Implementation of a PET scanner:

a guide to reconstruct data from your scanner in STIR

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STIR meeting, 3 December 2020

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Steps to reconstruct your data

- Read the raw data
- Read data for the Normalisation
- Estimate attenuation
- Align umap and PET image
- Estimate random and scattered events
- Use all the above into the reconstruction

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Raw data:

- If interfile, it is easy
- If vendor-specific format:
  - If not public, ask information to the vendor (will need NDA)
  - Collect information to create interfile header with script, implement a scanner object or projData derived class
  - Study the order of detectors and modules

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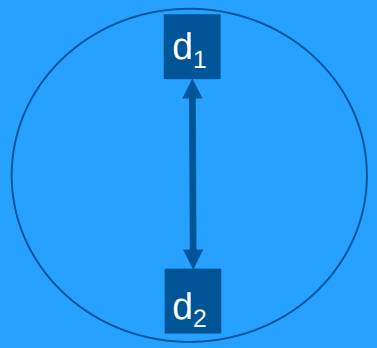
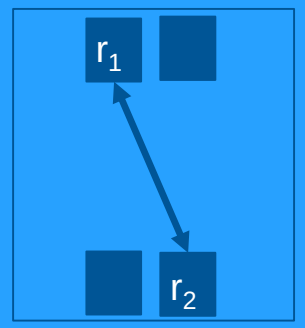
Raw data:





- Binary data is organised as a vector or matrix
- Each element (bin) represents a combination of d1, d2, r1, r2
- Need to order these bins in a STIR ProjData structure

How?

ProjDataInfoCylindricalNoArcCorr::
get_bin_for_det_pair(Bin& bin, DetectionPositionPair pair**)**

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Raw data: sinogram extraction utility (if vendor raw is a vector/histogram)

For (i=0; i<N_{tot} ; i++) {

- Calculate d1, r1, d2, r2 from i
- proj_info. get_bin_for_det_pos_pair(Bin, pair)
- Save bin in memory: proj_mem.set_bin_value(bin);

}

proj_mem.write_to_file(out_data_filename);

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Normalisation: Detector efficiencies

- Similarly to raw data can be saved in vectors (text or binary)
- Need to transform to STIR projData
- apply_normfactors3D needs norm terms in a specific order: $S= t+m*N_t +r*N_t*N_m$
- Important to reorder the values accordingly: create simple utility to manipulate text or binary (ifstream,ofstream)
- Run **apply_normfactors3D** with input your STIR-efficiencies file

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Normalisation: Dead-time

- Similarly to efficiencies can be saved in vectors (text or binary)
- Need to transform to STIR ProjData,
- 1 factor for each pair coincidence allowed
- Create look-up table between dead-time index and pair indices
- **ProjDataInfoCylindricalNoArcCorr** Proj_data_info
- For(all the sinogram bins){
- Proj_data_info.get_det_pos_pair_for_bin(pair,bin); (only span 1)
- get pair.pos1 and pair.pos2
- Access table[pos1][pos2]=i and bin.set_bin_value(DT_table[i])
- Proj_mem.set_bin_value(bin)
- }

- Proj_mem.write_to_file(out_data_filename)

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Attenuation:

Extract the umap from the scanner or use the CT image. If CT image:

- Use **ctac_to_mu_values**, to get a umap ex:
  ctac_to_mu_values -o umap.hv -i CT.dcm -j STIR/src/utilities/share/stir/ct_slopes.json -m mediso -k 511

- Need to subsample ex:
  zoom_image --scaling preserve_values –template temp.hv zoomed_umap.hv umap.hv

- Before Calculate_attenuation_coefficient we need to register the umap to the PET image
  - Quick recon of PET (no corrections), need to convert to .nii
  - niftyReg**: reg_aladin** -ref NAC.nii -flo zoomed_umap.nii -res registration –rigOnly

- Calculate acfsino: **calculate_attenuation_coefficients** --PMRT --ACF acfsino zoomed_umap.hv sino_template.hs

- **stir_math** --mult -s normacfsino_t normsino acfsino
- Also multiply the dead-time similarly to get fullnormsino

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Randoms and scatter:

- Provided with single rates
- Like the efficiencies we need a script to reorder the index (same scripts works)
- Create rondoms using:
  construct_randoms_from_singles randoms.hs S input_sino 5

- **Scatter_and_recon.sh** script (one for mMR and one for GESigna)
  - All parfiles and scripts are in STIR/example/sample
  - If normsino and/or randoms and/or acfsino is not saved you need to estimate again.
  - Output is total_additive…hs/s

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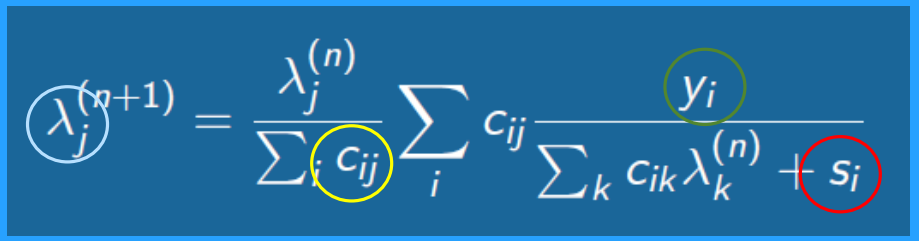
Reconstruction: run OSMAPOSL OSMAPOSL.par



- OSMAPOSLParameters :=
- objective function type:= PoissonLogLikelihoodWithLinearModelForMeanAndProjData
- PoissonLogLikelihoodWithLinearModelForMeanAndProjData Parameters:=
- input file := ${input_sino}
- maximum absolute segment number to process := -1
- zero end planes of segment 0 := 1
- projector pair type := Matrix
- Projector Pair Using Matrix Parameters :=
- Matrix type := Ray Tracing
- Ray Tracing Matrix Parameters:=
- number of rays in tangential direction to trace for each bin := 10
- End Ray Tracing Matrix Parameters:=
- End Projector Pair Using Matrix Parameters :=
- recompute sensitivity := 1
- use subset sensitivities := 1
- ; optional. if not set, the subset sensitities won't be saved
- subset sensitivity filenames:= ${recon_prefix}_sens_%d.hv
- Bin Normalisation type:=From ProjData
- Bin Normalisation From ProjData :=
- normalisation projdata filename:= ${dtnormacfsino}
- End Bin Normalisation From ProjData:=
- additive sinogram := ${additive}.hs
- zoom:= 1
- xy output image size (in pixels) := ${image_size_xy}
- z output image size (in pixels) := ${image_size_z}
- end PoissonLogLikelihoodWithLinearModelForMeanAndProjData Parameters:=
- output filename prefix := ${recon_prefix}
- number of subsets:= ${subsets}
- number of subiterations:= ${subiter}
- ;start at subiteration number :=1
- Save estimates at subiteration intervals:= ${subiter_interval}
- END :=

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Thank you!

Questions?

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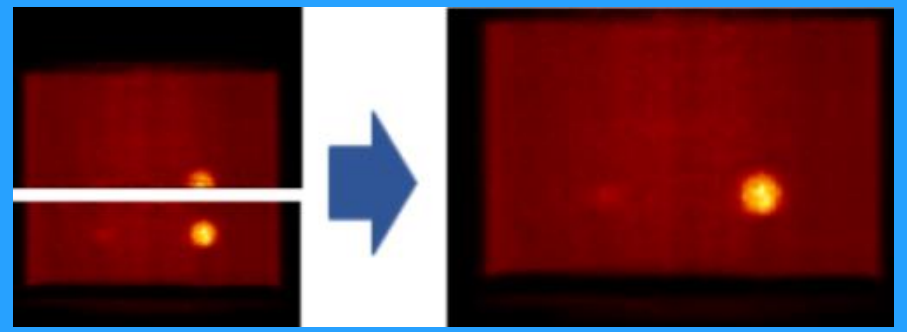
Multiple bed positions:

- Use bed position (BP) info to create a image template for each z offset
- Use **zoom_image** with template to crop umap into multiple BPs
- Created **combine_multiple_bed_position** ex:
  combine_multiple_bed_positions <out_im_prefix> <num_bed_pos> <iter_num> <bedpost_temp> <image_prefix> <sens_prefix>

- Iterates over the number of BPs
- Bigger image is created
- Overlapped region is obtained using weighted mean
- weight=sensitivity



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Work in progress

- BinNormalisationWithCalibration
- Allows calibration, branching ratio factors
- Radionuclide database
- Decay correction

Thank you!

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