Pass	500.0		



Click the printer icon to generate a print report.

Use the tabs to navigate through the print settings options.

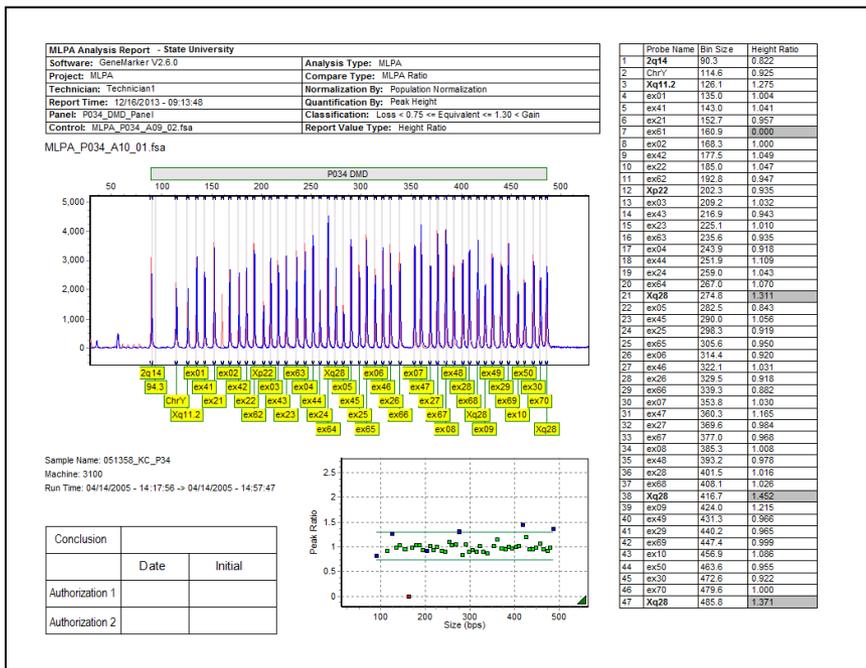
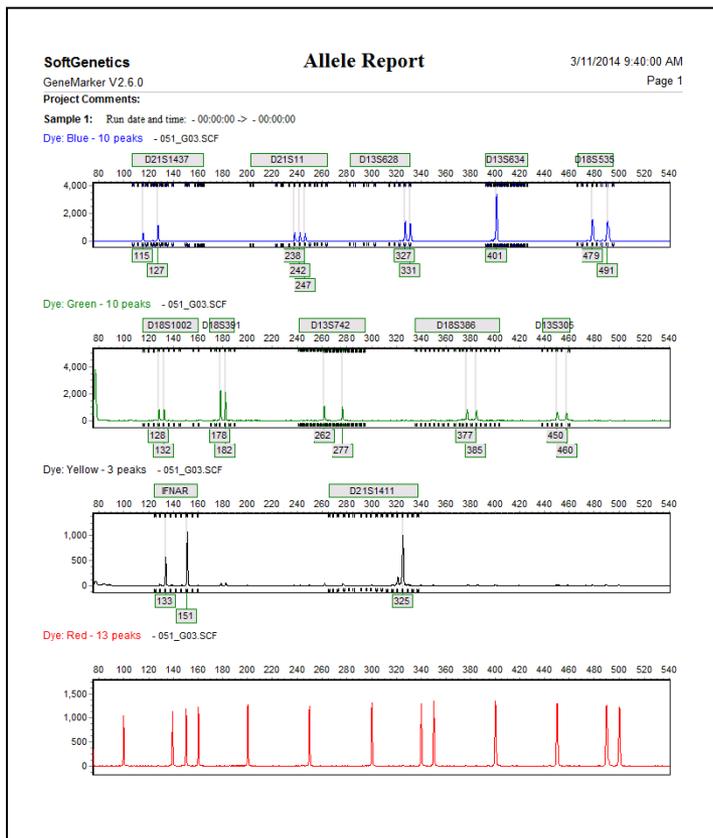
Input a Template name and click Save below to save your settings for future reports.

Click Preview to view the report prior to printing.

GeneMarker Supports Numerous Reporting Options

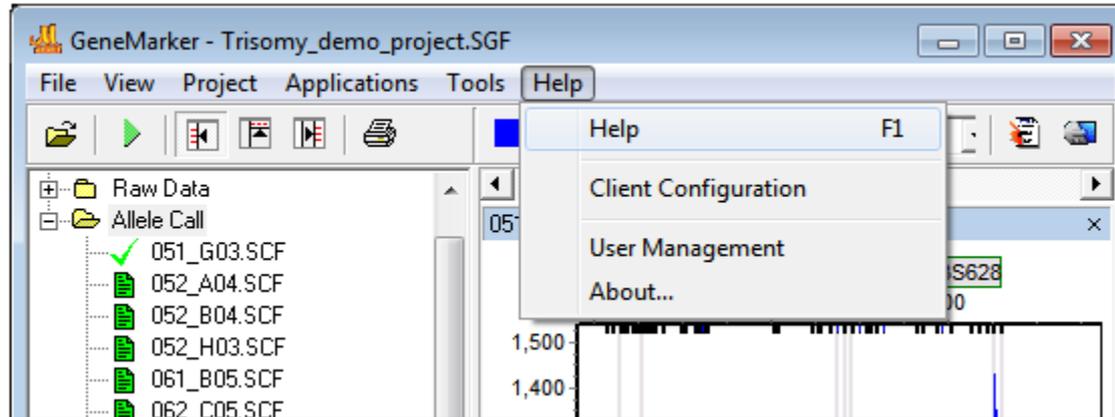
Below are two example reports that can be generated in GeneMarker. Each post-genotyping application has its own unique report format that can be extensively customized. Reports can be printed directly or saved as PNG and JPG image files.

A typical print report from one of the many post-genotyping applications (MLPA):



Need Assistance?

Access the User Manual anytime by navigating to Help > Help



You can view webinars on GeneMarker here:
http://softgenetics.com/GeneMarker_reference.html

Or, Please Email: tech_support@softgenetics.com

Or Please Call: 814-237-9340

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