A₂₆₀ iPhone App

User Guide

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1 Overview

This app calculates the solution concentration of a nucleic acid (DNA, RNA) or nucleotide from an absorbance measurement at 260 nm.

Dilution factors can be automatically calculated from stock and final volumes.

The app operates in one of two modes: novice or expert.

In novice mode, the user is guided by a question and answer format.

In expert mode the user can enter parameters in any order as well as:

- Set the dilution volume units
- Set the spectrophotometer path length

- Set low and high limits for warning the user when an absorbance reading is outside the recommended range.

2 Main Screen

The main screen view depends on whether you are in novice or expert mode.

The following sections present each main view and any secondary views for each.

2.1 Novice Main Screen

iPod	10:2	7 AM				
Sele	ect Molecule	ssDNA				
Did you measure a diluted solution?						
	Yes	No				
Enter Stock Volume (µl): 5.0						
Ente	Enter Final Volume (µl): 400.0					
E	Enter A260 Reading: 0.3580					
Con	centration:	1.06	µg/µl			
Go to Expert Mode						

2.1.1 Data Entry Process

This screen progressively displays the data question/input fields from top to bottom.

Data is entered into the fields by tapping the data display field.

Once the molecule type has been selected, the user is asked whether a diluted solution was used for the absorbance reading.

If so, the user is then prompted to enter stock and final volumes in μ l (in this mode volume units are fixed).

If not, the next prompt is for the A_{260} reading. The path length defaults to one (1) centimeter but the novice mode will use whatever path length is set in the information screen available through the expert mode. This allows an expert to set the application configuration and then change to novice mode for use by another user.

Once the absorbance reading is entered the concentration is automatically calculated and displayed. The concentration units can be toggled by tapping the units field. The units alternate between $\mu g/\mu l$ and $\mu g/m l$ for DNA/RNA and between μM and mM for nucleotides.

At any time the user can tap any of the already entered answer/input fields and the process will restart from that point.

2.2 Expert Main Screen



2.2.1 Data Entry Process

This screen displays all data input fields simultaneously. Data can be entered into the fields in any order by tapping the desired data display field.

Either the concentration or absorbance can be calculated in this mode.

If the absorbance is set, the concentration will be calculated when any changes are made to the molecule type, volume or volume units fields.

If the concentration is set, the absorbance is calculated when any changes are made to the volume, volume units, molecule type, or concentration units fields.

The concentration units can be toggled by tapping the concentration units field. The units alternate between μ g/ μ l and μ g/ml for DNA/RNA and between μ M and mM for nucleotides.

The stock and final volume units can be changed independently by tapping the appropriate units field. These units can be any of the following:

- nl (nanoliters)
- μl (microliters)
- ml (milliliters)
- I (liters)

2.2.2 Setup

Touching the small "I" in the lower right corner of the screen activates the setup screen. (See <u>the</u> Information Screen section for details)

3 Information Screen



3.1 Path Length

The absorbance path length can be set to any positive number of centimeters.

3.2 A₂₆₀ Warning Low Limit

If an absorbance value less than this limit is entered, the user is warned that this is outside the normal operating limits for this spectrophotometer. The user can choose to use this value anyway or reject it and use another value.

3.3 A₂₆₀ Warning High Limit

If an absorbance value greater than this limit is entered, the user is warned that this is outside the normal operating limits for this spectrophotometer. The user can choose to use this value anyway or reject it and use another value.

3.4 Cancel

If the setup screen is canceled, any changes made will be ignored and the previous parameter values used.