

# Software User Manual

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
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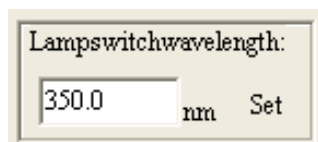
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# 1. Function Introduce

The main functions of UV Solution 3.0 is the photometric measurement, wavelength scan (spectral measurement), time scan measurement (dynamics), quantitative work, DNA/protein work, and multi-wavelength work; auxiliary function is spectrum operations (addition, subtraction, multiplication, and division), spectrum derivative, overlay, etc.

## 1.1 Main Function

### **Photometric Measurement:**

The absorbance or transmittance of sample by single wavelength measuring

### **Wavelength Scan:**

Interval of scan (0.1, 0.2, 0.5, 1.0, 2.0 and 5.0nm)

Scan curve display way: wavelength-transmittance, wavelength-absorbance and wavelength-energy.

### **Time Scan:**

Interval of scan (0.2, 0.5, 1.0, 2.0 and 5.0s)

Scan curve display way: time-transmittance and time-absorbance.

### **Quantitative Work:**

Two ways to build standard curve: Standard sample calibration method and coefficient method

Most build 15 standard samples or directly enter curvilinear equation.

Standard curve approximate by four ways: (first-order linear approximate, third-order and second-order and broken line).

### **DNA/Protein Analysis:**

2 analyses way build-in

Measurement parameter can set.

### **Multi-wavelength work:**

Test 8 wavelength

## **1.2 Auxiliary Function**

**Spectrum data display**  
**Peak valley value automatically search**  
**Scale map**  
**Spectrum derivative**  
**Spectrum operations**

## **2. Software Installation**

### **2.1 System Requirements**

Operation system: Windows XP or later  
CD-ROM drive  
Two or more USD ports  
RAM: 256MB or more  
Memory: 32MB or more  
Disk Space: 50MB or more

### **2. 2 Installation UV Solution 3.0**

1. Power on the computer and start Windows operation system.
2. Insert CD into CD or DVD drive and run the Explore of WINDOWS.
3. Select "CD or DVD drive (X:)" in the Explore window. X is the drive letter.
4. Double click "Setup" file in the files' list of the Explore.
5. Follows the operate instruction till the installation finished.



## 2.3 Uninstallation

Two methods to uninstall

1. Start → All program → SOT-UV → Uninstall SOT-UV
2. Control panel → add or remove programs →, selected in the current installation program list → SOT - UV , click Delete to uninstall.

## 2.4 Operation

Insert the USB line (attachment) respectively host on the right side of the square and the USB port of PC, then Insert "encryption dog" to the USB port of PC.

When a host in the main menu interface has two methods to run SOT-UV software

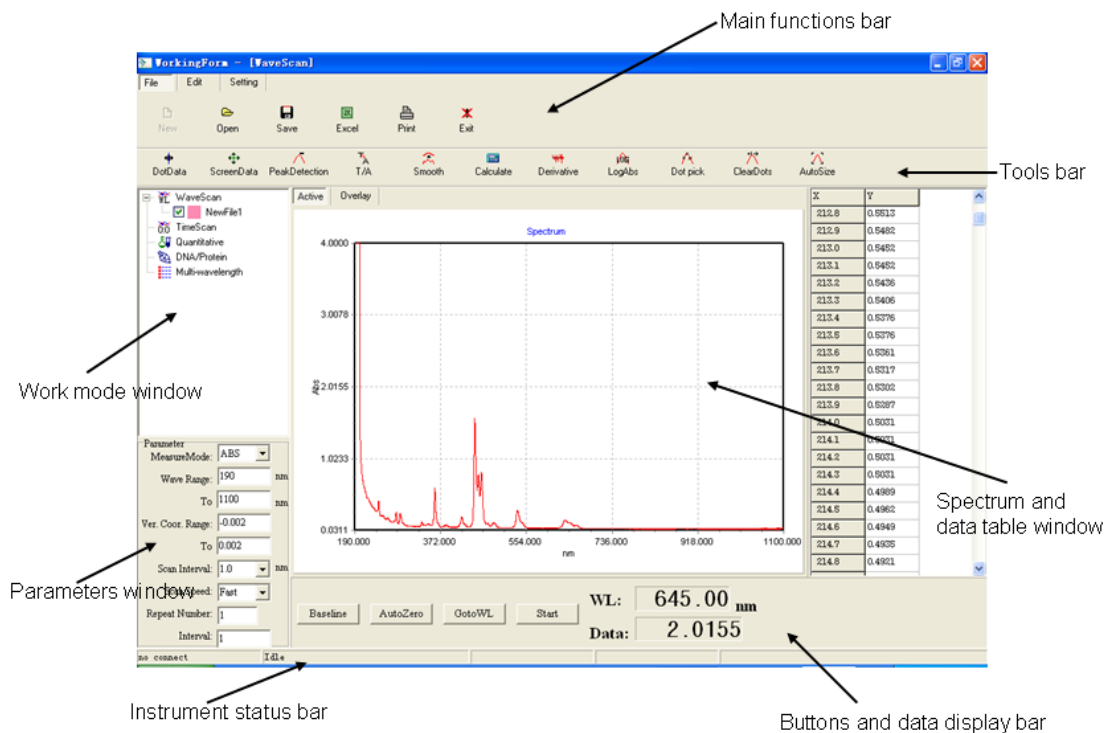
1. Start → All program → SOT-UV → click.
2. Double click the SOT-UV icon on the desktop.

Notice: When operating the software, please confirm the machine under the main menu.



# 3. Software Introduce

## 3.1 The main window is shown as below:



The main window can be separated into 7 windows: instrument status bar, parameters window, work mode window, tools bar, main functions bar, buttons and data display bar and spectrum and

data table window. Descriptions of each one are in the following sections.

## 3.2. Instrument Status Bar



The status of instrument connecting, working and model will be shown in the status bar.

Status of instrument connecting:

When instrument is disconnected, display “no connect”;

When instrument is connected, display “Connect” .

Status of working:

When waiting operation, display “Idle”

When adjusting zero, display “Blanking...”

When correcting baseline, display “Building Baseline...”

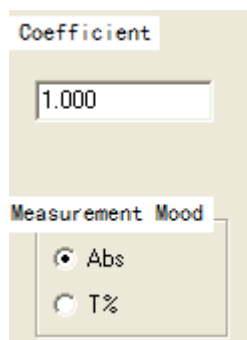
When scanning, display “Scanning...”

When changing wavelength, display “Moving Wavelength...”

Instrument model: Display the model if the instrument can be identified.

## 3.3. Parameters Window

### 3.3.1 Photometric measurement parameters



Use mouse to select mood. The coefficient do not set 0, the default setting is 1.000.

### 3.3.2 Wavelength scan parameters

#### Parameters window for T% and ABS measure modes :

Parameter	
MeasureMode:	ABS
Wave Range:	600 nm
To	700 nm
Ver. Coor. Range:	0
To	200
Scan Interval:	1.0 nm
Scan Speed:	Fast
Repeat Number:	1
Interval:	1

#### Parameters window for E measure mode :

Parameter	
MeasureMode:	E
Wave Range:	600 nm
To	700 nm
Ver. Coor. Range:	0
To	200
Scan Interval:	1.0 nm
Scan Speed:	Fast
Repeat Number:	1
Interval:	1
Lamp:	D2
Gain:	1

#### Measure Mode :

Three measure modes, T% , ABS and E can be selected in the list by a mouse. Parameter's items are different between E mode and the other two modes. Lamp and Gain can be set under E mode.

## **Wave Range:**

Set wavelength range for scanning. Wavelengths must input from short to long.

The short wavelength should be in 190-1100 nm range.

The long wavelength should be in the short wavelength to 1100 nm range.

## **Vertical Coordinate Range:**

Set suitable range based on the request of scan spectrum display. But the short wavelength must be larger than the long wavelength. And wavelengths should be input from short to long.

The largest should be smaller than the smallest (Mode: ABS, suggest set 0~4).

## **Scan Interval:**

Set the interval of the wavelengths between each data points when scanning.

6 values can be selected: 0.1, 0.2, 0.5, 1.0, 2.0 and 5.0 nm.(suggest set 1.0)

## **Scan Speed:**

3 levels can be selected: fast, normal and slow.

The scanning speed set suggested fast.

## **Repeat Number:**

If this number is more than 1, the scanning will be automatic repeated after a scanning is finished. The waiting time between twice scanning is set in the Interval box.

## **Interval:**

Set the time interval between twice scanning when the Repeat Number is more than 1. The unit is second.

The value should be more than 1s.

## **Lamp:**

Only be displayed and can be set under E mode.

Three modes, D2, WI and Auto can be selected.

D2: Only deuterium lamp is used in the whole scan process.

WI: Only tungsten lamp is used in the whole scan process.

Auto: D2 and WI lamp will be switched in the scan process based on the Lamp Switch Wavelength setting.

## Gain:

Only be displayed and can be set under E mode.

8 values, 1-8 can be selected.

## 3.3.3 Time scan parameters

### Parameters window for T% and ABS measure mode:

Parameter	
MeasureMode:	T% <input type="button" value="v"/>
Delay:	0 s
Time:	2 s
Ver. Coord. Range:	99
To:	101
Scan Interval:	0.2 s <input type="button" value="v"/>
Repeat Number:	1
Interval:	1

## Parameters window for measure E mode :

Parameter	
MeasureMode:	E
Delay:	0 s
Time:	2 s
Ver. Coord. Range:	99
To	101
Scan Interval:	0.2 s
Repeat Number:	1
Interval:	1
Lamp:	D2
Gain:	1

### Measure Mode :

Three measure modes, T% , ABS and E can be selected in the list by a mouse. Parameter's items are different between E mode and the other two modes. Lamp and Gain can be set under E mode.

### Delay :

Set how much time will delay before scan beginning. The unit is second.

### Time :

Set how long time the scan will be lasted. The unit is second.

### Vertical Coordinate Range :

Set suitable range based on the request of scan spectrum display. But the short wavelength must be larger than the long wavelength. And wavelengths should be input from short to long.

## **Sample Interval:**

When set scanning, the time between two point.  
5 values can be selected: 0.2, 0.5, 1.0, 2.0 and 5.0 s.

## **Repeat Number :**

When a scanning is finished, if this number is more than 1, the scanning will be automatic repeated after waiting setting time filled in the Interval position.

## **Repeat Number :**

If this number is more than 1, the scanning will be automatic repeated after a scanning is finished. The waiting time between twice scanning is set in the Interval box.

## **Interval:**

Set the time interval between twice scanning when the Repeat Number is more than 1. The unit is second.

The value should be more than 1s.

## **Lamp:**

Only be displayed and can be set under E mode.

Three modes, D2, WI and Auto can be selected.

D2: Only deuterium lamp is used in the whole scan process.

WI: Only tungsten lamp is used in the whole scan process.

Auto: D2 and WI lamp will be switched in the scan process based on the Lamp Switch Wavelength setting.

## **Gain:**

Only be displayed and can be set under E mode.

8 values, 1-8 can be selected.

### 3.3.4 Parameters for quantitative analysis

Wavelength1	
Wavelength:	500.0 nm
Coefficient:	1.0000
Wavelength2	
Wavelength:	0.0 nm
Coefficient:	0.0000
Wavelength3	
Wavelength:	0.0 nm
Mode	
<input checked="" type="radio"/> 1WL <input type="radio"/> 2WLs <input type="radio"/> 3WLs	

#### Wavelength1:

Wavelength: Set a value in the range of 190-1100 nm based on the request of the sample analysis.

Coefficient: Set a suitable value based on the request of the sample analysis except 0. The default value is 1.000.

The result will be that ABS value at the wavelength multiplies the coefficient.

#### Wavelength2:

Wavelength: Set a value in the range of 190-1100 nm based on the request of the sample analysis.

Coefficient: Set a suitable value based on the request of the sample analysis except 0. The default value is 1.000.

The result will be that ABS value at the wavelength multiplies the coefficient.

Operation result is  $K1 \cdot A1 - K2 \cdot A2$

#### Wavelength3:

Wavelength: Set a value in the range of 190-1100 nm based on the request of the sample analysis.

#### Mode:

There are three modes can be selected: one wavelength, two wavelengths and three wavelengths.



1WL represents that only wavelength1 is used for the quantitative analysis.  
2WLs represents that both wavelength1 and wavelength2 are used for the quantitative analysis.  
3WLs represents that wavelength1, wavelength2 and wavelength3 are used for the quantitative analysis.

### 3.3.5 Parameters for DNA/Protein analysis

Wavelength		
Wavelength1:	<input type="text" value="260.0"/>	nm
Wavelength2:	<input type="text" value="230.0"/>	nm
<input checked="" type="checkbox"/> Reference:	<input type="text" value="320.0"/>	nm
Factor:	<input type="text" value="1.0"/>	
DNA Coefficients		
Coefficient1:	<input type="text" value="49.1"/>	
Coefficient2:	<input type="text" value="3.48"/>	
Protein Coefficients		
Coefficient1:	<input type="text" value="183.0"/>	
Coefficient2:	<input type="text" value="75.8"/>	
Mode		
<input checked="" type="radio"/> Default1	<input type="radio"/> Default2	<input type="radio"/> Custom

#### Wavelength:

Set the wavelength for the analysis.

Wavelength1: When the mode is custom, it can be set to any value in the range of 190~1100nm. Under other modes, only default values can be used.

Default 1: 260nm

Default 2: 260nm

Wavelength 2: When the mode is custom, it can be set to any value in the range of 190~1100nm. Under other modes, only default values can be used.

Default 1: 230nm

Default 2: 280nm

Reference wavelength: When the mode is custom, it can be set to any value in the range of 190~1100nm. Under other modes, only default values can be used.

Default 1: 320nm

Default 2: 320nm

If the reference does not be checked, this wavelength will do not be used for the analysis.

## DNA Coefficients:

Coefficient 1: When the mode is custom, it can be set to any known value. Under other modes, only default values can be used.

Default 1: 49.1

Default 2: 62.9

Coefficient 2: When the mode is custom, it can be set to any known value. Under other modes, only default values can be used.

Default 1: 3.48

Default 2: 36.0

## Protein Coefficients:

Coefficient 1: When the mode is custom, it can be set to any known value. Under other modes, only default values can be used.

Default 1: 183.0

Default 2: 1552.0

Coefficient 2: When the mode is custom, it can be set to any known value. Under other modes, only default values can be used.

Default 1: 75.8

Default 2: 753.3

## Mode:

Three modes can be selected: default 1, default 2 and custom.

### 3.3.6 Parameters for multi-wavelength detection:

Parameter		
Wavelength1:	<input type="text" value="440.0"/>	nm
Wavelength2:	<input type="text" value="546.0"/>	nm
Wavelength3:	<input type="text" value="635.0"/>	nm
Wavelength4:	<input type="text"/>	nm
Wavelength5:	<input type="text"/>	nm
Wavelength6:	<input type="text"/>	nm
Wavelength7:	<input type="text"/>	nm
Wavelength8:	<input type="text"/>	nm
MeasureMode:	<input checked="" type="radio"/> T% <input type="radio"/> Abs	

## Wavelength :

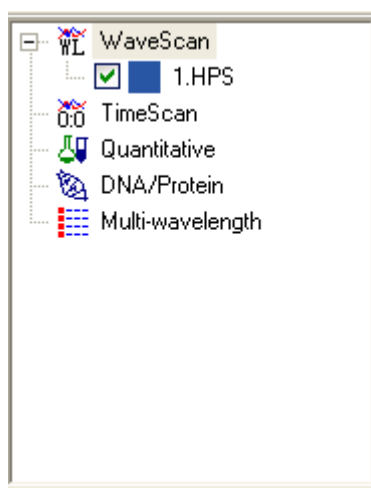
Each wavelength can be set in the range of 190~1100nm.

8 wavelengths can be set in the maximum for the analysis. If one of wavelengths is set to 0 or left blank, the wavelengths after it will not be used.





## Measure Mode :

Two modes can be select: T% and Abs.

## 3.4. Work Mode Window



5 work modes, WaveScan, TimeScan, Quantitative, DNA/Protein and Multi-wavelength can be selected in the work mode window. Selecting a mode only need click it by a mouse.

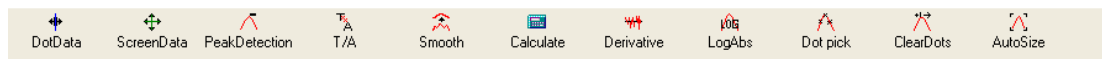
More than one files can be existed under wavelength scan and time scan work modes. A sign of “” or “” at the left of the work modes’ name means files are existed. “” means it is not the current work mode. “” represents it is the current work mode. The default of unsaved file’s name is “Newfile?” and before the system exited a prompt window will display to ask if save the file.

Quantitative, DNA/Protein and Multi-wavelength work modes only allow operating the current file. If another file opened, the current file will be overwritten. So please confirm that the work data has already been saved before open another file.

## 3.5. Tools Bar

The tools bar is different under different work modes.

Under wavelength scan and time scan work modes, the tools bar is shown as below:



Under quantitative work mode, the tools bar is shown as below:

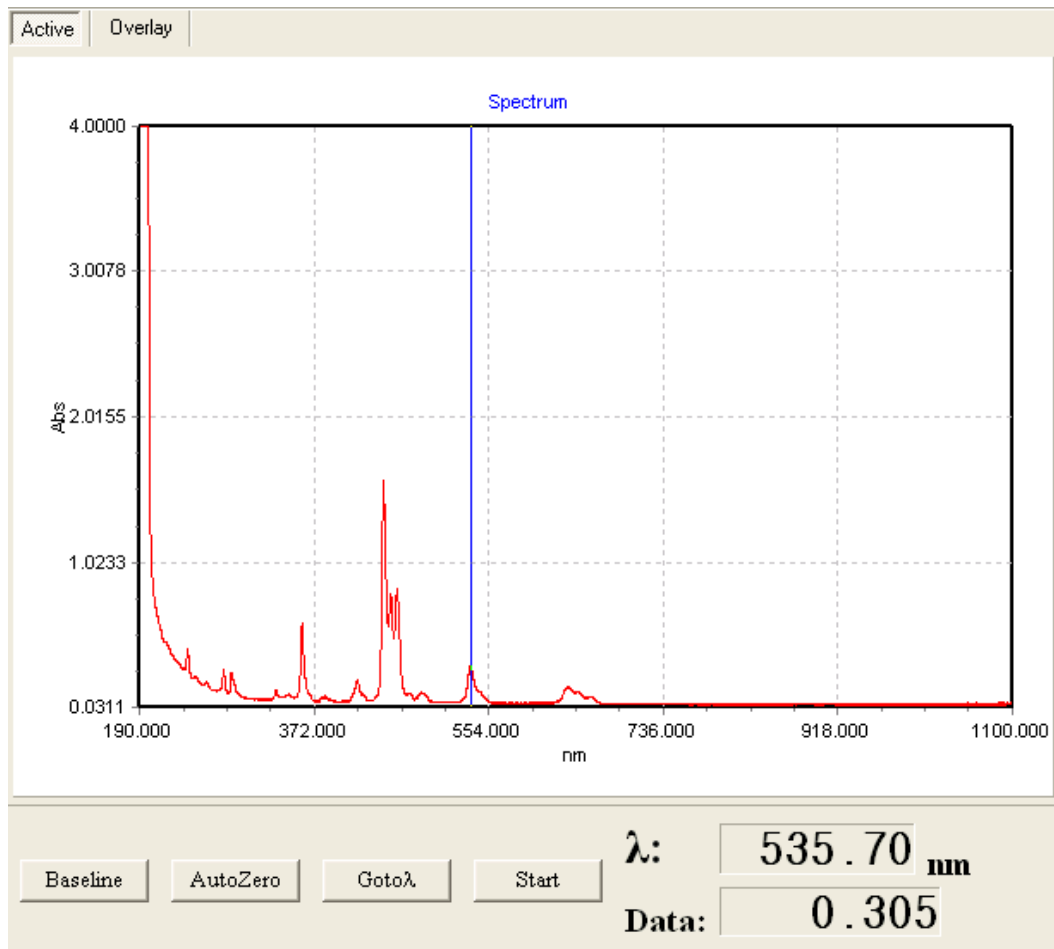


And the tools bar is not valuable under DNA/Protein and multi-wavelength work modes.



Under wavelength scan, time scan and quantitative work mode, this tool can display a vertical line on the spectrum. Data display bar will display the data at the point where the line cross the curve. This line can be moved by mouse dragging or the left or right arrow keys on the keyboard.

The example under wavelength scan work mode is shown.

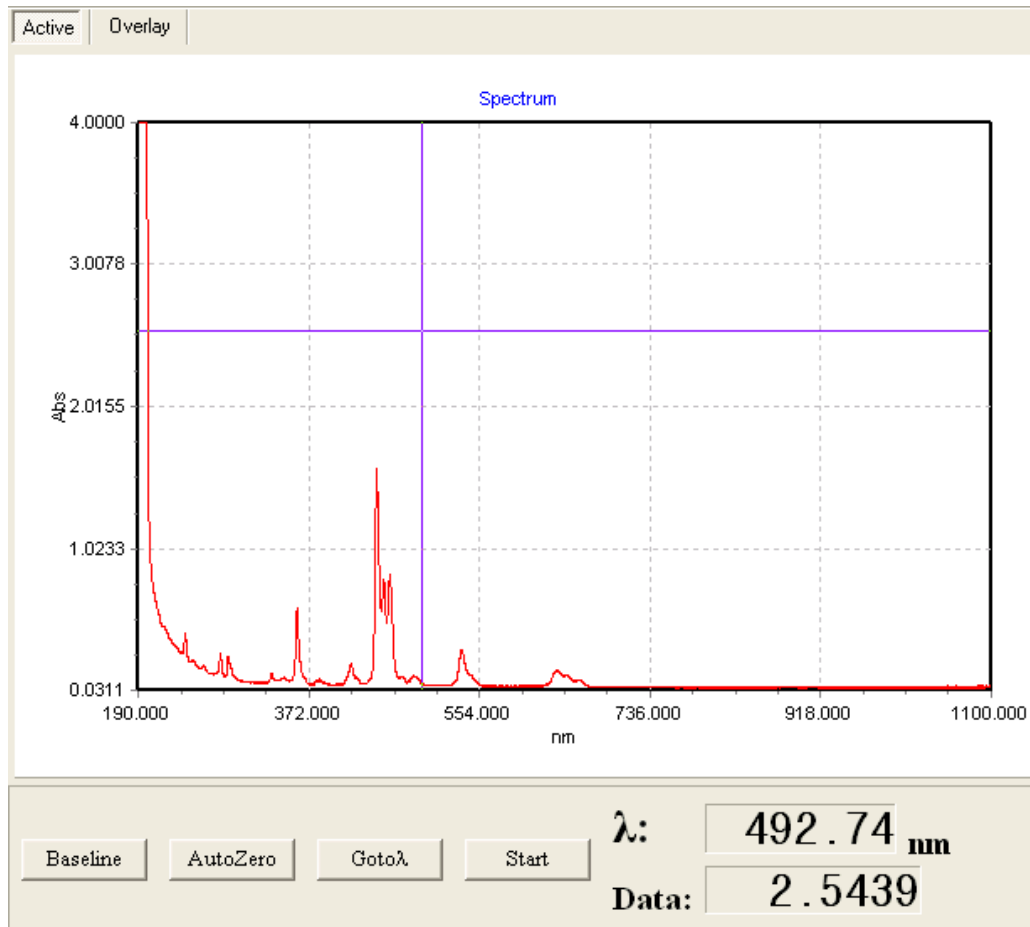


Note: This function is not valuable for overlay spectrum display mode under wavelength scan and time scan work modes.



Under the wavelength scan, time scan and quantitative work modes, this tool can display cross lines on the spectrum. Data display bar will display the X and Y data of the cross point. This point can be moved by mouse dragging.

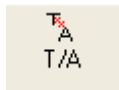
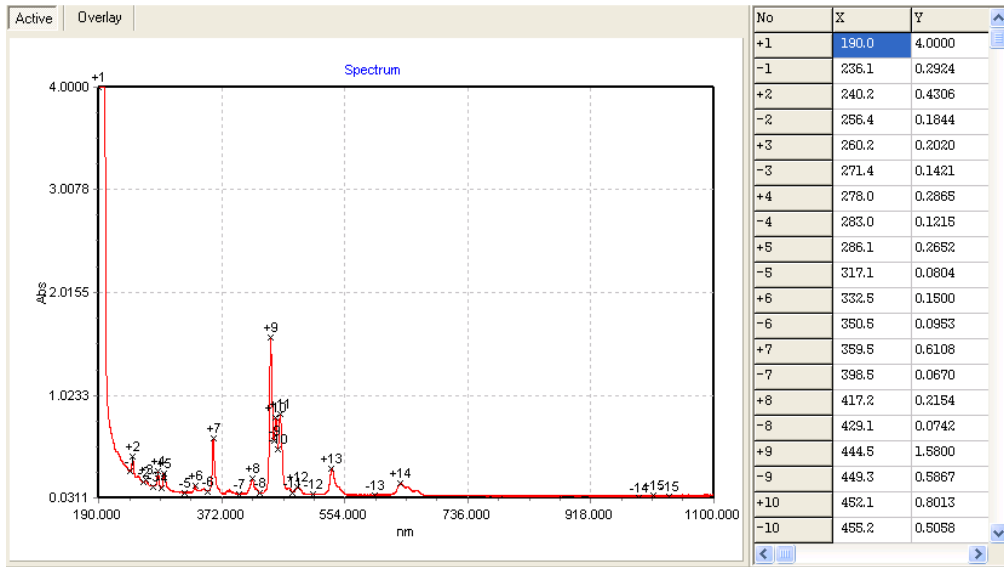
The example shown below is under wavelength scan work mode.



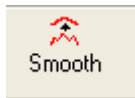
This function is valuable in the active spectrum window only.

It detects peaks and valleys data of the current curve and display results on the spectrum and data table at the right of the screen in the spectrum and data table window.

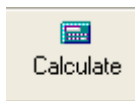
The example is under wavelength scan work mode.



This function is valuable in the active spectrum window only.  
 It is not valuable if the current spectrum is E mode.  
 It can transfer the spectrum between the T% and Abs modes.

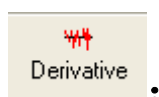
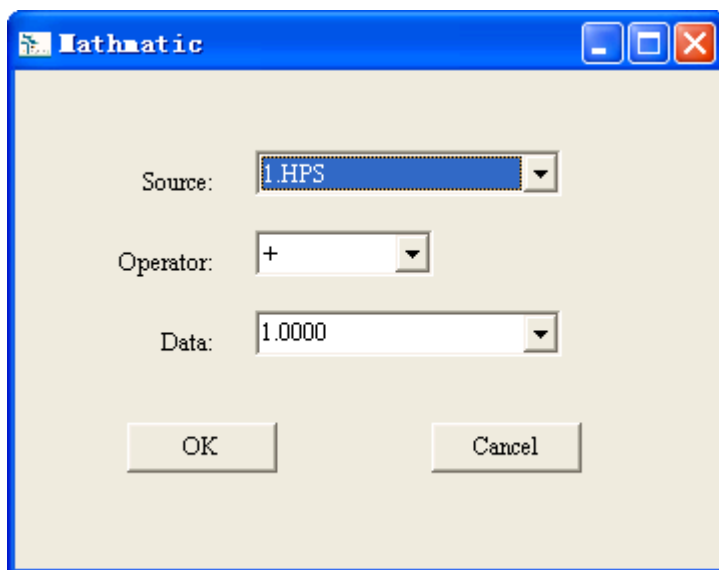


This function is valuable in the active spectrum window only.  
 It can smooth the current spectrum in a certain degree if the curve is not smooth.



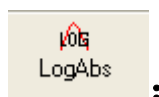
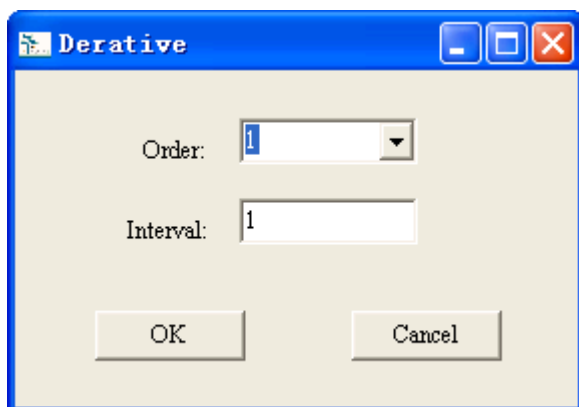
This function is valuable in the active spectrum window only.  
 It can add, subtract, multiply or divide the current spectrum with the current spectrum, other spectrum or a constant.

The calculation window looks like:



This function is valuable in the active spectrum window only.  
It calculates the derivative curve of the current curve in the selected order (1-4) and interval (the points which is used as one point for calculating purpose).

The setting window of order and interval looks like:



This function is valuable in the active spectrum window only.  
This function is not valuable if the spectrum is T% or E mode.  
It calculates the log curve of the current Abs spectrum.

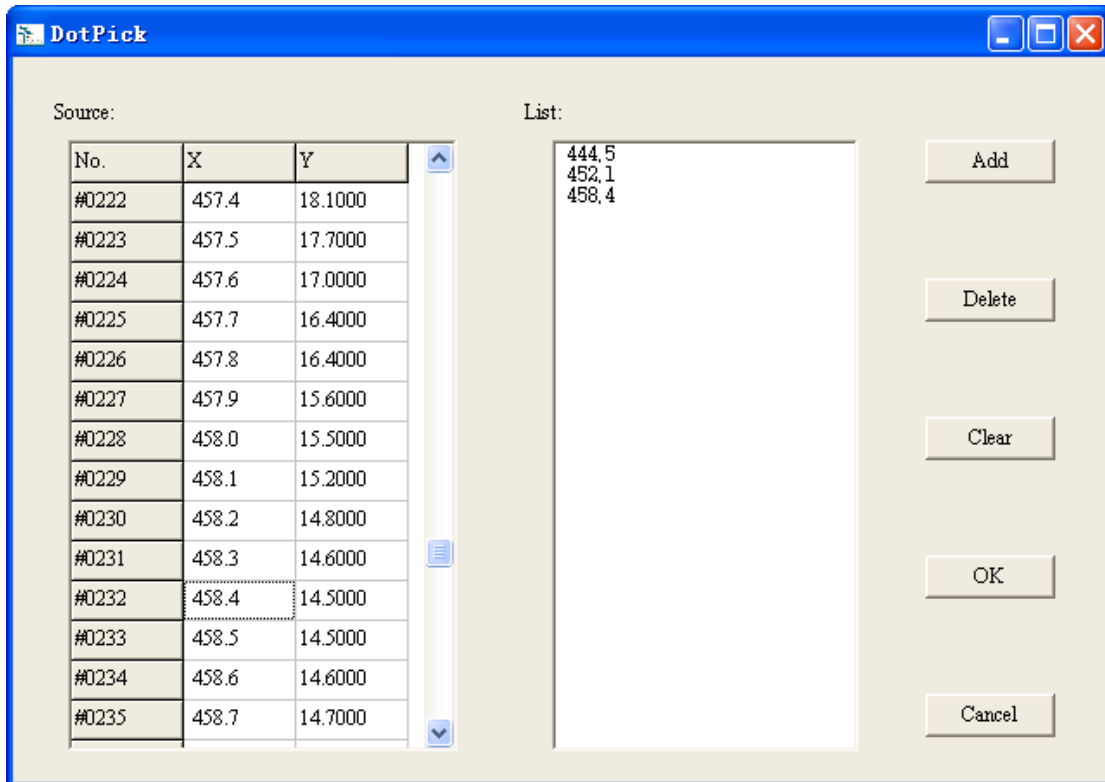




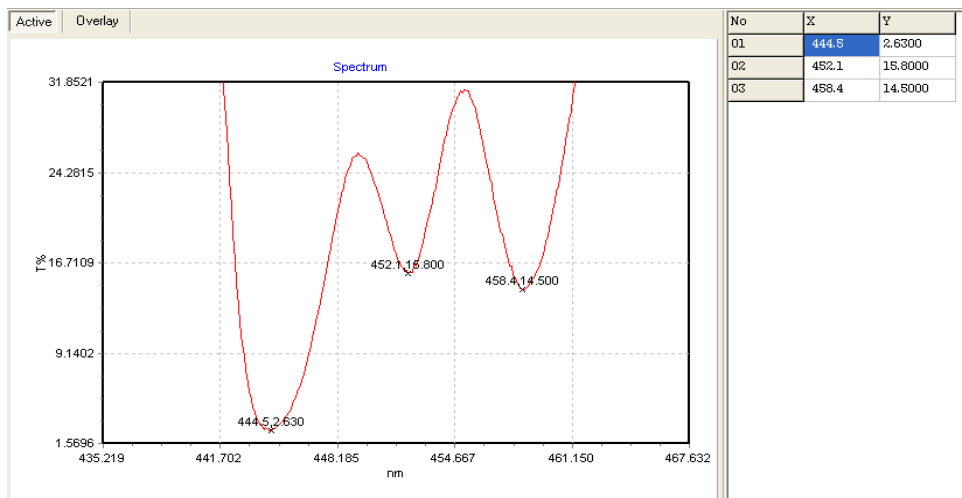
This function is valuable in the active spectrum window only.

It picks up points on the current curve that want to display data of them on the spectrum and in the data table in the spectrum and data table window.

Points selected window looks like:

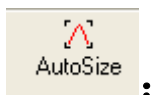


Result after selected:





Clear the selected points' marks on the spectrum.



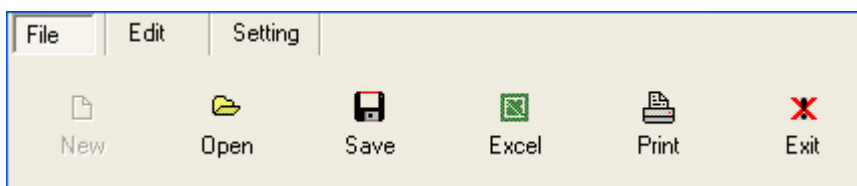
Auto rescales coordinate axes to fit the current curve.

## 3.6. Main Functions Bar

There are three functions groups: File, Edit and Setting.

### 3.6.1 File group

File functions group under wavelength scan, time scan work modes:

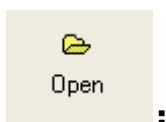


File functions group under quantitative, DNA/Protein and multi-wavelength work modes:



There is no "New" function under wavelength scan and time scan work modes.

This function is used for clearing all data in the data table under quantitative, DNA/Protein and multi-wavelength work modes. Please confirm useful data are already saved before using this function.



This function will open a file by selecting it in a file dialog window.

Under wavelength scan mode, the default file suffix is “HPS” or “CSV”. Data in the “HPS” suffix files format in binary. Data in the “CSV” files format in ASCII, so it can be opened directly by Microsoft Excel or Microsoft Word.

Under time scan mode, the default file suffix is “HPT” or “CSV”. Data in the “HPT” suffix files format in binary. Data in the “CSV” files format in ASCII, so it can be opened directly by Microsoft Excel or Microsoft Word.

Under quantitative mode, the default file suffix is “HPQ”. Data in files format in binary. When open a file and the current data are unsaved, a dialog will display to ask if need to save. When save is selected, a file dialog for saving is displayed. After saving, should select open function again to open a file. If decide no save, current data will be clear and data in the file is displayed.

Under DNA/Protein mode, the default file suffix is “DNA”. Data in files format in binary. When open a file and the current data are unsaved, a dialog will display to ask if need to save. When save is selected, a file dialog for saving is displayed. After saving, should select open function again to open a file. If decide no save, current data will be clear and data in the file is displayed.

Under multi-wavelength mode, the default file suffix is “MUL”. Data in files format in binary. When open a file and the current data are unsaved, a dialog will display to ask if need to save. When save is selected, a file dialog for saving is displayed. After saving, should select open function again to open a file. If decide no save, current data will be clear and data in the file is displayed.



This function is used to save data to the file. After click it a file saving dialog display for inputting file name. File name should fit with Windows system’s request.

Under wavelength scan work mode, the default file suffix is “HPS” or “CSV”. Data in the “HPS” suffix files are binary format. Data in the “CSV” files are ASCII format, so it can be opened directly by Microsoft Excel or Microsoft Word.

Under time scan work mode, the default file suffix is “HPT” or “CSV”. Data in the “HPT” suffix files are binary format. Data in the “CSV” files are ASCII format, so it can be opened directly by Microsoft Excel or Microsoft Word.

Under quantitative work mode, the default file suffix is “HPQ”. Data in the “HPQ” suffix files are binary format.

Under DNA/Protein work mode, the default file suffix is “DNA”, and data in these files are binary format.

Under multi-wavelength work mode, the default file suffix is “MUL” , and data in these files are binary format.



This function transfers the current data under the current work mode into Excel program in spreadsheet format.

The Microsoft Excel program must be already installed correctly. Otherwise, an error will be reported.

Under wavelength scan and time scan work modes, the data in the data table at the right of the screen will be transferred, not include scan parameters.

Under quantitative work mode, the data of the sample and standards are transferred, not include work parameters.

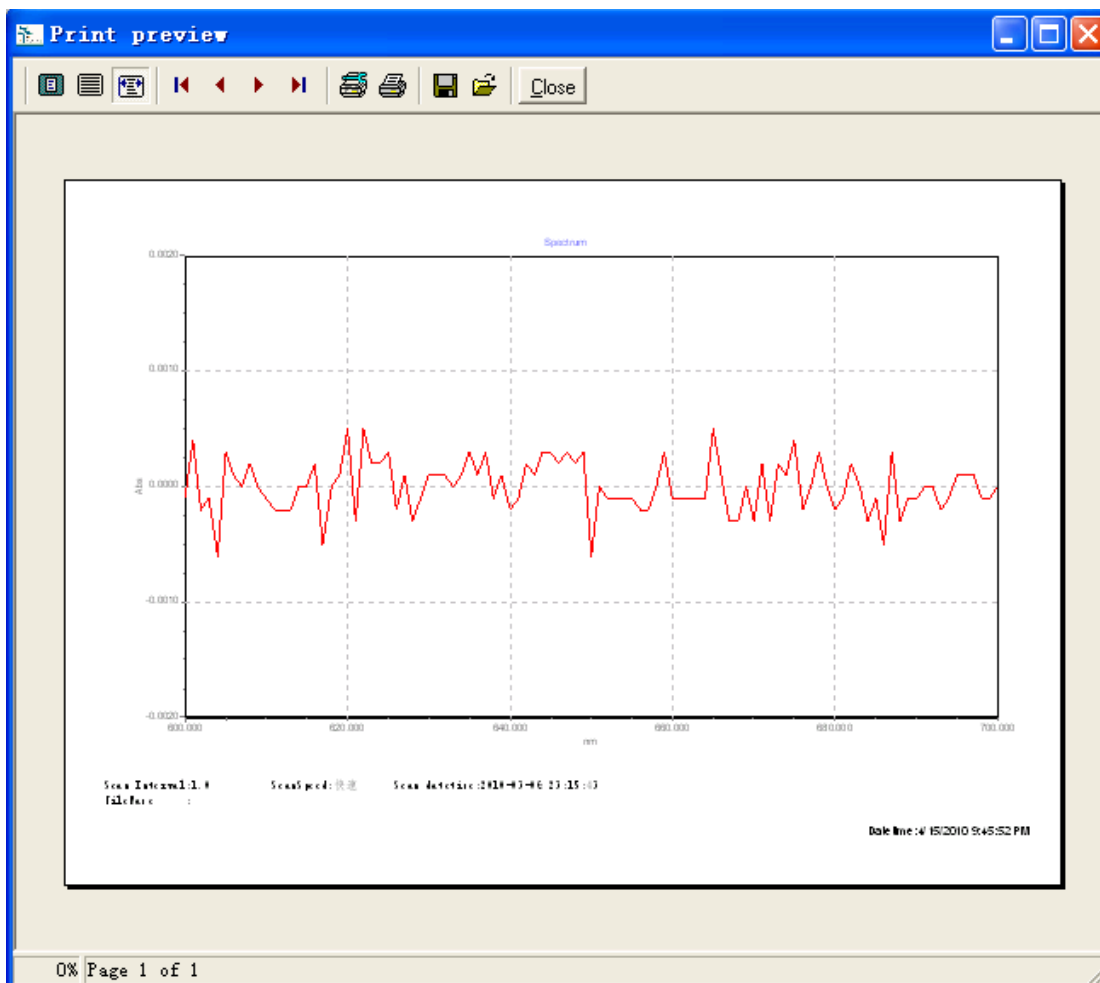
Under DNA/Protein and multi-wavelength work modes, the data in the data table at the right of the screen will be transferred, not include work parameter.



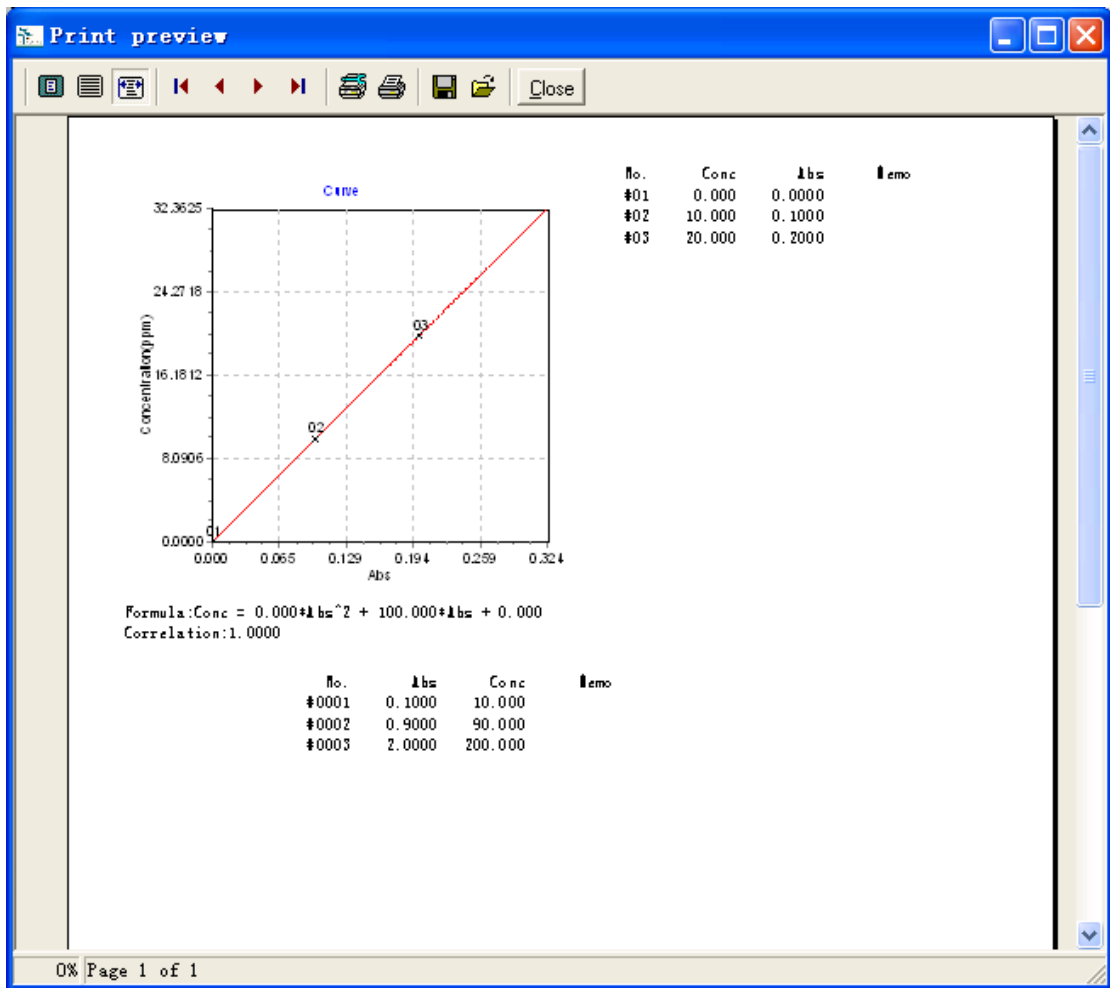
This function will display the data in a print preview mode based on work mode, then wait user decide if print it out.

Under wavelength scan and time scan work modes, the print format is same. For active spectrum printing, spectrum, scan interval, scan speed, scan time, file name and time will be printed out. For overlay spectrum, only spectrum and time will be printed, no other information.

The example figure is a printing of an active spectrum under wavelength scan work mode

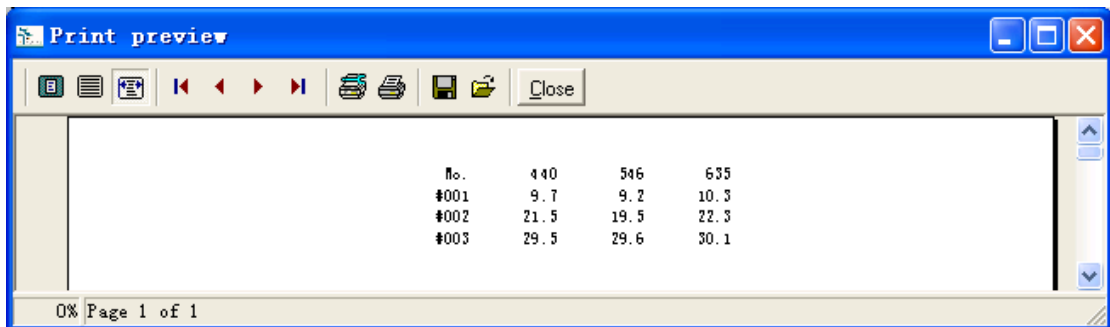


Under quantitative work mode, the work curve, curve equation, data of standards and data of the samples will be printed out.



Under DNA/Protein and multi-wavelength work modes, only data in the data table will be printed out.

The example is in multi-wavelength work mode.

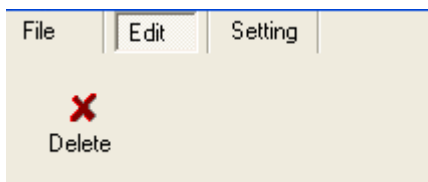


This function will exit the system.

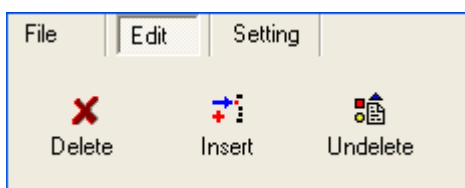
Before exiting, if there is any unsaved spectrum or data, the prompt window for saving will display. Select No if do not want to save. If select Yes, a file save dialog will display. Input file name and click save button to save it.

## 3.6.2 Edit group

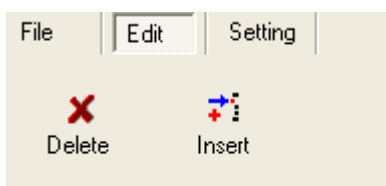
Edit functions group under wavelength scan and time scan work modes.



Edit functions group under quantitative work mode.



Edit functions group under DNA/Protein and multi-wavelength work modes.

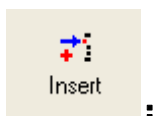


Delete function is different under different work modes.

Under wavelength scan and time scan work modes, this function delete the selected spectrum in the work modes window under current work mode.

Under quantitative work mode and in the standards data table, it is only marked data when use the delete function first time. The mark “\*” means the data do not be used in the calculation. The data is really deleted when using the function second time. In the samples data table, this function will delete the data in the current line.

Under DNA/Protein and multi-wavelength work modes, this function will delete the data in the current line.



There is no this function under wavelength scan and time scan work modes.

Under quantitative, DNA/Protein and multi-wavelength work modes, this function will insert

a record in the current line.

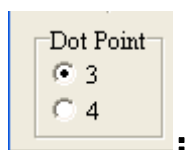


There is no this function under wavelength scan, time scan work, DNA/Protein and multi-wavelength modes.

Under quantitative work mode, this function will remove the deleting marks of standards data. And the data will be used in the calculation again.

### 3.6.3 Setting group

The functions in the setting group.

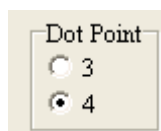


This check box used for setting the digits after the decimal point of the Abs value.

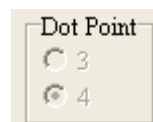
3 means the data format is FX.XXX, where F is the sign. When data is more than 0, the sign will not display. When less than 0, it will be “-”.

4 means the data format is FX.XXXX, where F is the sign. When data is more than 0, the sign will not display. When less than 0, it will be “-”.

After connect the instrument, it will display as



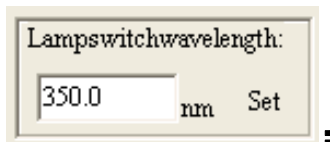
When the instrument do not be connected, it will looks like



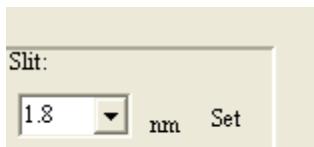




These check boxes are used to control the Deuterium and tungsten lamp on or off. This function can not work now.



This edit box is used to set the wavelength for switching lamps. The value can be set in the range of 294~364 nm.



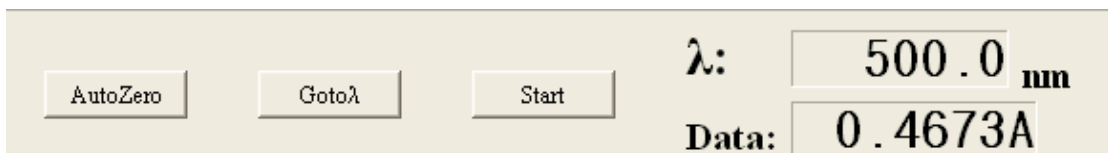
Slit Settings(Bandwidth): set slit bandwidth then press “set” button. The actual slit displays on the status area of instrument.

### 3.7. Buttons and Data Display Bar

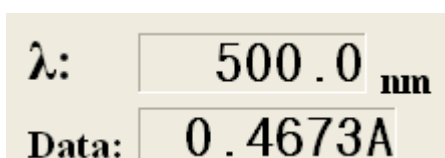
Under wavelength scan work mode



Under other work modes



#### 3.7.1 Data display:



Display the current wavelength and real-time data.

## Wavelength $\lambda$ :

When it is in the process of scanning under time scan work mode, the title will change to “Time” and the unit will change from “nm” to “s”. Under other work modes, it will be same as shown in the figure.

## Real-time data:

Display the real time data based on the current work modes. The last digit is different under different measure modes, “%” for T% mode, “A” for Abs mode and “E” for E mode.

Under “Dot Data” or “Screen Data” tools working status, it will display the curve data instead of real time data.

## 3.7.2 Buttons:

**Baseline** :

This button can not be used when the instrument do not be connected.

This button is only displayed under wavelength scan work mode.

This button is used for the baseline correction. It works based on setting wavelength range, scan interval and scan speed. The minimum of the scan interval is 0.1 nm. In the process of the baseline correction, the “Start” button will change to “Cancel”. Clicking it will cancel the baseline correction.

**AutoZero** :

This button can not be used when the instrument do not be connected.

This button can work in T% and Abs measure modes under all work modes. But it is pointless in E measure mode.

In T% and Abs measure modes, the instrument will adjust the gain to the best scale based on the current sampling data. Then the sampling data with closing the light screen is set to zero.


If more than one wavelength is requested for current measurement, the instrument will move to each wavelength, set zero at each point and move back to the beginning wavelength (the first setting wavelength).

**Gotoλ** :

This button can not be used when the instrument do not be connected.

The button can work under all work modes.

Clicking this button after connecting, wavelength inputting will be requested at the

wavelength display position . Input the expected wavelength in the edit box and press “Enter” key on the keyboard.

The wavelength range is in 190~1100nm.

In the process of wavelength moving, “Start” button will change to “Cancel”. Click it to cancel the wavelength moving.

**Start** :

This button can not be used when the instrument do not be connected.

The button can work under all work modes.

Under wavelength scan and time scan work modes, click the button to begin the scanning and the button changes to “cancel” button. In the scanning process, click this “cancel” button can stop the scanning.

Under quantitative, DNA/Protein and multi-wavelength work modes, this button is used for sampling. If the sampling wavelength is 1, it will stop after finished. If the wavelength is more than 1, it will move to the next wavelength and begin sampling after finished one sampling under a wavelength. After finished sampling under all wavelengths, it will move back to the first wavelength position (the first setting wavelength).

**Pool**

Only for UV2400 and UV2600. Click it for moving position of cuvette. R is for reference sample, S1-S7 is for sample. Window shows the position of cuvette.

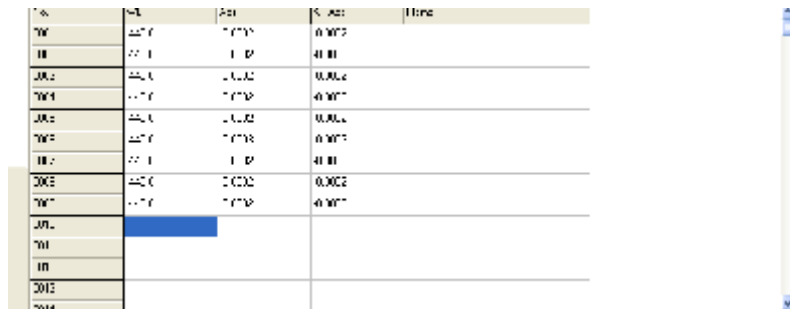
## 3.8. Spectrum and Data Table Window

### 3.8.1 Photometric Measurement

Under photometric measurement mood, no map area, only the data table

The first line shows the title data table

The title is shown as: "No", "probably", "Abs", "K \* Abs"...



No	probably	Abs	K * Abs
1	...	...	...
2	...	...	...
3	...	...	...
4	...	...	...
5	...	...	...
6	...	...	...
7	...	...	...
8	...	...	...
9	...	...	...
10	...	...	...
11	...	...	...
12	...	...	...
13	...	...	...
14	...	...	...
15	...	...	...
16	...	...	...
17	...	...	...
18	...	...	...
19	...	...	...
20	...	...	...
21	...	...	...
22	...	...	...
23	...	...	...
24	...	...	...
25	...	...	...
26	...	...	...
27	...	...	...
28	...	...	...
29	...	...	...
30	...	...	...
31	...	...	...
32	...	...	...
33	...	...	...
34	...	...	...
35	...	...	...
36	...	...	...
37	...	...	...
38	...	...	...
39	...	...	...
40	...	...	...
41	...	...	...
42	...	...	...
43	...	...	...
44	...	...	...
45	...	...	...
46	...	...	...
47	...	...	...
48	...	...	...
49	...	...	...
50	...	...	...

Clear data:

Through the "file" → "new"

Delete the data:

Through a "edit" → "delete"

Insert the data:

Through the "edit" → "insert"

Save the file:

Through the "file" → "save"

Open the file:

Through a "open" → "file"

Transfer to Excel

Through the "file" → "Excel"

print

Through the "file" → "print"

### 3.8.2 Under wavelength scan and time scan modes

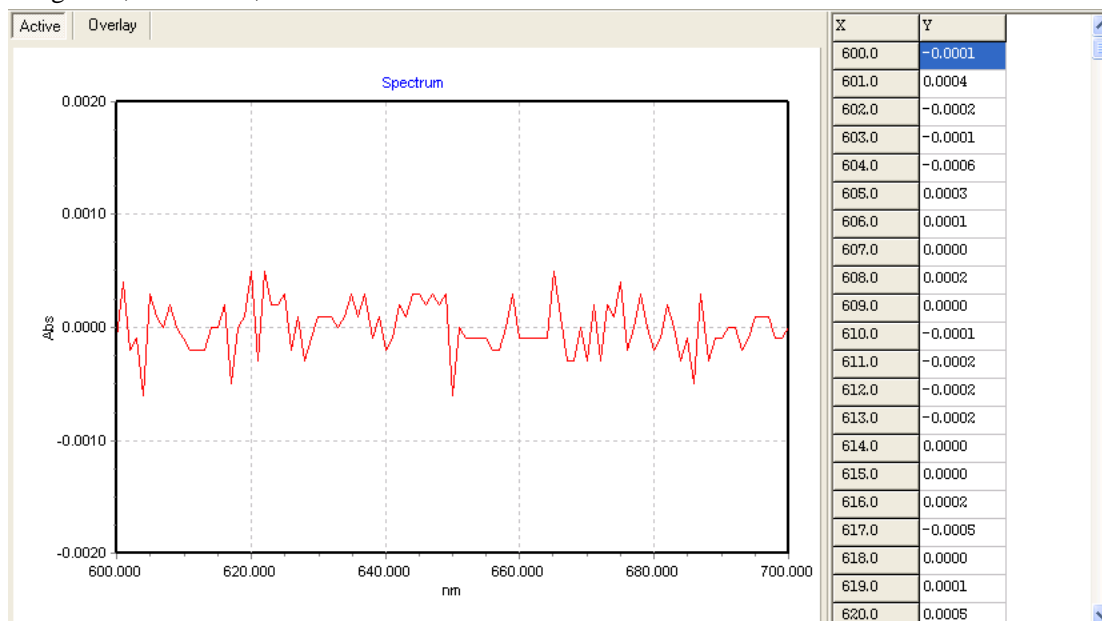
The spectrum have active and overlay windows under wavelength scan and time scan work modes.

#### Active window:

The current scan spectrum or user selected spectrum will display in this window. User selected spectrum is opened by double clicking the file name in the work modes window under the current work mode, or by open file function.

The data displayed in the data table is X, Y axis values of the current spectrum. When the spectrum is enlarged, the data displayed in the table will be changed with the spectrum displaying.

The “DotData”, “ScreenData”, “PeakDetection”, “T/A”, “Smooth”, “Calculate”, “Derivative”, “LogAbs”, “DotPick”, “ClearDots” and “AutoSize” functions can work in this window.

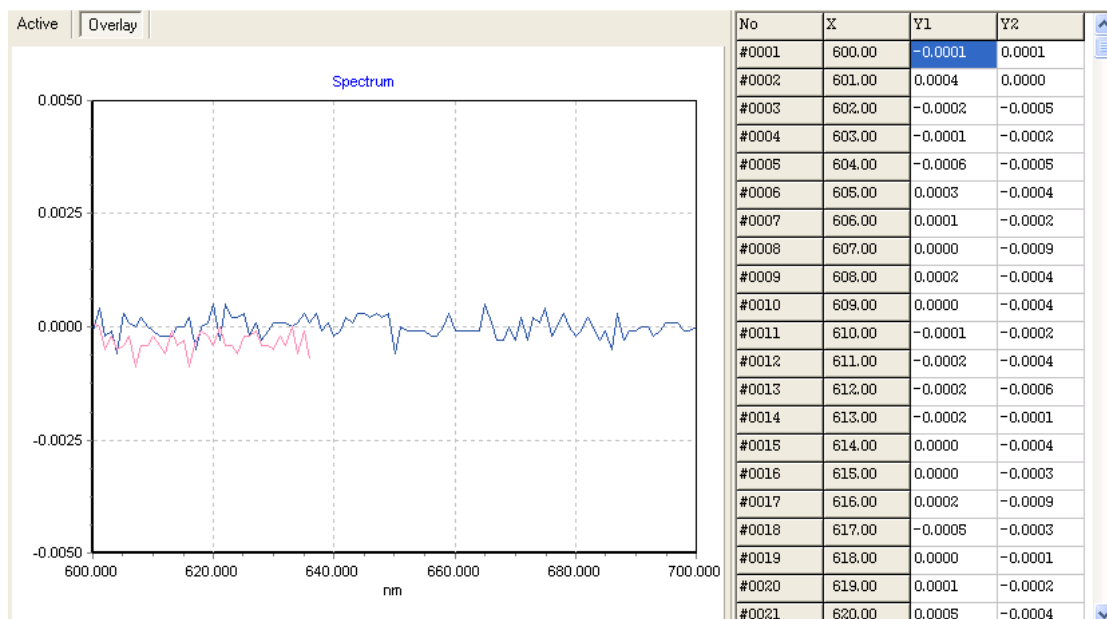


## Overlay window :

All spectrums will display in this window.

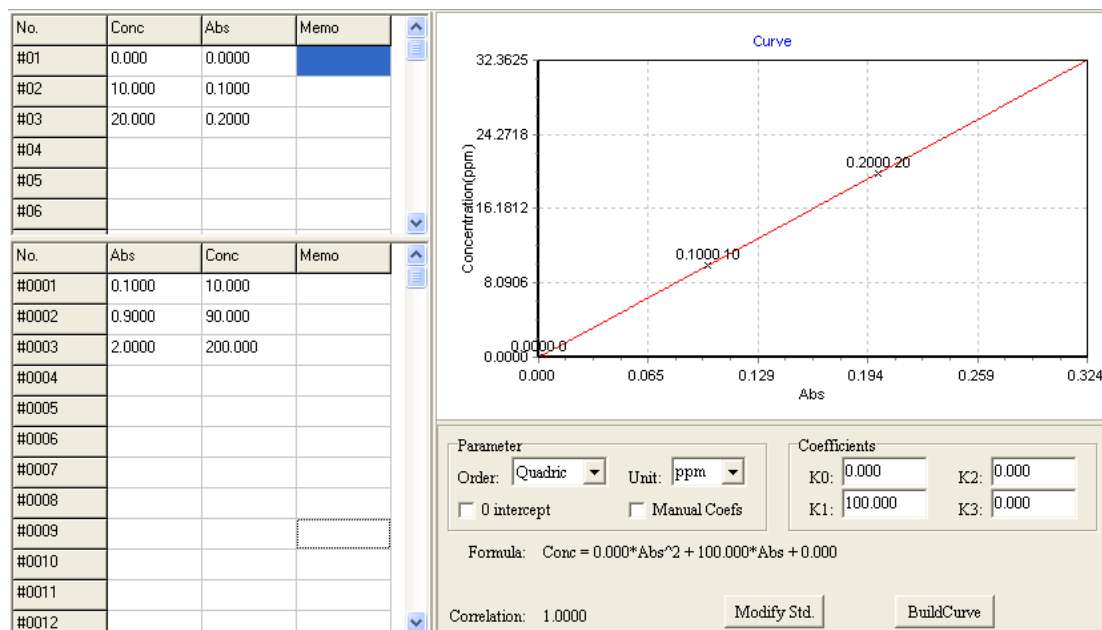
The data displayed in the data table is X, Y axis values of the current spectrum. When the spectrum is enlarged, the data displayed in the table will be changed with the spectrum displaying.

The “ScreenData”, “ClearDots” and “AutoSize” functions can work in this window.



### 3.8.3 Under quantitative work mode

Under quantitative work mode, the work curve and the curve parameters will display in the spectrum window. The data of standards and samples display in the data table.



### Standards data table

No.	Conc	Abs	Memo
#01	0.000	0.0000	
#02	10.000	0.1000	
#03	20.000	0.2000	
#04			
#05			
#06			

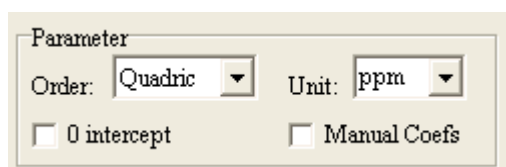
### Input concentrations

Input the concentrations into the table in the low to high concentrations order based on the number of standards. If a wrong order is input, the calculated result will be wrong.

## Measure Abs values

Put the standard into the sample room and cover it. Select the requested line in the table by a mouse and press “Start” button (Refer to start button in the 3.6.2 buttons section). The Abs value will be displayed in the table after measurement finished. And the input focus will move to the next line. If need to repeat measurement, repeat steps above till finished all.

## Build curve



Parameter

Order:  Unit:

0 intercept  Manual Coefs

Set parameters according to the request.

### Order:

Four modes, “Linear”, “Quadric”, “Cubic” and “Polygonal” can be selected.

“Linear”, “Quadric” and “Cubic” will have

Formula:  $\text{Conc} = 0.000 \cdot \text{Abs}^2 + 100.000 \cdot \text{Abs} + 0.000$  and Correlation: 1.0000

But the “Polygonal” do not have them.

### Unit:

“%”, “ppm”, “ppb”, “g/L”, “mg/mL”, “ng/mL”, “M/L”, “ug/mL” and Null 9 modes can be selected according to the request.

### 0 intercept:

If checked, the K0 of the curve will be set to 0.

### Manual Coefs:

If check this, coefficients need to be input manually. Input K0, K1, K2 and K3 and press “BuildCurve” button to build a curve.

If do not check this, press “Modify Std” button after setting parameters for quantitative. Input a serial of concentrations in the standards data table and measure Abs values as the description above.



## Samples data table

No.	Abs	Conc	Memo
#0001	0.1000	10.000	
#0002	0.9000	90.000	
#0003	2.0000	200.000	
#0004			
#0005			
#0006			
#0007			
#0008			
#0009			
#0010			
#0011			
#0012			

## Measure samples

Before samples measurement, must measure standards and build the curve, or build the curve by manual inputting coefficients, or get the curve by opening a file.

Put the sample want to be measured into the sample room and cover it. Select the requested line in the table by a mouse and press “Start” button (Refer to start button in the 3.6.2 buttons section). The Abs value will be displayed in the table after measurement finished. And the input focus will move to the next line.

### 3.8.4 Under DNA/Protein work mode

Under DNA/Protein work mode, no spectrum window display, only the data table display.

Titles are display in the first line of the data table.

When no reference wavelength exist, titles will be:

“No.”, “A(WL1)”, “A (WL2)”, “A1/A2”, “Result (DNA)” and “Result (Protein)” .

When the reference wavelength exist, titles will be:

“No.”, “A(WL1)”, “A (WL2)”, “A (RefWL)”, “A1/A2”, “Result (DNA)” and “Result (Protein)”

Example with having reference wavelength

No.	A(260.0)	A(230.0)	A(320.0)	A1/A2	Result(DNA)	Result(Protein)
#001						
#002						
#003						
#004						
#005						
#006						
#007						
#008						
#009						
#010						
#011						
#012						
#013						
#014						
#015						
#016						
#017						
#018						
#019						

Clear data:

Function “File” → “New” .

Delete data:

Function “Edit” → “Delete” .

Insert data::

Function “Edit” → “Insert” .

Save file:

Function “File” → “Save” .

Open file:

Function “File” → “Open” .

Transfer to Excel

Function “File” → “Excel” .

Print

Function “File” → “Print” .

### 3.8.5 Under multi-wavelength work mode

Under DNA/Protein work mode, no spectrum window display, only the data table display.

Titles are displayed in the first line of the data table.

Based on setting wavelengths, titles will be: “No”, “WL1”, “WL2”, “WL3”...

No.	440	546	635
#001			
#002			
#003			
#004			
#005			
#006			
#007			
#008			
#009			
#010			
#011			
#012			
#013			
#014			
#015			
#016			
#017			
#018			
#019			
#020			

Clear data:

Function “File” → “New” .

Delete data:

Function “Edit” → “Delete” .

Insert data::

Function “Edit” → “Insert” .

Save file:

Function “File” → “Save” .

Open file:

Function “File” → “Open” .

Transfer to Excel

Function “File” → “Excel” .

Print







Function “File” → “Print” .

# 4. Operation

## 4.1 Photometric Measurement

This chapter introduces how to measure single wavelength absorbance or transmittance.

### 4.1.1 Measurement

1. Click  **Photometric Measurement** in the work mood.
2. In the parameters window, select measure mood and enter coefficient value.
3. Click , enter wavelength value and press: “Enter”, the meachine will goto wavelength automatically.
4. UV2400, UV2600: put the reference samples (blank) in optical path, and then press the . The instrument does zero for the reference sample. After zero, put the samples in optical path, then press .  
UV2800, UV2800S: put the reference samples (blank) on the shelf R and shelf S, close cover, press the . After zero, take the reference samples away, put the sample want tested, then press .

### 4.1.2 Save Data

1. Select “File” → “Save”
2. Under save file window, choose save the file directory and file name, click save.
3. The data is saved as extension \*. SPC photometric data files.

### 4.1.3 Transmit Data






Select “File” → “Excel”

### 4.1.4 Print Report

Select “File” → “Print” , set print parameters and click print.

## 4.2 Wavelength Scan

### 4.2.1 Measurement

1. Select  Wavelength Scan under work mood.
2. Under parameters window, select measurement mood, scan wavelength range, vertical coordinate range, scan interval and scan speed.  
(Under ASB mood, suggest user to choose 0-4 of vertical coordinate range, 1nm scan interval and fast scan speed.)
3. UV2400, UV2600: put the reference samples (blank) in optical path, and then press the . The instrument does baseline for the reference sample. After baseline, put the samples in optical path, then press .  
UV2800, UV2800S: put the reference samples (blank) on the shelf R and shelf S, close cover, press the . After baseline, take the reference samples away, put the sample want tested, then press .

### 4.2.2 Map Display Changing Scaling

Under map display, modify the coordinates of the upper and lower limits and press "Enter" button.

### 4.2.3 Search Peak and Valley

This button is for searching peak valley data, and marks the result on the map.

### 4.2.4 Save Data

1. Double click file name, then select "File" → "Save" .
2. Under save file window, choose save the file directory and file name, click save.
3. The data is saved as extension \*. HPS photometric data files.
4. Click right bottom of mouse, display "copy". Then click copy to stick on the Word or Excel.

### 4.2.5 Transmit Data


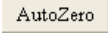
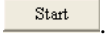


Select "File" → "Excel"

## 4.2.6 Print Report

Select “File” → “Print” , set print parameters and click print.

## 4.3 Time Scan

### 4.3.1 Measurement

1. Select  Time Scan under work mood.
2. Under parameters window, select measurement mood, scan wavelength range, vertical coordinate range, scan interval and scan speed.  
(Under ASB mood, suggest user to choose 0-4 of vertical coordinate range and 1s interval)
3. UV2400, UV2600: put the reference samples (blank) in optical path, and then press the . The instrument does zero for the reference sample. After zero, put the samples in optical path, then press .  
UV2800, UV2800S: put the reference samples (blank) on the shelf R and shelf S, close cover, press the . After zero, take the reference samples away, put the sample want tested, then press .

### 4.3.2 Map Display Changing Scaling

Under map display, modify the coordinates of the upper and lower limits and press "Enter" button.

### 4.3.3 Search Peak and Valley

This button is for searching peak valley data, and marks the result on the map.

### 4.3.4 Save Data

1. Double click file name, then select “File” → “Save” .
2. Under save file window, choose save the file directory and file name, click save.
3. The data is saved as extension \*. HPS photometric data files.
4. Click right bottom of mouse, display “copy”. Then click copy to stick on the Word or Excel.

### 4.3.5 Transmit Data

Select “File” → “Excel”


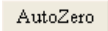

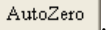

### 4.3.6 Print Report

Select “File” → “Print” , set print parameters and click print.

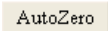

## 4.4 Quantitative Analysis

### 4.4.1 Measurement

#### a. Standard sample demarcate method (Multiple Point)

1. Click  Quantitative Analysis in the work mood.
2. In the parameters window, select measure mood and enter wavelength value and coefficient value. (Generally choose 1 wavelength method)
3. Choose line type and unit (suggest lint type: straight line)
4. UV2400, UV2600: put the reference samples (blank) in optical path, and then press the . The instrument does zero for the reference sample. After zero, put the samples in optical path, then press .
- UV2800, UV2800S: put the reference samples (blank) on the shelf R and shelf S, close cover, press the . After zero, take the reference samples away, put the sample want tested, then press .
5. According to the number of sample and Conc, to enter concentration from small to large. If the order is wrong, lead to calculate fault.
6. Corresponding to the input concentration, put the samples on sample room in the light path, close cover, use the mouse to select the current need Abs (absorbance) prototype line, and then press the "start" button. After completion of sampling, Abs value will display in the table, at the same time the input focus will automatically move down the next line. If you need to get again, please repeat the operation, until you get as so far.
7. After completion of measurement, press the "curve" button, the curve, equation and phase relationship automatically displayed in the table. If any error, press "modify", enter value. then "get Abs value", "establishing curve" button again, the curve equation and correlation coefficient display in the table.
8. Corresponding to the input concentration, put the samples on sample room in the light path, close cover, use the mouse to select the current need Abs (absorbance) prototype line, and then press the "start" button. After completion of sampling, Abs value will display in the table, at the same time the input focus will automatically move down the next line. If you need to get again, please repeat the operation, until you get as so far.

#### b. Coefficient method

1. In the parameters window, select measure mood and enter wavelength value and coefficient value. (Generally choose 1 wavelength method)
2. Choose unit.
3. Choose "manual coefficient" and enter known coefficient and press "curve". The curve equation and correlation coefficient display in the table.
4. UV2400, UV2600: put the reference samples (blank) in optical path, and then press the . The instrument does zero for the reference sample. After zero, put the samples in optical path, then press .
- UV2800, UV2800S: put the reference samples (blank) on the shelf R and shelf S, close cover,



press the **AutoZero**. After zero, take the reference samples away, put the sample want tested, then press **Start**.

5. Put the samples on sample room in the light path, close cover, use the mouse to select the current need Abs (absorbance) prototype line, and then press the "start" button. After completion of sampling, Abs value will display in the table, at the same time the input focus will automatically move down the next line. If you need to get again, please repeat the operation, until you get as so far.

## **4.4.2 Save Data**

- 1.Select “File” → “Save”
- 2.Under save file window, choose save the file directory and file name, click save.
3. The data is saved as extension \*. HPQ photometric data files.

## **4.4.3 Transmit Data**

Select “File” → “Excel”

## **4.4.4 Print Report**

Select “File” → “Print” , set print parameters and click print.

## 4.5 DNA/Protein Analysis

### 4.5.1 Measurement

1. Click **DNA/Protein Analysis** in the work mood.
2. Under parameters window, select measurement mood.
3. UV2400, UV2600: put the reference samples (blank) in optical path, and then press the **AutoZero**. The instrument does zero for the reference sample. After zero, put the samples in optical path, then press **Start**.

UV2800, UV2800S: put the reference samples (blank) on the shelf R and shelf S, close cover, press the **AutoZero**. After zero, take the reference samples away, put the sample want tested, then press **Start**.

### 4.5.2 Save Data

1. Select “File” → “Save”
2. Under save file window, choose save the file directory and file name, click save.
3. The data is saved as extension \*. HPQ photometric data files.

### 4.5.3 Transmit Data


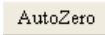

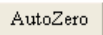

Select “File” → “Excel”

### 4.5.4 Print Report

Select “File” → “Print” , set print parameters and click print.

## 4.6 Multi-wavelength Measurement

### 4.6.1 Measurement

1. Click  Multi-Wavelength Measure in the work mood.
2. Under parameters window, select measurement mood and enter wavelength.
3. UV2400, UV2600: put the reference samples (blank) in optical path, and then press the . The instrument does zero for the reference sample. After zero, put the samples in optical path, then press .
- UV2800, UV2800S: put the reference samples (blank) on the shelf R and shelf S, close cover, press the . After zero, take the reference samples away, put the sample want tested, then press .

### 4.6.2 Save Data

1. Select “File” → “Save”
2. Under save file window, choose save the file directory and file name, click save.
3. The data is saved as extension \*. HPQ photometric data files.

### 4.6.3 Transmit Data

Select “File” → “Excel”

### 4.6.4 Print Report

Select “File” → “Print” , set print parameters and click print.