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WORKSHOP

# **PET data quantification using SAKE**

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**SAKE project:**  
<http://bio.dei.unipd.it/sake/>

*Ref: Veronese M, Rizzo G, Turkheimer FE, Bertoldo A. SAKE: a new quantification tool for positron emission tomography studies. Comput Methods Programs Biomed. 2013 Jul;111(1):199-213.*

# Practical: PET data quantification using SAKE

## TUTORIAL 1: Quantification at ROI level.

In this tutorial we will apply Spectral Analysis based methods (standard and rank shaping) for *region-wise* quantification of [11C](r)-Rolipram brain PET data.

## TUTORIAL 2: Quantification at Voxel level.

In this tutorial we will apply Spectral Analysis based methods (standard and rank shaping) for *voxel-wise quantification* of [11C](r)-Rolipram brain PET data.

## TUTORIAL 3: Analysis of Results.

Critical evaluation of spectral analysis quantification results on [18F]FDG brain PET data.

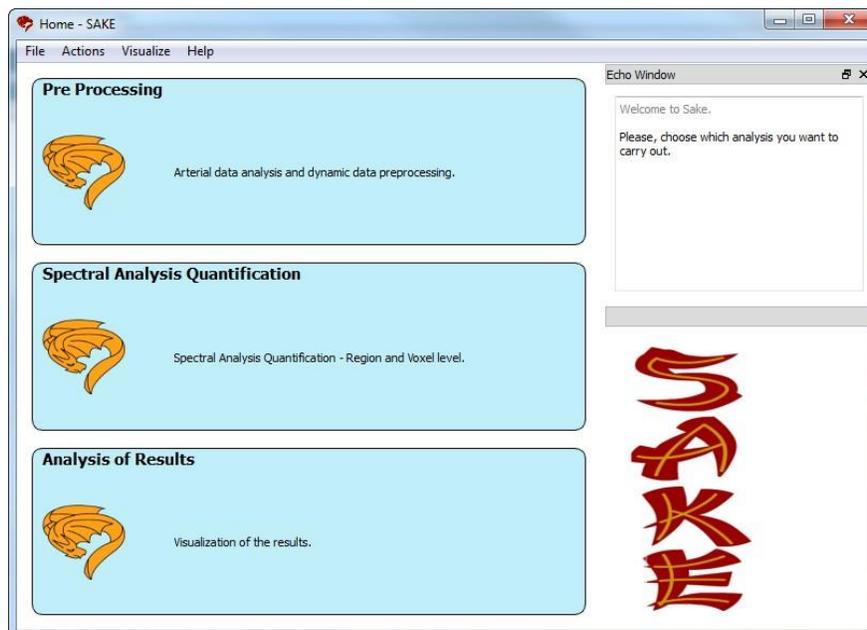
**Note:** These tutorials are meant to provide illustrative examples of how to use the modelling software to carry out PET data analysis. They do not necessarily provide the optimal choice of parameters or methods for the particular application area.

## Tutorial 1: Quantification at ROI level

This part of tutorial consists in quantifying [ $^{11}\text{C}$ ](r)-Rolipram brain PET data using Spectral Analysis based methods. [ $^{11}\text{C}$ ](r)-Rolipram is a ligand for phosphodiesterase 4 (an enzyme that metabolizes cyclic adenosine monophosphate (cAMP)). It is usually associated with reversible kinetics and modelled with a 2TCM.

Ref: Rizzo G, Veronese M, Zanotti-Fregonara P, Bertoldo A. *Voxelwise quantification of [(11)C](R)-rolipram PET data: a comparison between model-based and data-driven methods. J Cereb Blood Flow Metab. 2013 Jul;33(7):1032-40.*

### Step 1: Open SAKE and Check the data



**SAKE's home page.**

- Double click on SAKE's icon (red dragon)
- From SAKE's home page click on "Pre Processing"
- To evaluate arterial data click on "Arterial Input Function", "Load File", and in the working folder of SA\tutorial1 load Rolipram\_arterial.txt  
*Q: Do the data require extra modelling?*
- To evaluate measured tissue PET data, return to SAKE's home, click on "Pre Processing" and "PET Data at region level". Load Rolipram\_region.txt from the SA\tutorial1 working directory.  
*Q: How does the NSD (Noise Standard Deviation) time course look like? Is it consistent with PET acquisition protocol?*

To note that both arterial and tissue data are already corrected for tracer decay (both) and tracer delay (arterial).

## Step 2: Quantification via Standard Spectral Analysis

- From SAKE's home page click on "*Spectral Analysis Quantification*", select "*Standard Spectral Analysis*" and "*REGION LEVEL*". Click on "*Next*" icon.
- The data should be already loaded (if you have just completed the step 1). Otherwise, load Rolipram\_arterial.txt and Rolipram\_region.txt from the SA\tutorial1 working directory as "*Arterial File*" and "*Exam File*" respectively.
- Perform the analysis with the default values by clicking on "*Apply*" icon.
- Select an existing workspace directory, for example the working directory SA\tutorial1
- Write the output file prefix: "*Default*"
- Click on "*Go To Result Analysis*"

*Q: How is the fit of the data? How many lines did you expected? How many lines are detected?*

## Step 3: Quantification via Spectral Analysis Rank Shaping

First attempt.

- From SAKE's home click on "*Spectral Analysis Quantification*" and select "*Spectral Analysis Rank Shaping*" and "*Region Level*". Click on "*Next*" icon.
- Load Rolipram\_arterial.txt and Rolipram\_region.txt from the SA\tutorial1 working directory as "*Arterial File*" and "*Exam File*" respectively.
- Perform the analysis with the default values by clicking on "*Apply*" icon.
- Select an existing workspace directory, for example the working directory SA\tutorial1
- Write the output file prefix: "*Default*".
- Click on "*Go To Result Analysis*".

*Q: How is the fit of the data? How many lines did you expected?*

Second attempt.

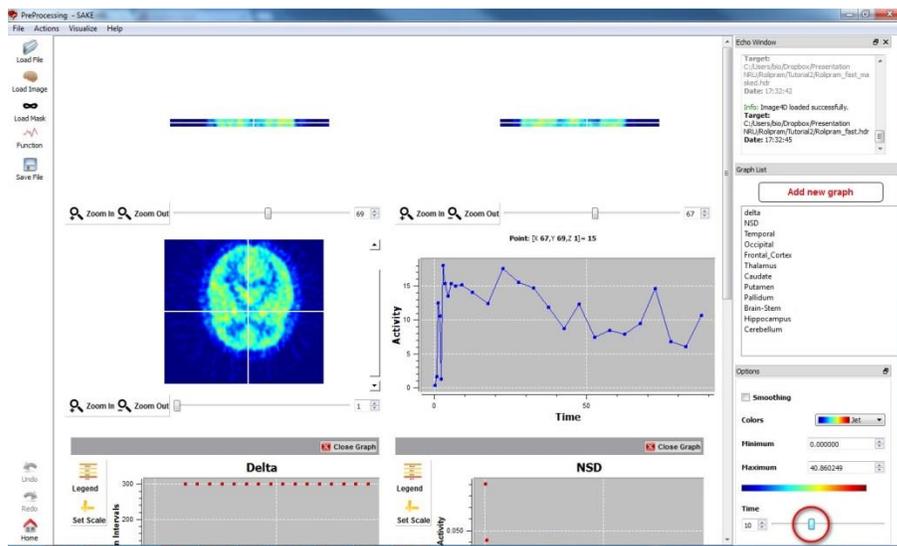
- Return to home and repeat the same analysis with a different algorithm setting [Number of Components = 100; Beta min=0.0001; Beta max=1; SNR from 0.001 to 0.1]. Use as output file prefix "*AlternativeGrid*".
- Click on "*Go To Result Analysis*".

*Q: How is the fit of the data? How is the precision of the estimated parameters?*

## Tutorial 2: Quantification at voxel level

### Step 1: Open SAKE and Check the data

- To evaluate voxel-wise measured tissue PET data return to SAKE's home, click on "Pre Processing" and "PET Data at voxel level".
- Load Rolipram\_region.txt from the SA\tutorial2 working directory using "Load File" icon.
- Load Rolipram\_fast.img from the SA\tutorial2 working directory using "Load Image" icon. Scroll the time line on the bottom right of the GUI and check the distribution of the data.



- Load Rolipram\_fast\_masked.img from the SA\tutorial2 directory successfully using "Load Mask" icon.

### Step 2: Create the Added image

- Click on "Function" and on "Summed PET". To note that the data are already decay corrected.
- Type the output file name, like "Added\_image" and click on "Save". The added image should appear on the GUI.

### Step 3: Quantification via Standard Spectral Analysis

- From SAKE's home click on "Spectral Analysis Quantification" and select "Standard Spectral Analysis" and "VOXEL LEVEL".
- Load Rolipram\_arterial.txt as "Arterial File" from SA\tutorial2 working directory. The other files should already be loaded, otherwise load them from SA\tutorial2 working directory.
- Apply the analysis with the default values.
- Select an existing workspace directory, for example the working directory SA\tutorial2.
- Write the output file prefix: "Default".
- Click on "Go To Result Analysis" when the analysis is completed.

*Q: How do the obtained parametric maps look like?*

- Map Vt: .....
- Map Ki: .....
- Map Vb: .....

*Q: How is MapOrder (estimated number of components)? Is it consistent with the characteristics of the tracer?*

- To assess the voxel-wise fit, load Rolipram\_fast.img from the SA\tutorial2 working directory using “Load Source” icon and click on one of the visualized maps. How is the fit of the data?

#### **Step 4: Quantification via Spectral Analysis Rank Shaping**

You can try to repeat the same analysis by using Spectral Analysis Rank Shaping.

*Q: How does the setting impact on the results?*

### **Tutorial 3: Analysis of results**

- From SAKE’s home click on “Analysis of Results”.
- Load FDG\_Saif\_Image.sake from the SA\tutorial3 working directory using “Load File” icon.
- Load “FDG\_PET.img” from the SA\tutorial3 working directory using “Load Source” icon.

*Q: How do the obtained parametric maps look like?*

- Map Vt: .....
- Map Ki: .....
- Map Vb: .....

*Q: How is MapOrder (estimated number of components)? Is it consistent with the characteristics of the tracer?*