

Processing a patient image with the DaTQUANT™ application

Selecting your data

A

Data can be imported into the licensed version of the DaTQUANT application via three methods:

- If the data is stored on your PC, you can import it from a folder
- If the data is stored on a flash drive or disk, you can import the data from the drive/disk
- The most common way to import data is over your network via DICOM®

B

Select the patient from the database.

C

Select series to be processed (raw data or transaxial slices) and click “Start”.

D

Saving:
Save via DICOM or save locally.



NOTE: The DaTQUANT application will accept raw SPECT data, reconstructed transaxial slices or result series from DaTQUANT as input.

DICOM: digital imaging and communications in medicine
PC: personal computer
SPECT: single-photon emission computed tomography



Processing

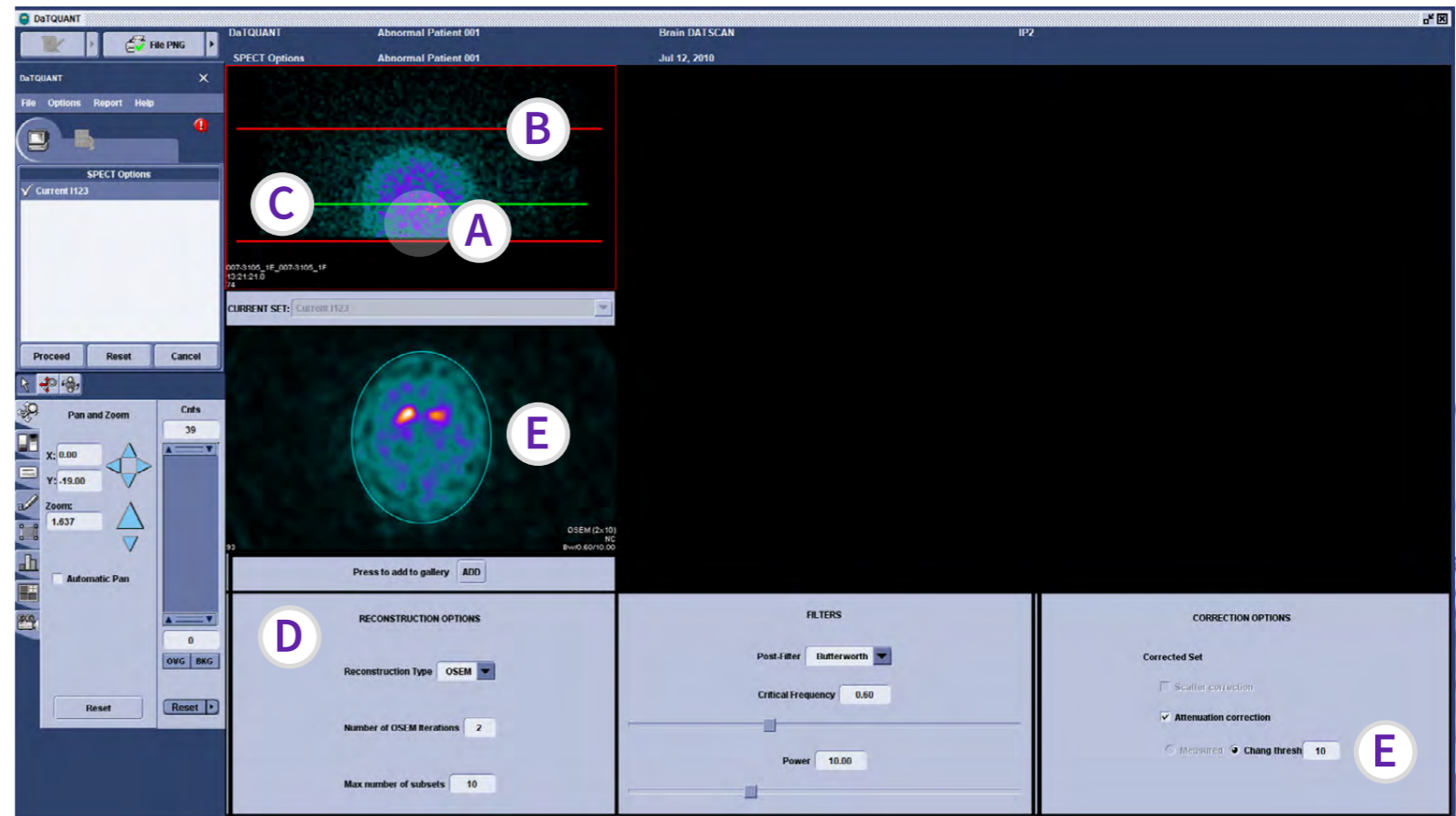
A Original raw data.

B The red lines represent the limits between which the data will be reconstructed - ensure that the volume includes from the top of the head to below the striatum.

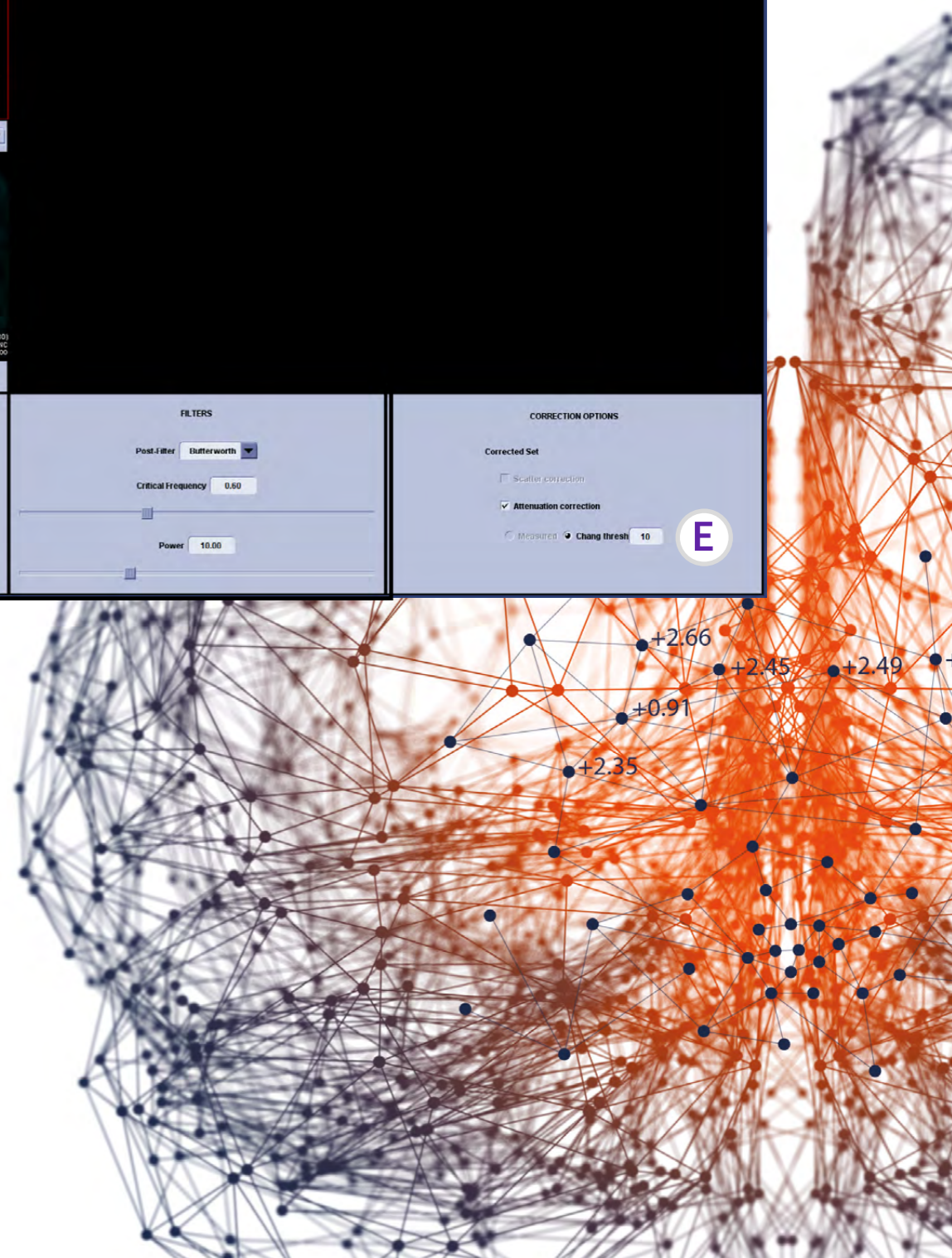
C The green line represents the slice that is visible in the window below - ensure that the striatum is visible in this slice.

D The default reconstruction setting is based on raw data from the normal database. Raw data from the 118 normal, age-matched controls was collated and reconstructed with these parameters.

- Both filtered-back reconstruction and iterative reconstruction are available
- Changing the reconstruction and filter parameters can affect quantitative values
- For accurate comparison, the parameters should match those of the normal database to be used



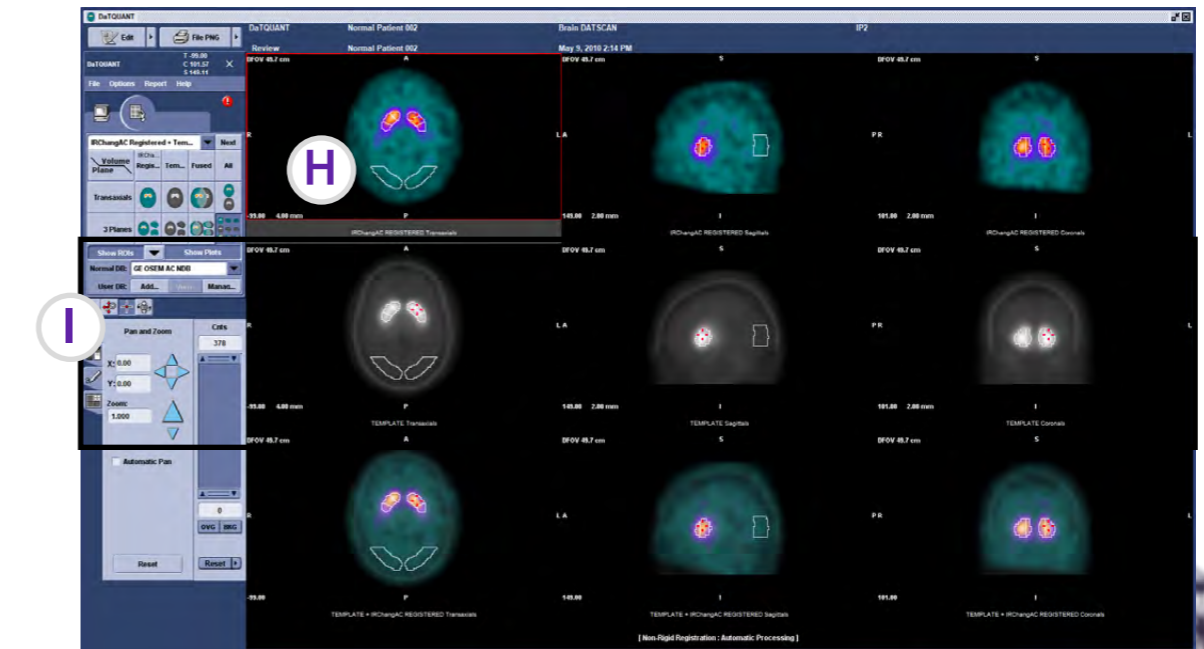
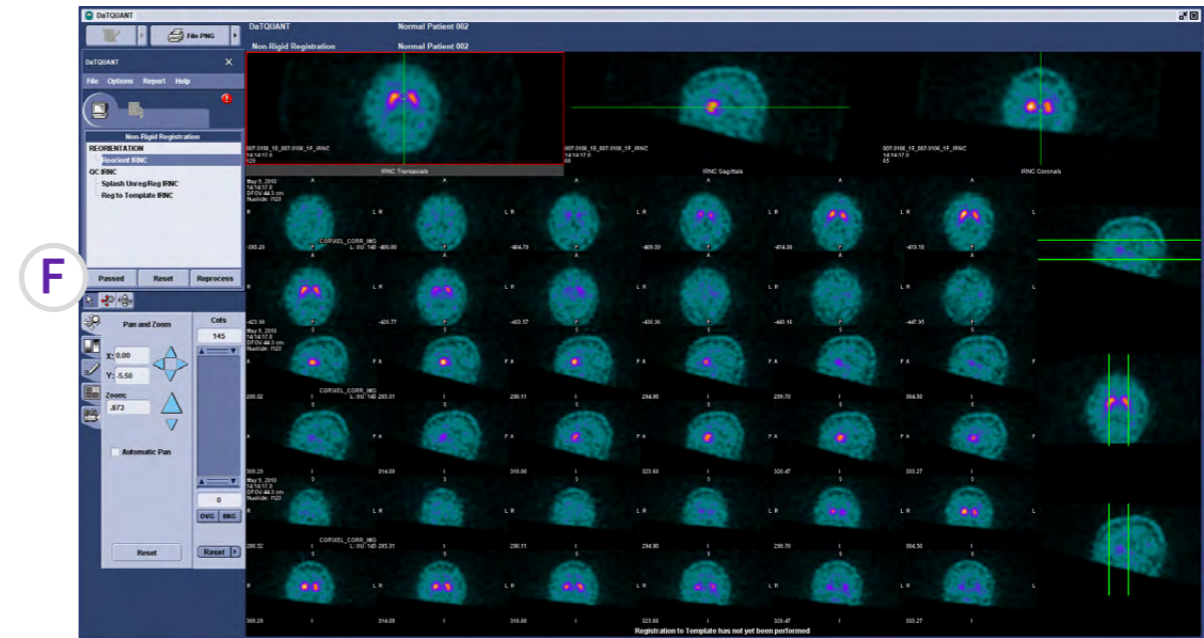
E When using Chang or linear attenuation correction, select a threshold value for which the ellipse closely follows the contours of the head in all slices.



Processing

The DaTQUANT application will automatically reconstruct raw data, if necessary, and your images will appear on screen. You will need to verify if the images have been processed correctly:

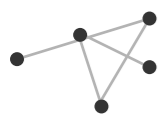
- F** Verify that reconstruction or importing of images is correct. To verify a successful process, click “Passed” – this will trigger image registration. If the reconstruction settings need to be changed, click “Reprocess”.
- G** Once verified, the DaTQUANT application will perform a non-rigid registration of the images, registering the data 3-dimensionally, and VOIs will be applied automatically.
 - Images are automatically corrected for head tilt
- H** The VOI from the template is displayed on the patient’s image.
 - Verify correct placement of both striatal and background VOIs
 - 95% of cases require no user intervention to accurately register to the VOI template¹
 - VOI placement can be manually adjusted, if desired (next page)
- I** The “template” is an average of ¹²³I-ioflupane distribution in the brain of multiple normal subjects and is used to orient the patient image and place the VOIs.



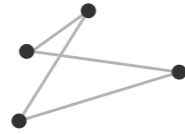
Reference: 1. Data on file. Internal verification data. GE HealthCare; 2015. VOI: volume of interest



Processing



If the ROIs are incorrectly placed, select **“Edit ROIs”** and manually reposition as needed



Confirm that the ROIs are properly located and click **“Passed”**

The screenshot shows the DaQUANT software interface. A central window displays brain scan images with ROIs. A 'QCheck' dialog box is open, prompting for patient information. Below the images is a table of measured values and Z-scores for various brain regions.

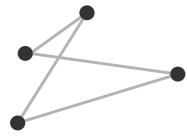
	Striatum Right	Putamen Left SBR	Caudatus Right SBR	Caudatus Left SBR
Measured	+2.29	+1.99	+2.61	+2.24
Mean (± 1 SD)	+2.41 (± 0.40)	+2.39 (± 0.42)	+2.33 (± 0.39)	+2.28 (± 0.41)
Deviation	-5%	-13%	-7%	-13%
Z-Score	-0.29	-0.75	-0.43	-0.72

K A window may appear, prompting you to enter additional information that was not located in the header of the image. If known, it is important to enter this information so that comparison to the most appropriate normal database can be made. If you are using DICOM, some of the data will be pre-populated from the image header and cannot be changed.

DICOM: digital imaging and communications in medicine
ROI: region of interest



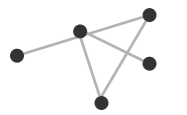
Generating a report



A screen containing the quantitative results will be displayed. These can be edited and included in the report.



A Select the table layout that gives the desired information. A “Custom” table can also be created by the user.



The report can be saved either as a .pdf, DICOM screen capture uploaded to PACS or sent directly to a printer.

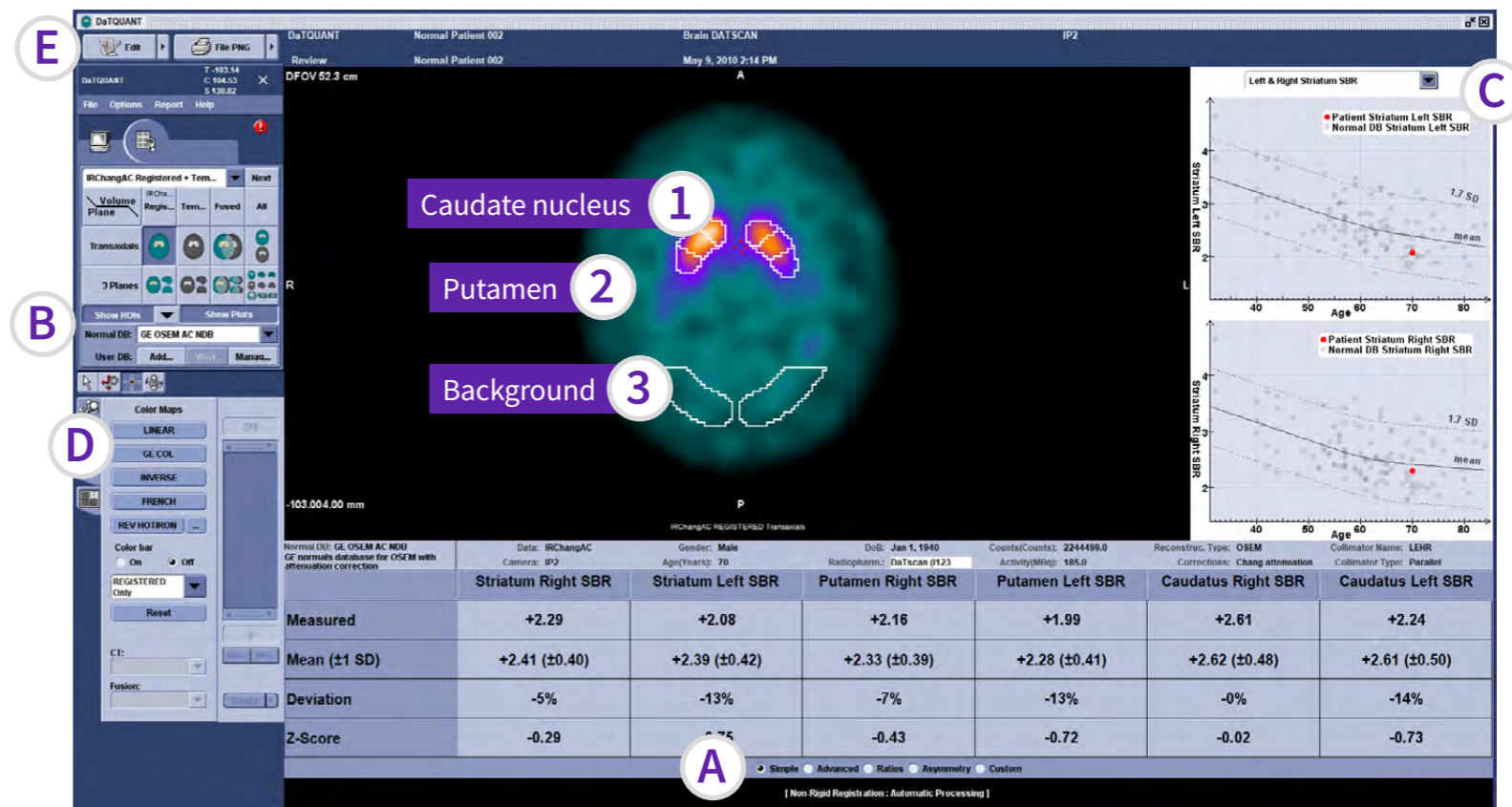


B Choose whether to view or hide ROIs. ROIs can not be edited in this view.



C Select which graph you would like to view. Click on the graph to select the value of the SD lines.

DICOM: digital imaging and communications in medicine
 PACS: picture archiving and communication system
 ROI: region of interest
 SBR: striatal binding ratio
 SD: standard deviation



D If desired, the color map can be altered. The preset GE HealthCare color map is recommended, as it provides the correct balance in specificity and sensitivity for visual assessment.



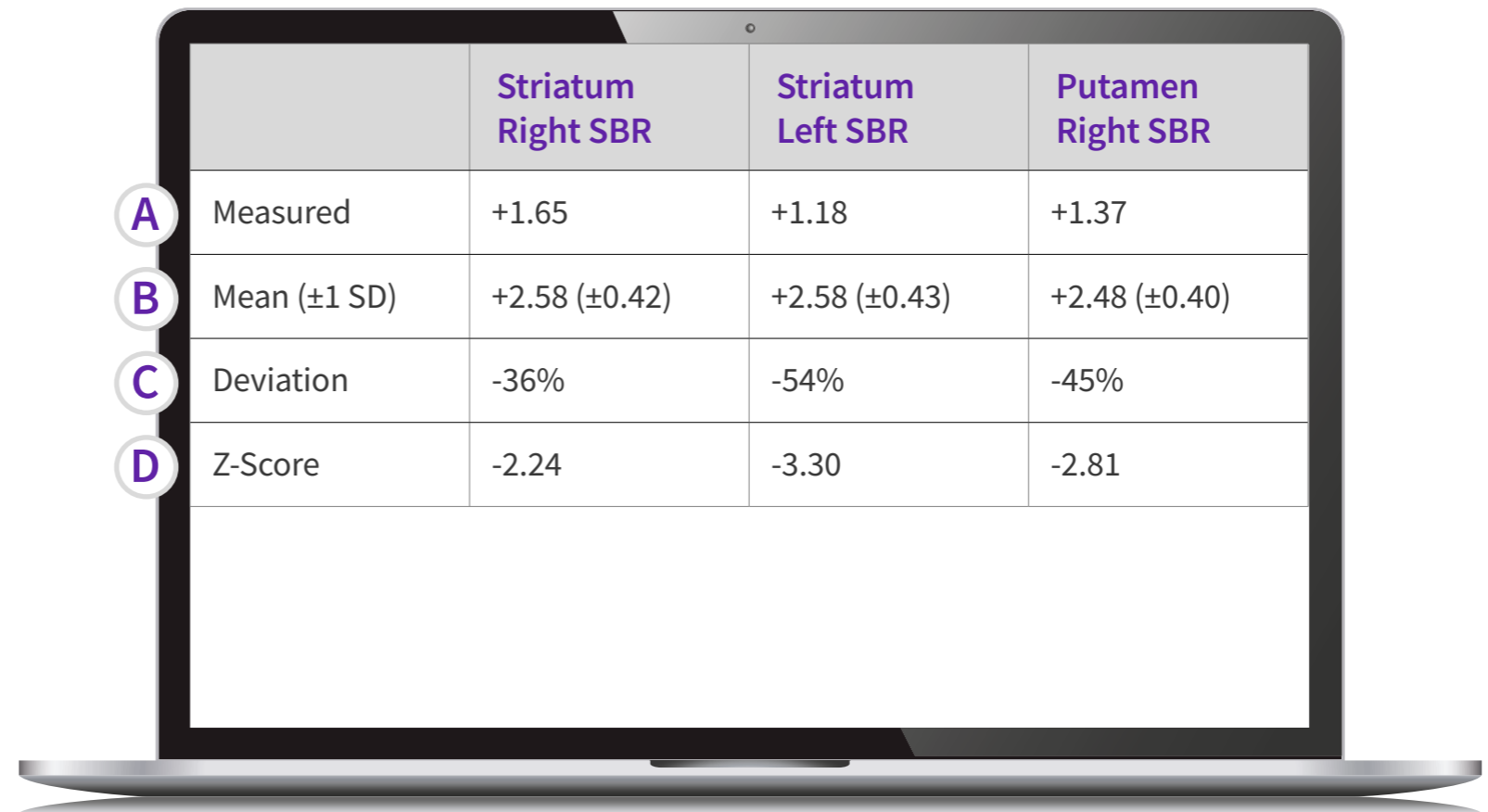
E Click the button in the upper right corner to edit or save the report. Additional views can be added by pressing Ctrl + R.

This image is of the “Simple” report, revealing SBRs in specific areas of the brain.

Influence diagnoses with accurate interpretation

Data-driven, reliable assessment

- A** Striatal value in each region as compared to the occipital cortex background region.
- B** Mean uptake in the same region for the same-aged subjects from the normal database.
- C** Percentage of deviation from the normal database represented by the patient data.
- D** Number of standard deviations from normal for the same age groups.
 - For SBR and putamen to caudatus ratio, a negative Z-score indicates that the patient's measured value is less than the age-matched mean value
 - For asymmetry, a positive Z-score indicates that the patient's measured asymmetry is greater than the age-matched mean value



	Striatum Right SBR	Striatum Left SBR	Putamen Right SBR
A Measured	+1.65	+1.18	+1.37
B Mean (± 1 SD)	+2.58 (± 0.42)	+2.58 (± 0.43)	+2.48 (± 0.40)
C Deviation	-36%	-54%	-45%
D Z-Score	-2.24	-3.30	-2.81

Values are for illustrative purposes only.

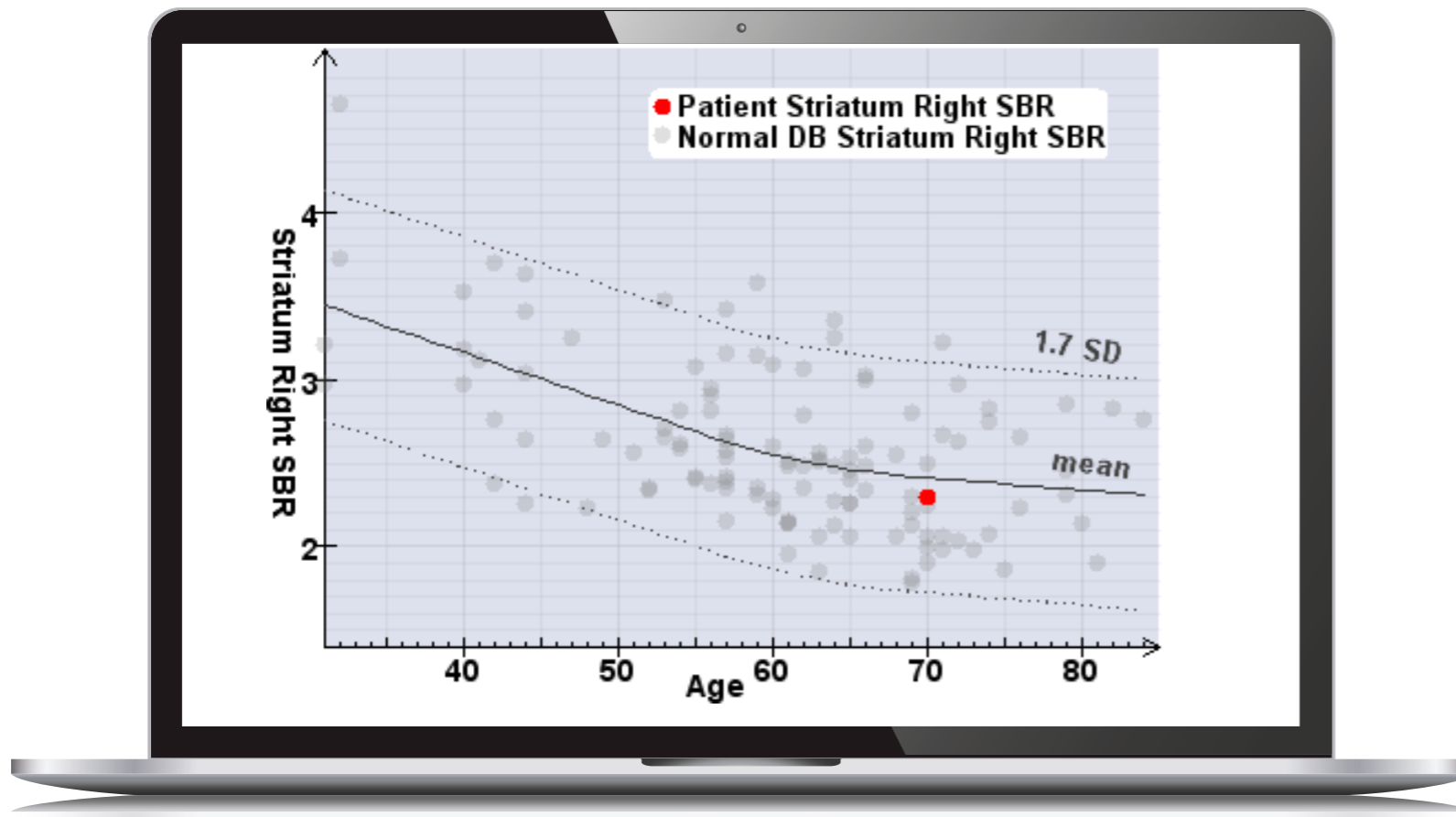
NOTE: The SBR is the ratio of specific to non-specific binding for the selected striatal region. The formula for SBR is as follows:

$$\frac{(\text{mean counts in the specific striatal region} - \text{mean counts in the background region})}{(\text{mean counts in the background region})}$$

SD: standard deviation
SBR: striatal binding ratio



Visualization of quantification results



Values are for illustrative purposes only.

Key:

- Normal database (118 healthy volunteers imaged in PPMI)
- User-selected standard deviation line which corresponds to confidence interval
- Mean of the normal value for the age represented
- ROI value for the patient being assessed

DB: database
PPMI: Progressive Parkinson Marker Study
ROI: region of interest
SBR: striatal binding ratio



DaTQUANT is CE marked



GE Healthcare Limited, Pollards Wood, Nightingales Lane,
Chalfont St Giles, Buckinghamshire, England HP8 4SP
www.gehealthcare.com

© 2024 GE HealthCare
DaTQUANT is a trademark of GE HealthCare.
GE is a trademark of General Electric Company used under trademark license.
DICOM is the registered trademark of the National Electrical Manufacturers Association for its standards publications relating to digital communications of medical information.

Any third-party trademarks are the property of their respective owners.

All images displayed are of participants from the PPMI study.

09-2024 JB03750UK/DGT/OS UK