PSEG PET Image Segmentation

Image Segmentation

Image segmentation plays an important role in objective image assessment. Segmented anatomic structures are the basis for a multitude of quantitative approaches analyzing shape, texture and dynamic uptake of tracer. PSEG supports tailored segmentation workflows for static and dynamic imaging scenarios.

PERCIST-type Segmentation

PERCIST[1,2] defines an objective methodology to assess the tumor burden and treatment response from static FDG PET images. Lesions are segmented based on the uptake in a reference organ, and their relevant properties (SUVpeak, MTV, TLG, etc.) listed in a report. In PSEG, the same workflow is also applicable when segmenting on an absolute threshold in SUVlbm or other calibrated units.

PERCIST-type lesion segmentation in PSEG is comprehensive and flexible.

Functional Organ Segmentation

Dynamic rodent PET studies are often used early in tracer or drug development. PSEG includes a patented clustering approach for grouping image pixels with similar kinetics in a local neighborhood[3]. Semi-automatic segmentation of such studies can be achieved within only a few minutes.

K-Means Segmentation

The K-means method is a general clustering approach. The implementation in PSEG is aimed at subdividing a dynamic image into clusters of “kinetically similar” pixels[4]. It uses the time-weighted Euclidean distance as the measure of dissimilarity (or distance) between TACs.

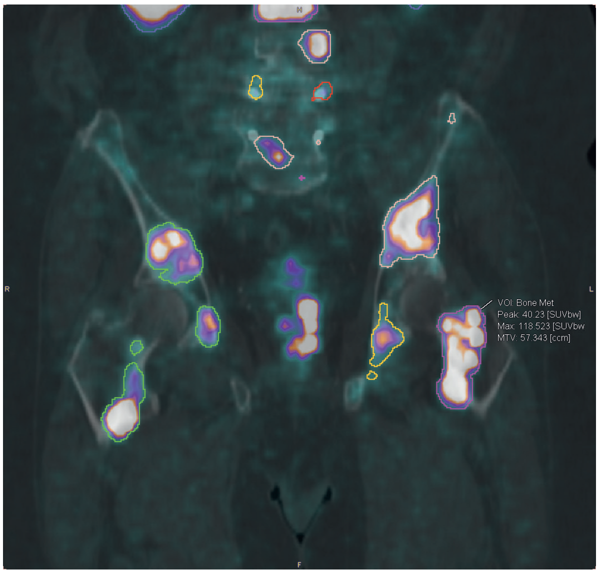
PSEG supports the semi-automatic segmentation of dynamic rodent PET studies within just a few minutes.

Supervised Segmentation

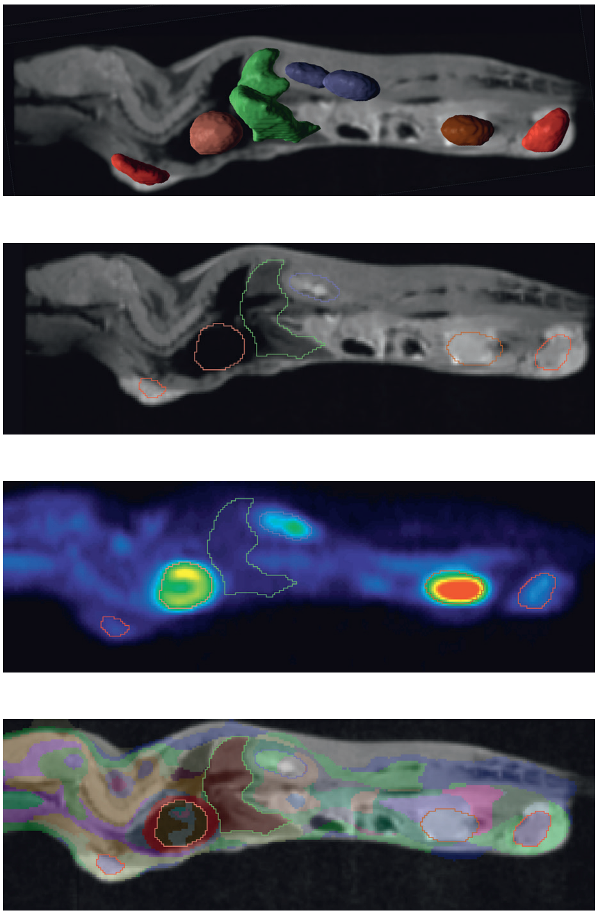
Whereas K-means is completely data-driven, supervised clustering is driven by a set of time-activity curves specified by the user[5]. They represent the kinetic behavior of the tissues of interest, which are to be segmented from the data. This approach has been developed for data-driven reference region determination.

AI-based Segmentation (Option)

PMOD’s Artificial Intelligence framework (PAI) builds on the PSEG tool. It allows users developing segmentation solutions based on artificial neural networks.



Segmentation of human PSMA PET on SUVbw = 3.5 threshold



Organs and lesions derived by segmentation of dynamic FDG PET, shown in overlay on sagittal mouse MR sections.

Workflow
All methods use a consistent workflow:
- Load the functional data to be segmented
- Option: Load matched anatomical data
- Crop to relevant volume
- Interpolate to suitable resolution
- Generate a segmentation mask
- Apply segmentation method within mask
- Analyze the functional data within the segments
- Save protocol file for exact reproduction

PERCIST Segmentation
Implements the PERCIST methodology for the oncologic assessment of static human FDG PET images[1, 2]:
- Interactive placement of 3cm diameter sphere in liver or blood
- Automatic iso-contouring on "minimal level of tumor uptake"
- Lesion sorting by SUVpeak
- Report of hottest lesions with exploratory measures incl. SUVmax, MTV, TLG, max. diameter

Special features:
- Texture analysis within lesions
- Segmentation on absolute SUV thresholds
- Comparison baseline – follow-up
- Label map generation of lesions as input to machine learning
- Applicable for animal data (reference sphere scales automatically)

Functional Organ Segmentation
Local means analysis method licensed from CEA, Orsay, France[3] for dynamic PET data. Segments "functional organs" characterized by independent pharmacokinetics.
- Localization of pixels in the organ centers
- Computation of local pharmacokinetics and global noise
- Parcellation of mask volume into a configurable number of regions
- Hierarchical fusion of regions forming increasingly larger regions
- Interactive assignment of organs to segments on suitable hierarchy levels
- Organ time-activity curve (TAC) calculation, optionally with partial volume correction
- Transfer of TACs to kinetic modeling tool

K-Means Segmentation
General k-means clustering for subdividing dynamic data into clusters of "kinetically similar" pixels[4]. The time-weighted Euclidean distance is used as the measure of distance between TACs. Performs the following steps for a specified number N of clusters:
- Randomly selects N pixels as initial cluster centroids
- Assigns each pixel to the centroid with minimal distance between the TACs
- Calculates new centroid TAC as average TAC of all cluster pixels
- Repeats cycle: 1) Assign each pixel to centroid with minimal distance, 2) Recalculate centroid TAC, until no pixel is assigned to a different cluster, or iteration exceeds a prescribed maximum.

As no geometric information is used in the process, the resulting clusters likely include spatially disconnected pixels.

Supervised Segmentation
Method for subdividing dynamic data into clusters following distinct kinetic behavior. Developed for derivation of reference brain region in [11C]PK11195 studies[5]. Requires preparation of representative class TACs. Implements the variant described for use with [11C]PIB[6]:
- Fits pixel TAC by linear combination of all kinetic class curves with non-negative coefficients (NNLS)
- Assigns pixel to class with highest coefficient
  Special feature:
- Mechanism (weight ratio) to assign only pixels with clear preference for one class curve

Morphological Segmentation
- Use of standard morphological operators for creating segments (threshold, range, region growing, Otsu, hottest pixels, hottest connected pixels

AI-based Segmentation (Option)
- See PAI product description

References
[1] Wahl RL et al.: From RECIST to PERCIST: Evolving Considerations for PET response criteria in solid tumors. J Nucl Med 2009, 50 Suppl 1: 122S–150S.
[2] O JH, Lodge MA, Wahl RL: Practical PERCIST: A Sim- plified Guide to PET Response Criteria in Solid Tu- mors 1.0. Radiology 2016, 280(2): 576–584.
[3] Maroy R et al. Segmentation of rodent whole-body dynamic PET images: an unsupervised method based on voxel dynamics. IEEE Trans Med Imag. 2008; 27(3): 342–54.
[4] Velamuru PK et al. Robust Clustering of Positron Emission Tomography Data. Paper presented 2005; St. Louis.
[5] Turkheimer FE et al: Reference and target region modeling of 11C-PK11195 brain studies. J Nucl Med 2007, 48(1): 158–167.
[6] Ikoma Y et al: Reference region automatic extraction in dynamic 11C-PIB. J Cereb Blood Flow Metab 2013, 33(11): 1725–1731.