

# **Protein Pressure-Temperature Phase Diagram Fit module**

**version v0.6.1**

**USER GUIDE**

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# Contents

<b>1</b>	<b>Copyright</b>	<b>2</b>
<b>2</b>	<b>License of the code</b>	<b>2</b>
<b>3</b>	<b>System Requirements</b>	<b>2</b>
3.1	Operating system	2
3.2	Software	2
<b>4</b>	<b>Installation</b>	<b>3</b>
4.1	phaseTPfit.tar.gz	3
4.2	Python Configuration Files	3
4.3	Buttons attachment	4
4.4	QtiPlot's template's	5
<b>5</b>	<b>Working with Protein Pressure–Temperature Phase Diagram Fit package</b>	<b>6</b>
<b>6</b>	<b>Results log</b>	<b>9</b>
	<b>Reference list</b>	<b>9</b>
<b>7</b>	<b>GNU Free Documentation License</b>	<b>11</b>
7.1	APPLICABILITY AND DEFINITIONS	11
7.2	VERBATIM COPYING	12
7.3	COPYING IN QUANTITY	13
7.4	MODIFICATIONS	13
7.5	COMBINING DOCUMENTS	15
7.6	COLLECTIONS OF DOCUMENTS	15
7.7	AGGREGATION WITH INDEPENDENT WORKS	15
7.8	TRANSLATION	15
7.9	TERMINATION	16
7.10	FUTURE REVISIONS OF THIS LICENSE	16
7.11	RELICENSING	16
7.12	ADDENDUM: How to use this License for your documents	17

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## 3 System Requirements

### 3.1 Operating system

Packages should work correctly on all systems that support other programs that are mentioned below. All the actions are tested on WINDOWS 8 and LINUX MINT 17. So it can be expected good performance on WINDOWS XP/VISTA/7 and LINUX DEBIAN, UBUNTU, KUBUNTU, ETC.

### 3.2 Software

To run the packages the following programs/packages should be installed on your Computer:

- QTIPLLOT [3] with PYTHON [6] scripting
- PYTHON 2.7.\*
  - On commonly used LINUX distributions this program is installed by default, but consumer should install PYTHON-DEV (developer) from SOFTWARE MANAGER or by copying following command in the TERMINAL *sudo apt-get install python-dev*
- PYTHON packages:

- NUMPY [2]
  - \* Download instructions for use are here
- SCIPY [5]
  - \* Download instructions for use are here
- LMFIT [1]
  - \* Download instructions for use are here
- PyQt4 [4]
  - \* Download instructions for use are here

## 4 Installation

All section's **System Requirements** requirements should be accomplished. To install module must perform following steps:

1. Extract **phaseTPfit.tar.gz** containing files to QTIPLLOT'S **Python Configuration Files** path. Merge files if needed.
2. Attach scripting action named **PmLtGen.py** from extracted folder **dialogs** (look at section 4.1) to QTIPLLOT'S button. Instructions shown in section 4.3.
3. Copy qti template named **dose\_curves\_analysis\_template.qti** from extracted folder **templates** (look at section 4.1) to your working directory.

### 4.1 phaseTPfit.tar.gz

This compressed file contains these files:

- *dialogs* folder which contains scripting action and version file
- *manual* folder which contains user guide pdf
- *modules* folder which contains py files
- *templates* folder which contains QTIPLLOT'S templates
- *psaFit.py* py file

### 4.2 Python Configuration Files

*Python Configuration Files* path can be found in the QTIPLLOT'S preferences after these actions (shown in figure 1):

1. Left click on menu bar Edit → Preferences...
2. On the opened settings window click *General* → *File Locations*.
3. Path is in the field *Python Configuration Files*. In the example path is /usr/share/qtiplot.

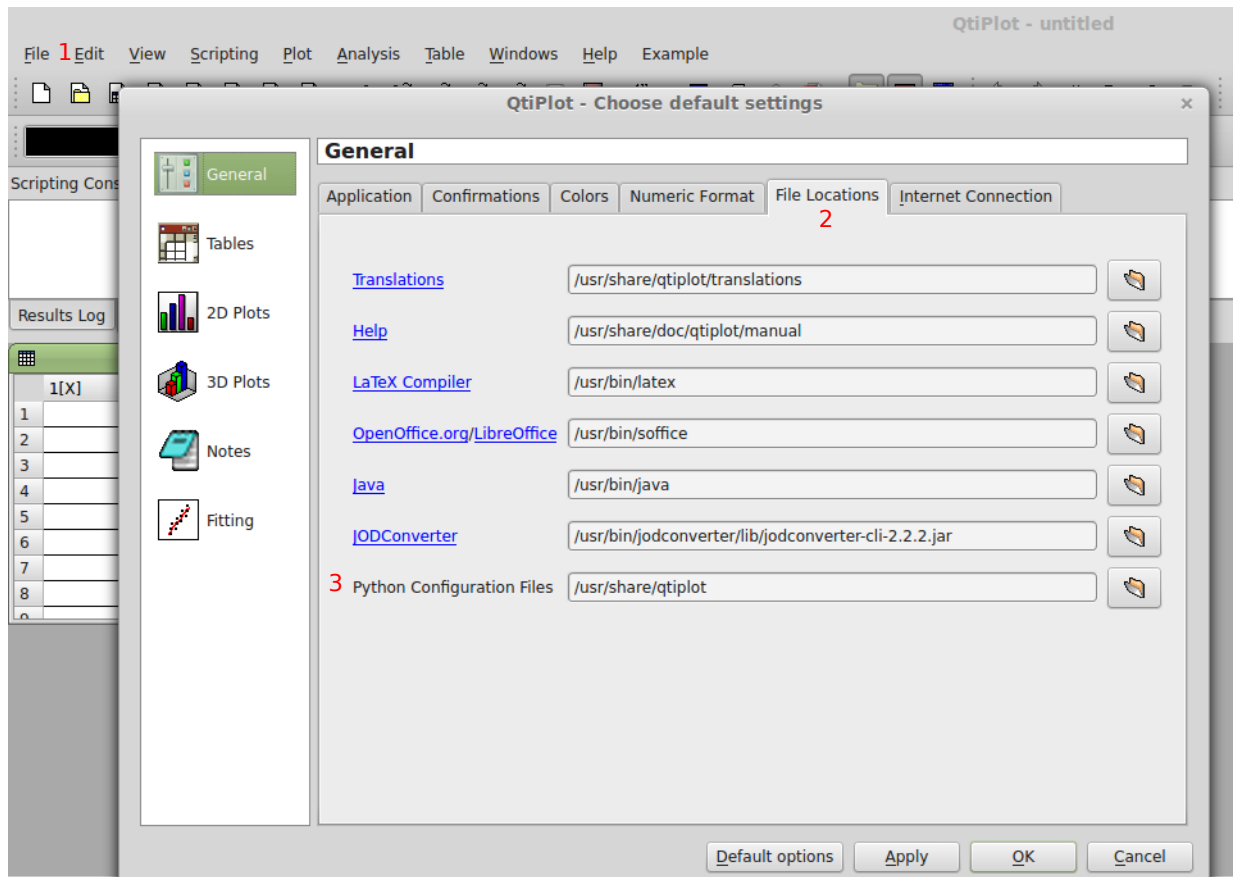


Figure 1 – Finding path of the Python Configuration Files.

### 4.3 Buttons attachment

There is possibility in QTIPLLOT to create buttons and attach them to the custom scripts/actions instead of creating NOTE objects on the QTIPLLOT'S PROJECT EXPLORER. This can be done in the following steps (shown in figure 2):

1. Open QTIPLLOT.
2. Left click on the menu bar *Scripting* → *Add Custom Script Action...*
3. Left click on the button *Choose Folder* in the pop-up window *Add Custom Action* and select the location where the created buttons and menu objects files should be saved. It is recommended to create new folder for this task.
4. Left click on the button *Choose Script* and select the script (*i.e. someAction.py file*).
5. Left click on the button *Choose Icon* and select the image for currently selected script action.
6. Fill the *Text* field. That text will be a name of the created button.
7. Fill the *Tool Tip Text* field. That field data will be a text of the pop-up tool tip. Only works then button is in the *Tool Bar*, not in the *Menu*.
8. Fill the *Shortcut* field. It is recommended but not required option. The command must be unique.

9. Choose the place it the QTIPLLOT's environmet where the button should be placed. Possible options:
  - (a) Already existing *Menu*.
  - (b) *Tool Bar*.
  - (c) *New Menu*. First create menu then choose it from already existing ones.
10. *Add* new button or *Save* corrected one.

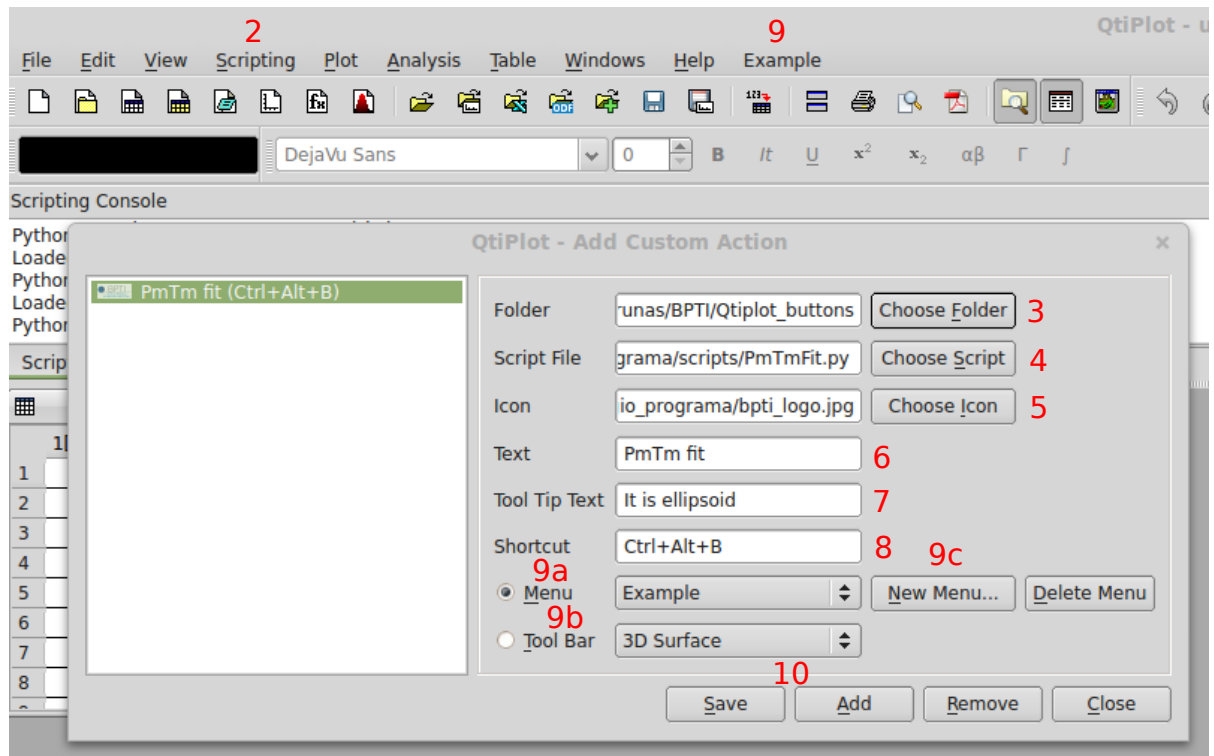


Figure 2 – Steps of QTIPLLOT's buttons attachement.

#### 4.4 QtiPlot's template's

Modules which perform curves **fitting** will work with this table (shown in figure 3):

1. Table to manage fit process called **fitWizard**. This table contains these columns:
  - (a) **parameter** – name of the parameter.
  - (b) **value** – value of the parameter. Default value is 0.0 (zero point zero).
  - (c) **vary** – parameter to allow fitting program to vary parameter value from initiadet one (value column or default 0.0). Default value is 1 (means TRUE → vary). If 0 (FALSE) is set on the parameter will not be varied.
  - (d) **min** – minimum value that can be reached during fitting process. Default value is  $-\infty$  (negative infinity).
  - (e) **max** – maximum value that can be reached during fitting process. Default value is  $+\infty$  (positive infinity).

	1a	Parameter[X]	value[Y]	1b	vary[Y]	1c	min[Y]	1d	max[Y]	1e	
1		DuG	9000		1						MODEL'S PARAMETERS
2		DuV	-1		1			-100		0	
3		DuBeta	-0.1		1						
4		DuAlpha	0.7		1						
5		DuCp	6800								
6		DuH	70500								
7											REFERENCE
8											
9		Pr	0.1								
10		T	298								
11											
12											
13											
14											

Figure 3 – *fitWizard* table.

## 5 Working with Protein Pressure–Temperature Phase Diagram Fit package

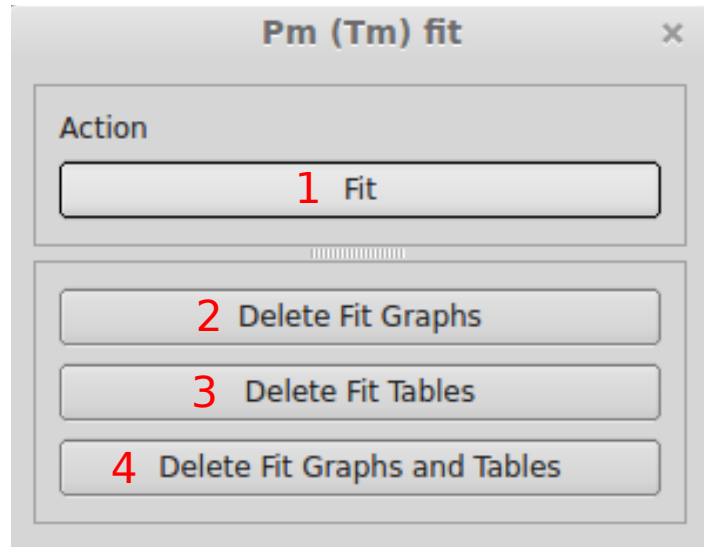


Figure 4 – *Protein Pressure–Temperature Phase Diagram Fit* module.

While running *Dose Curves Analysis* button there is four possible actions (shown in figure 4):

1. **Fit** – this button fit experimental data to protein pressure–temperature phase diagram (solutions eq. 1) [7] ( $P_m(T_m)$ ,  $P_m$  – melting pressure,  $T_m$  – melting temperature). More precisely, when Gibbs free energy change between protein native and unfolded states  $\Delta G = G_N - G_u$  is approaching to 0 the temperature and pressure values goes to its *melting* values. The solution of eq. 1 ( $\Delta G = 0$ ) is in eq. 6 (equations 2, 3, 4, 5 are written for simplicity).

Definition of the parameters that are used in eq. 1:  $P_r$  – reference pressure,  $P$  – system pressure,  $T_r$  – temperature,  $T$  – system temperature,  $\Delta_U G$  – protein [U]nfolding Gibbs free energy change,  $\Delta_U V$  – protein [U]nfolding volume change,  $D_U C_p$  – protein [U]nfolding isobaric specific heat change,  $\Delta_U H$  – protein [U]nfolding enthalpy change,  $\Delta_U \beta$  – protein

Table 1 – *Explanation of parameters names and naming which are used in literature and program code.*

Lit. mark	Code mark	Meaning	Example lit. $\equiv$ code
$D_U^*$	Du*	protein [U]nfolding * change	$D_U V \equiv \text{Du}V$
$^* \star G$	$^* \star G$	* Gibbs free energy *	$D_U G \equiv \text{Du}G$
$^* \star V$	$^* \star V$	* volume *	$D_U V \equiv \text{Du}V$
$^* \star H$	$^* \star H$	* enthalpy *	$D_U H \equiv \text{Du}H$
$^* \star C_p$	$^* \star C_p$	* isobaric specific heat *	$D_U C_p \equiv \text{Du}C_p$
$^* \star \beta$	$^* \star \text{Beta}$	* isothermal compressibility *	$D_U \beta \equiv \text{Du} \text{Beta}$
$^* \star \alpha$	$^* \star \text{Alpha}$	* thermal expansion *	$D_U \alpha \equiv \text{Du} \text{Alpha}$
$P_r$	Pr	reference pressure	$P_r \equiv \text{Pr}$
$T_r$	T	reference temperature	$T_r \equiv \text{T}$
$T$	x	system temperature	$T \equiv \text{T}$

[U]nfolding isothermal compressibility change,  $\Delta_U \alpha$  – thermal expansion factor. More information about parameters names are shown in table 1.

$$\Delta G = \frac{\Delta_U \beta}{2}(P - P_r)^2 + \Delta_U V(P - P_r) + \Delta_U \alpha(P - P_r)(T - T_r) - \Delta C_p \left[ T \left( \ln \frac{T}{T_r} - 1 \right) + T_r \right] - (\Delta_U H - \Delta_U G) \left( \frac{T}{T_r} - 1 \right) + \Delta_U G \quad (1)$$

$$a = \frac{\Delta \beta}{2} \quad (2)$$

$$b = \Delta_U V + \Delta_U \alpha(T_m - T_r) \quad (3)$$

$$c = -\Delta C_p \left[ T \left( \ln \frac{T}{T_r} - 1 \right) + T_0 \right] - (\Delta_U H - \Delta_U G) \left( \frac{T}{T_r} - 1 \right) + \Delta_U G \quad (4)$$

$$D = b^2 - 4ac \quad (5)$$

$$P_m = \frac{-b \pm \sqrt{D}}{2a} + P_0 \quad (6)$$

Perform following steps for protein dose curves fitting:

- (a) Check and edit fitting parameters (look at the System Requirements) – value, vary, min, max (1 b-f in figure 3) in *fitWizard* table.
- (b) Select  $x$  and  $y$  columns. There is no limit for  $y$  columns number.
- (c) Push **Fit** button (1 in figure 4).
- (d) Look at the output:
  - i. Graph (shown in figure 5) named *GfitElip\_\** – this object contains plotted experimental and fit data curves. Meaning of the name: *G* – graph, *fit* – fit, *Elip* – elliptical shape of phase diagram, \* number for name’s uniqueness. i.e. *GfitElip\_3*.



- ii. Table (shown in figure 5) named  $TfitResElip\_*$  – this object contains experimental and fit data curves. Meaning of the name:  $T$  – table,  $fit$  – fit,  $Res$  – results,  $Elip$  – elliptical shape of phase diagram,  $*$  number for name's uniqueness. i.e.  $TfitResElip\_4$ . Graph is plotted from this table.
- iii. Table (shown in figure 6) named  $TfitParElip\_*$  – this object contains fitted parameters on the left side, messages about fit operations in the middle and  $fitWizard$  table data on the left. Meaning of the name:  $T$  – table,  $fit$  – fit,  $Par$  – parameters,  $Elip$  – elliptical shape of phase diagram,  $*$  number for name's uniqueness. i.e.  $TfitParElip\_4$ .
- iv. All information about every fit action is printed to the QTIPLoT's Results Log (shown in figure 7).

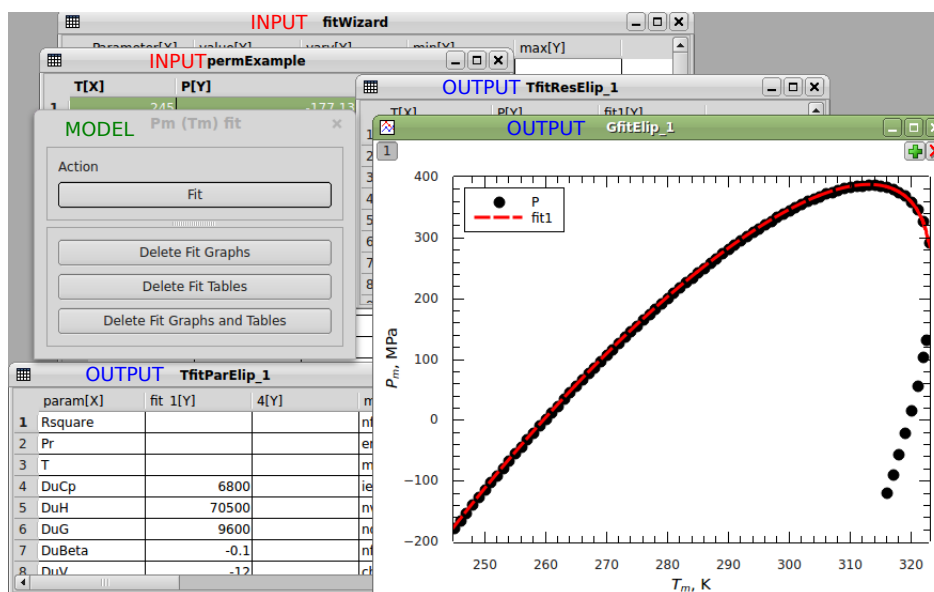


Figure 5 – Protein pressure – temperature phase diagram fit output.

FITTED PARAMETERS			MESSAGES ABOUT OPERATIONS			FIT WIZARD				
param[X]	fit 1[Y]	4[Y]	mnmzize p[Y]	mnmzize p v[Y]	7[Y]	fit param[Y]	value[Y]	min[Y]	max[Y]	vary[Y]
1 Rsquare			nfev	43		DuCp	6800	-inf	inf	0
2 Pr			errorbars	True		DuH	70500	-inf	inf	0
3 T			message	Tolerance seems		DuG	9000	-inf	inf	1
4 DuCp	6800		ier		2	DuBeta	-0.1	-inf	inf	1
5 DuH	70500		nvarys		4	DuV	-1	-100	0	1
6 DuG	9600		ndata		87	DuAlpha	0.7	-inf	inf	1
7 DuBeta	-0.1		nfree		83					
8 DuV	-12		chisqr	140361106e-20						
9 DuAlpha	1.4		redchi	385977237e-22						
10			input table	permExample						
11			output table	TfitParElip_1						
12			fit_result	fitRezTName						
13			date/time	2015-03-13 09:3						

Figure 6 – Protein pressure – temperature phase diagram fit parameters result table.

2. **Delete Fit Graphs** (2 in figure 4) – this button deletes graphs that are created by **Fit** button (1 in figure 4).

3. **Delete tables** (3 in figure 4) – this button deletes tables that are created by **Fit** button (1 in figure 4).
4. **Delete Graphs and Tables** – this button runs 2 and 3 buttons actions at once.

## 6 Results log

Results log is useful Qtiplo's tool. Purpose of this tool in all psaFit modules is to log main information about every experiment:

- Date and time
- Input/Output graphs and tables
- Model and statistical parameters of experiment

Example results log is shown in figure 7.

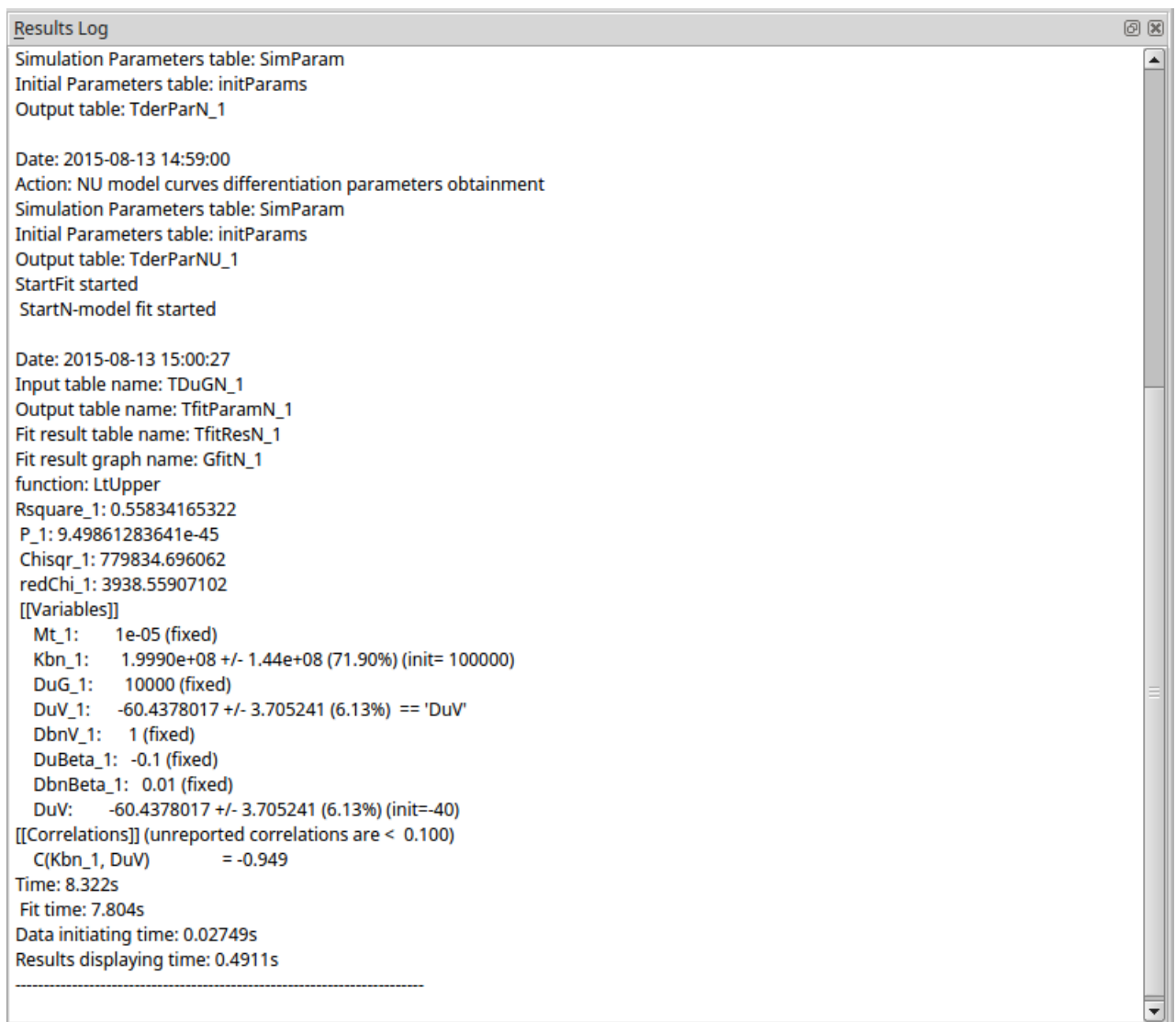


Figure 7 – Example Qtiplo's results log.

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