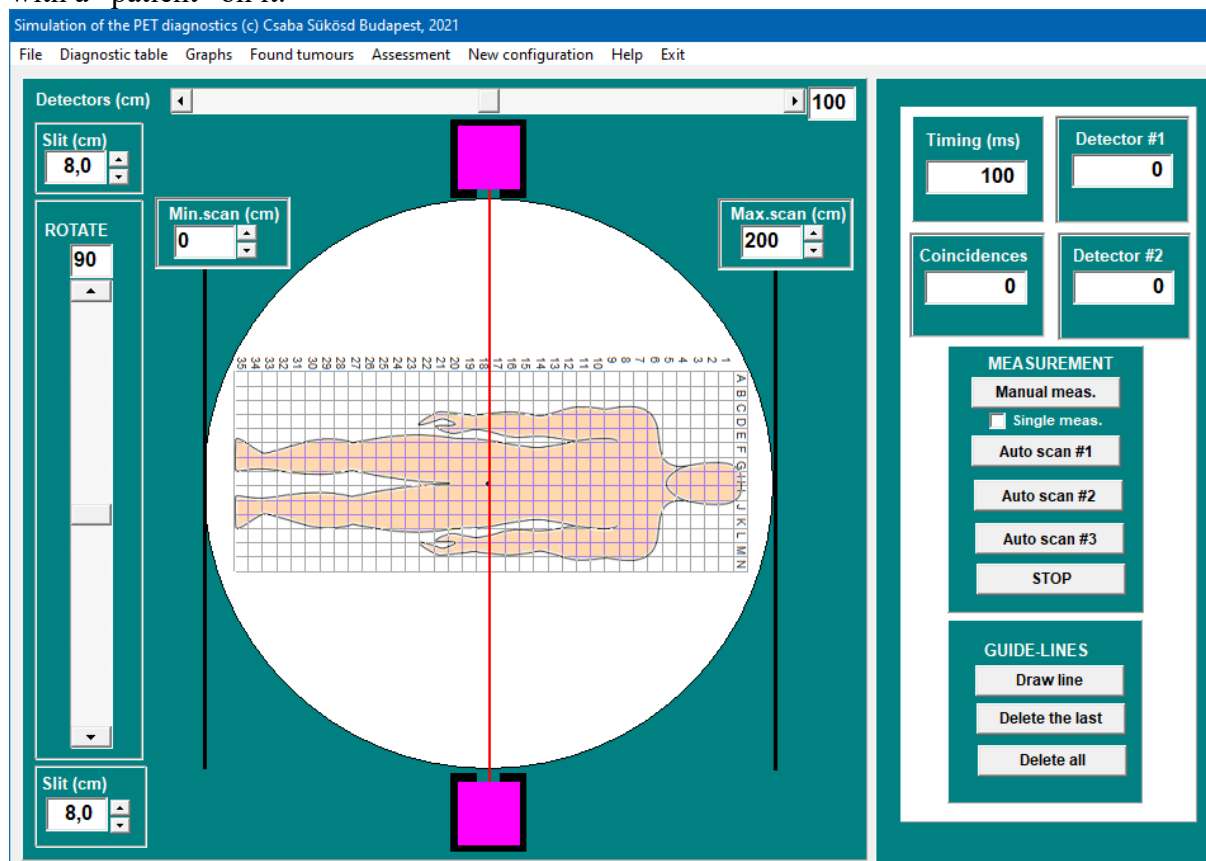




## Modelling Positron Annihilation Tomography (PET) diagnostics

After starting the program (and logging in), a picture of the “Diagnostic Table” can be seen with a “patient” on it.



A grid is drawn on the patient. The coordinates of the cancerous tumours can be given according to the grid coordinates. The two purple squares indicate the two detectors, which are surrounded by a radiation shielding lead cover (black). Radiation can only reach the detectors through the aperture of the “slits” (however, radiation can enter the slit from any direction, not just from the direction of the red line connecting the two detectors!). The aperture can be changed with the controls labelled *Slit (cm)* at the top and bottom left. The table can be rotated between 0° and 180° with the slider on the left as well. The detectors can be moved horizontally between 0 and 200 cm with the slider above. The screen is divided into two parts: the larger part on the left can be alternated with the *Diagnostic Table* and *Graphs* menu.

### THE CONTROLS OF THE RIGHT PANEL

The four fields of the upper panel show the parameters and data of a single measuring point:

**Timing:** measuring time for one single point

**Detector#1:** number of counts detected by Detector#1 during the *Timing* time.

**Detector#2:** number of counts detected by Detector#2 during the *Timing* time

**Coincidences:** number of detected coincidences (real + random) during the *Timing* time.

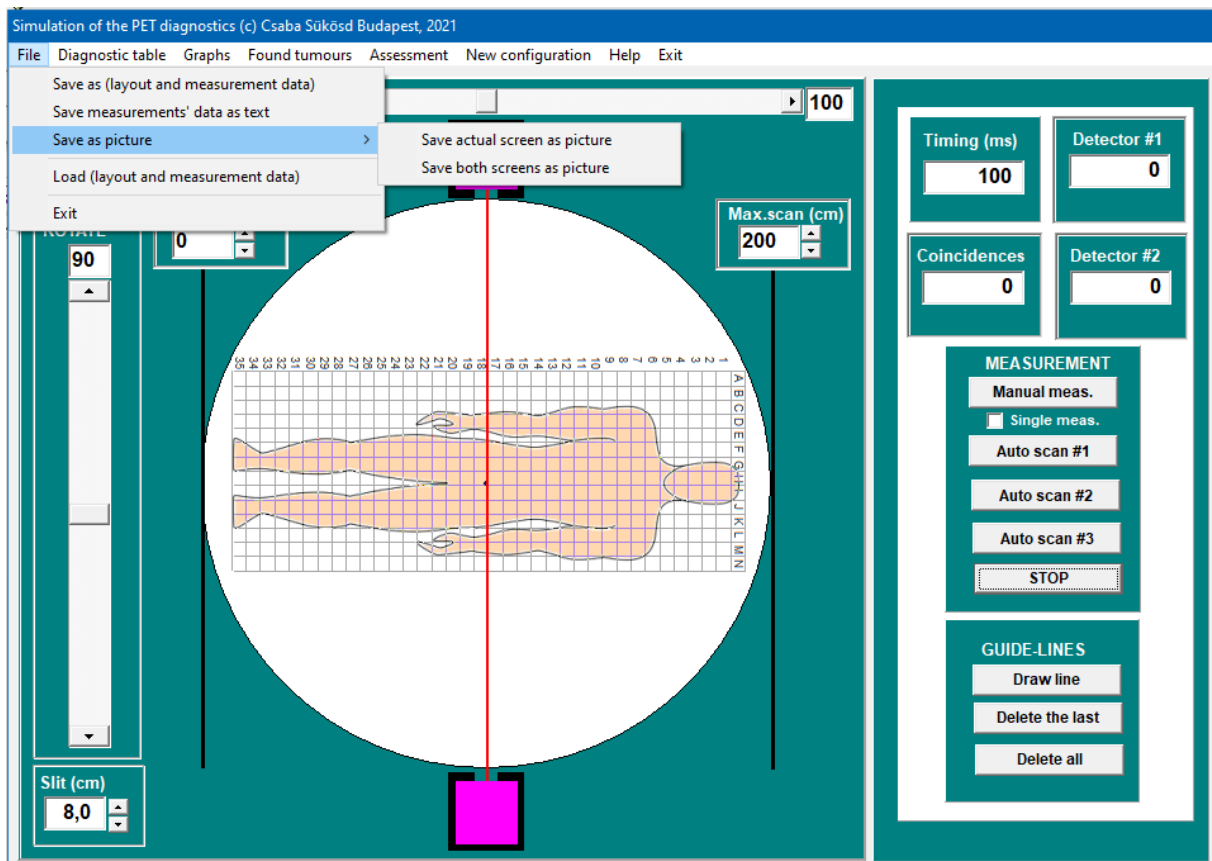
## MEASUREMENT

- **Manual meas.**: starts a single measurement manually.  
If **Single meas.** is checked, the measurement stops after the **Timing** time expires, otherwise it measures continuously.
- **STOP**: Stops all current measurements.
- **Autoscan#1,#2,#3**: The detectors scan the patient within the limits that can be set on the diagnostic table (vertical black lines). During the scan, in all positions (centimetre-wide horizontal “jumps”), the detectors measure during the time set in the **Timing**, and store the number of detected (true + random) coincidences, which can be viewed on the graphs available from the “**Graphs**” main menu item.

**GUIDE-LINES**: Use the buttons on the bottom panel to draw lines. If you feel that you have found a position that also has real coincidences, you can use the **Draw Line** button to insert a guide-line in the figure. The guide-line is created in place of the red line connecting the two detectors. It is important that these guide-lines always remain there until they are erased, and they also move (rotate) with the patient! Use the **Delete Last** and **Delete All** buttons to get rid of unwanted guide-lines. It is also important to know that the number of these lines is not limited. Any number of guide-lines can be drawn at any angles and detector positions!

**MAIN MENU** further items

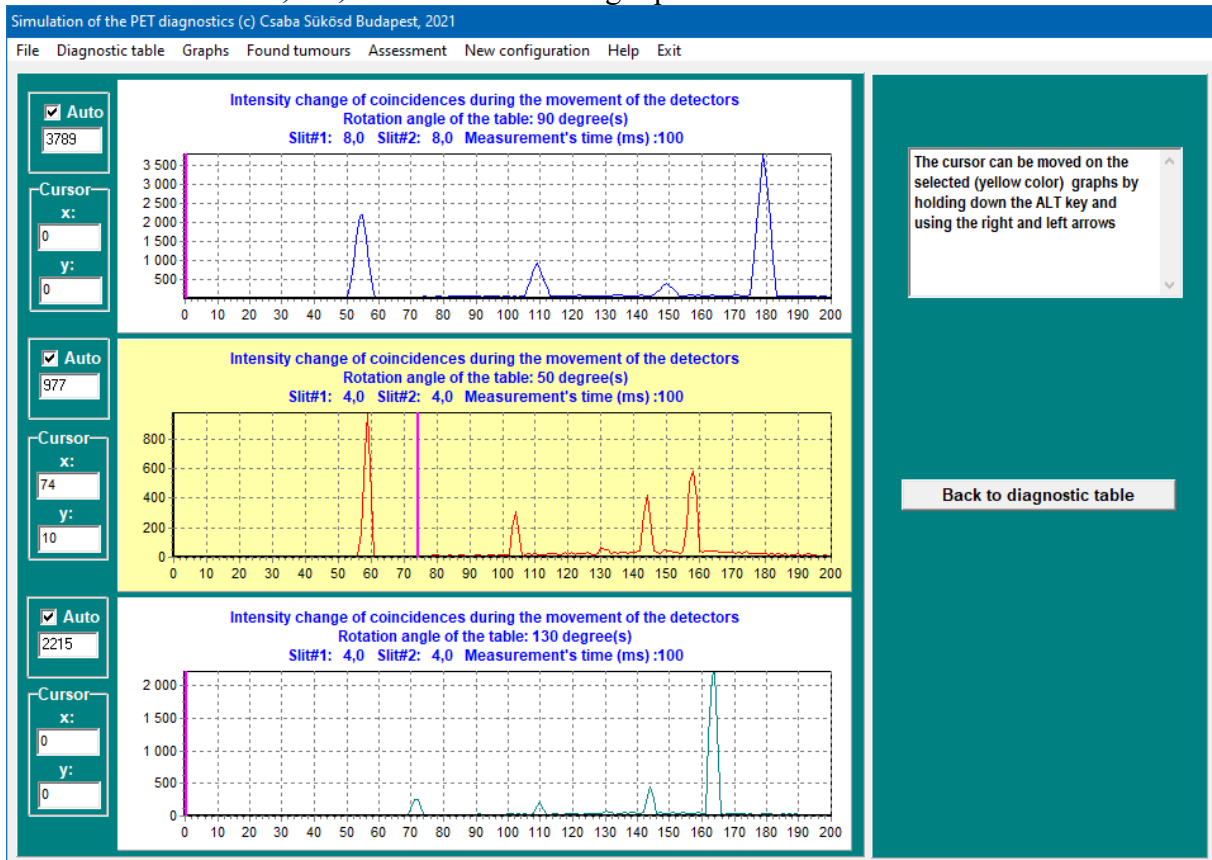
- **File**: The controls of the different saving and loading options are here. The following picture shows the possibilities:



The most important are the menu items "**Save as (layout and measurement data)**" and "**Load (layout and measurement data)**". These menu items save (or load) the entire measurement layout and all measurement data in (from) a binary file. A file name requesting window will appear, where you can specify the filename. By default, a subdirectory called "Data" opens,

which is part of the directory that contains the program file. “*Save measurement’s data as text*” only saves the measurement data to an ASCII text file, so that they can be accessed by other programs if necessary. The two sub-items of the “*Save as picture*” menu item either save only the current program window in a JPG file, or both of the images of the *Diagnostic table* and *Graphs* in a single JPG file.

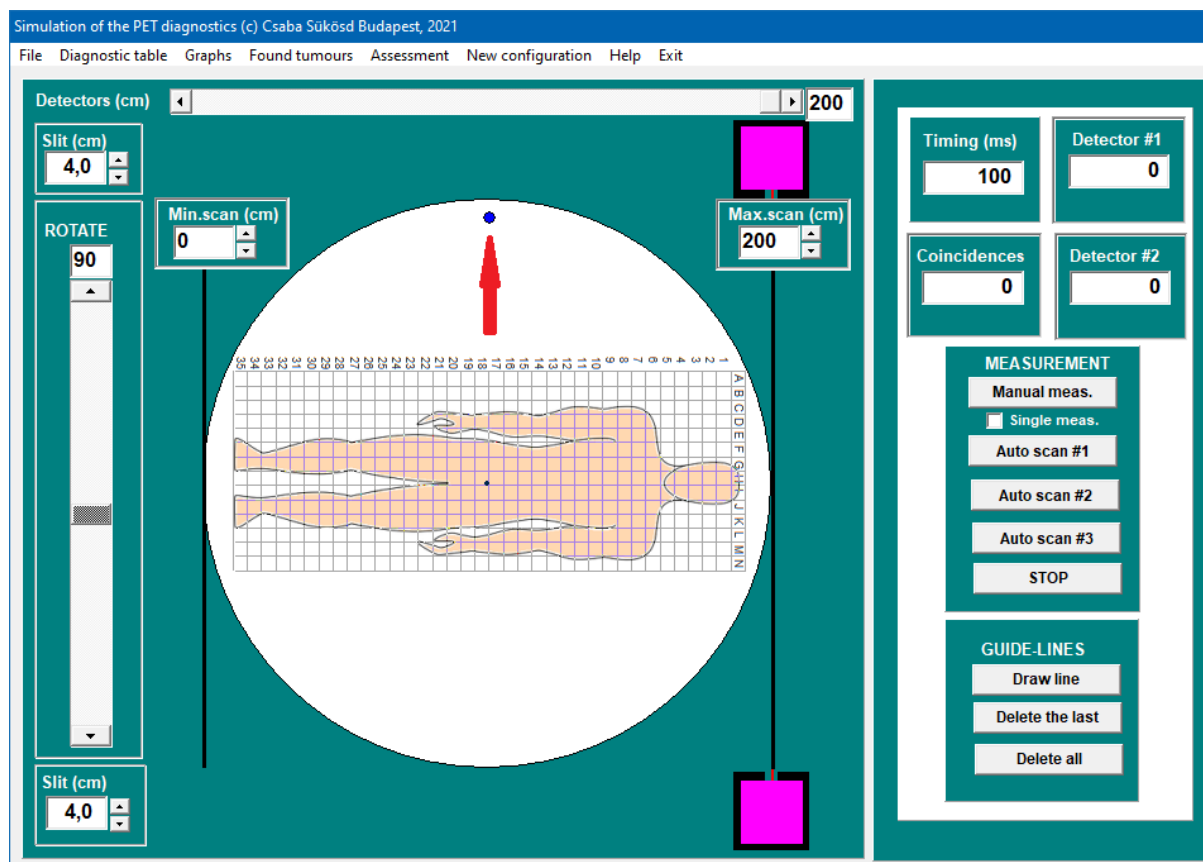
- **Graphs:** Instead of the diagnostic table, three graphs appear in the wider left part of the screen. These graphs represent the measurement results of the automatic scans started with the *Autoscan # 1, # 2, # 3* buttons in the right panel.



On the horizontal axis the horizontal position of the detectors is shown, on the vertical axis the number of coincidences are depicted, which were measured at the given location during the *Timing*. Only data from three scans can be displayed, if more than three angles are needed, we need to overwrite the data from a previously measured scan. Next (left) to the graphs, the maximum of the vertical axis can be entered. When the *Auto* field is selected, the program determines the display maximum, based on the data in the graph. By clicking on one of the graphs, you can “select” it, then its colour will change to light yellow. You can move the cursor on the selected graph by pressing the ALT key together with the right and left arrows. The x and y coordinates of the current cursor position can be read from the “*Cursor*” field on the left next to the graph. Clicking on the graphs with the right mouse button will bring up another menu. This allows to save the data of the graphs to a text file (for later, possible EXCEL processing), to list the data, and to save the images of the simulation in JPG format.

- **Tumours found:** Some sub-items also open here. By selecting “*Place a new tumour*”, we can place a blue dot on the body where we thought we found a tumour. By clicking on this sub-item, the program places a blue dot (see the figure below) in the diagnostic window, which can be “grabbed” with the mouse and dragged to the desired location (drag / drop). When the point is “dropped”, a window pops up where the coordinates of the point can be

fine-tuned. The additional subsections allow some operations in relation to the “fictional” tumours we have placed in this way: “*Delete Last*” or “*Delete All*”.



- **Assessment:** Here, the program compares the cancerous tumours we have “guessed” with the position of the hidden “real” tumours. In this case, it displays the real, hidden tumours in red on the diagnostic table, and the ones we guessed in blue. It also displays some informative data in a window: the number of real tumours found, number of those not found and the number of tumours we suggested but which are actually in excess, and false. Also, a score is calculated that also takes into account how accurately we were able to hit the hidden tumours. The higher this score, the better the result.
- **New Layout:** The program generates a new “hidden” layout of tumours at random, to allow the program to be played multiple times. The new arrangement is random not only in terms of the position of the tumours, but also in terms of the number of them. However, you can specify the maximum number of tumours. This makes the task easier, because e.g. for a maximum of 1 tumour, of course, the program only generates one. The maximum number that can be entered is 10.
- **Help** includes an *About* box, as well as a *Theoretical Introduction and Description of Tasks*, and this *Users’ Guide*.
- **Exit** It terminates the program, but before exiting, it asks whether everything important has been saved.