Bundesministerium für Bildung und Forschung

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The NUKDOS software for treatment planning in MRT

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NUKDOS

Klinik und Poliklinik für Nuklearmedizin
Direktor: Prof. Dr. A. Buck

Introduction

- NUKDOS was developed to provide a software tool for therapy planning in molecular radiotherapy

- Available software packages:

  - include only methods for one or several working steps and/or are only commercially available
  - do not include an estimate of the overall error of the absorbed doses

Aims

- One software tool for all relevant steps
- Implementation of robust and objective methods
- Calculation of an overall error (uncertainty) for the doses
- User-friendly

→ Improve quality and acceptance of dosimetry

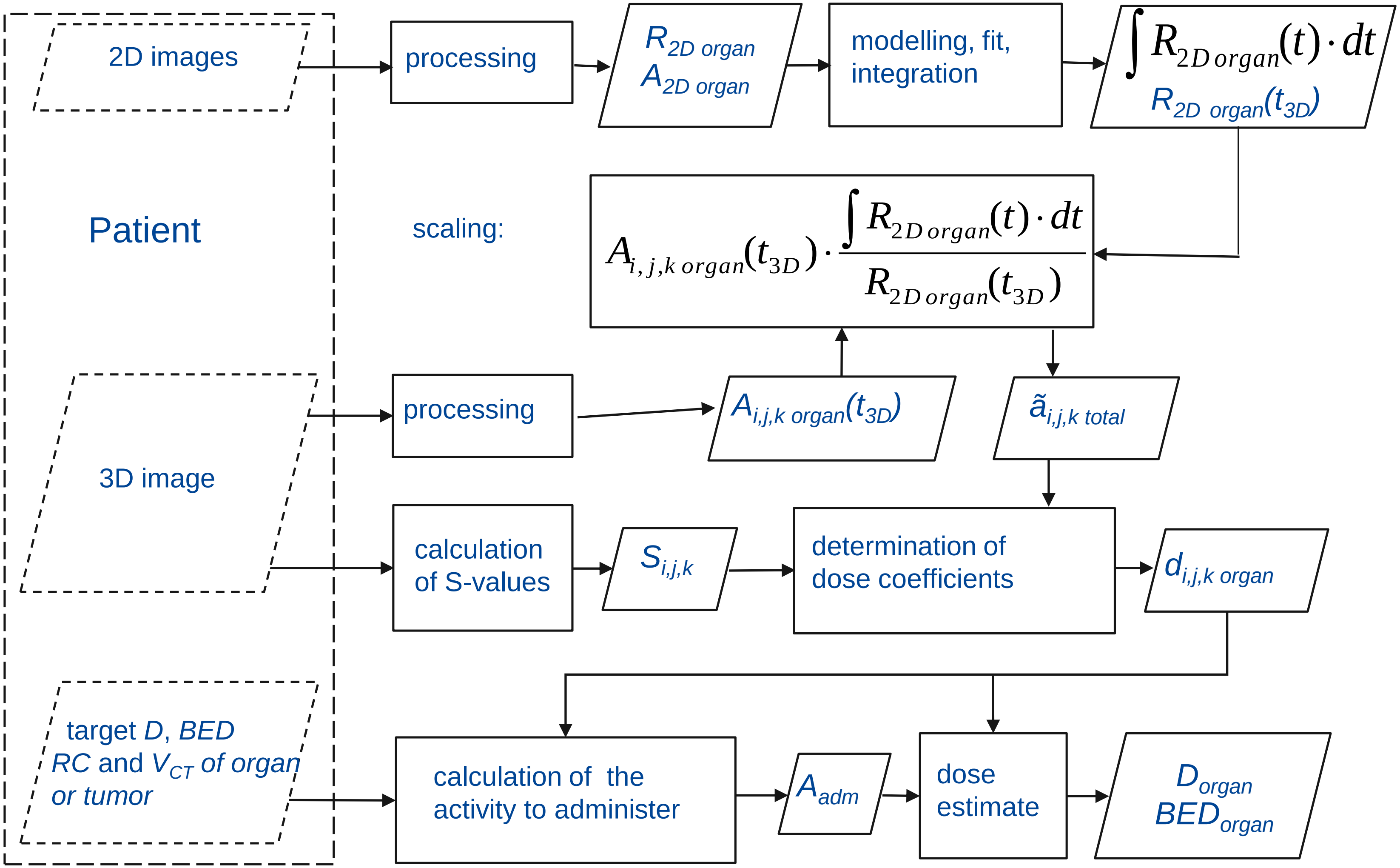
Methods

- NUKDOS is written in MATLAB

Focus on:

- A series of gamma camera images plus one SPECT/CT (e.g. for PRRT)
- Inclusion of data from
  - External Counting
  - Blood sampling
- MIRD formalism on the voxel level
  - One SPECT/CT (per organ) → voxel based activity
  - Conjugate view gamma camera images → organ/lesion kinetics
  - S values implemented for 3 nuclides → ^{90}Y, ^{131}I und ^{177}Lu
- Includes EANM SOPs for DTC and Benign Thyroid disease

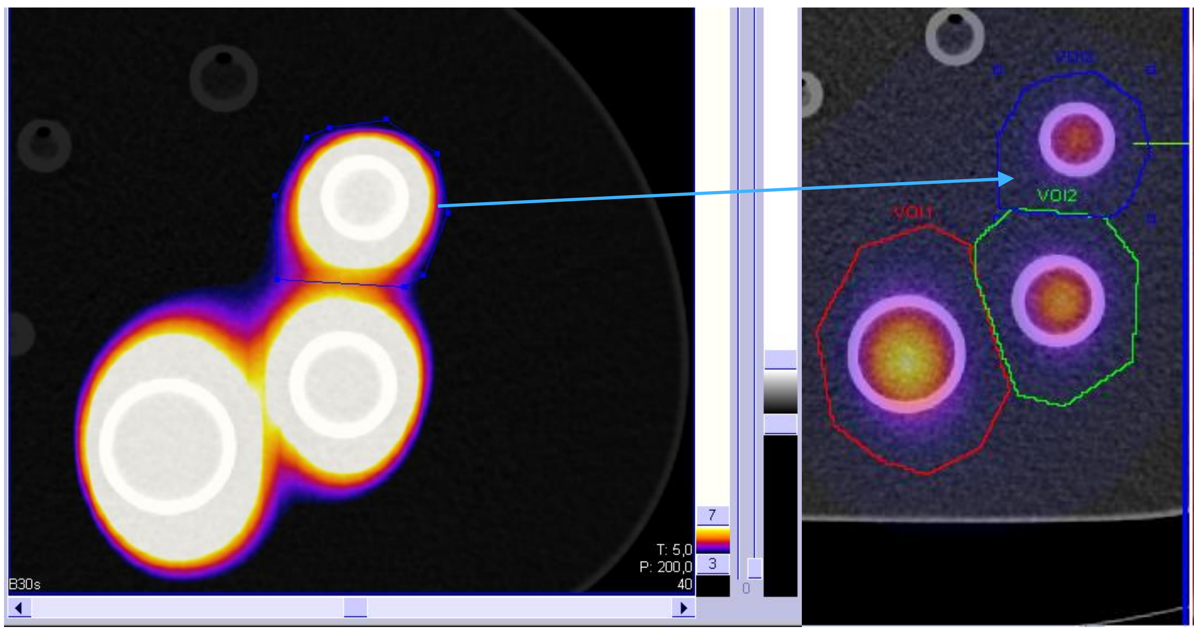
Workflow: Series of planar gamma camera images and one SPECT/CT

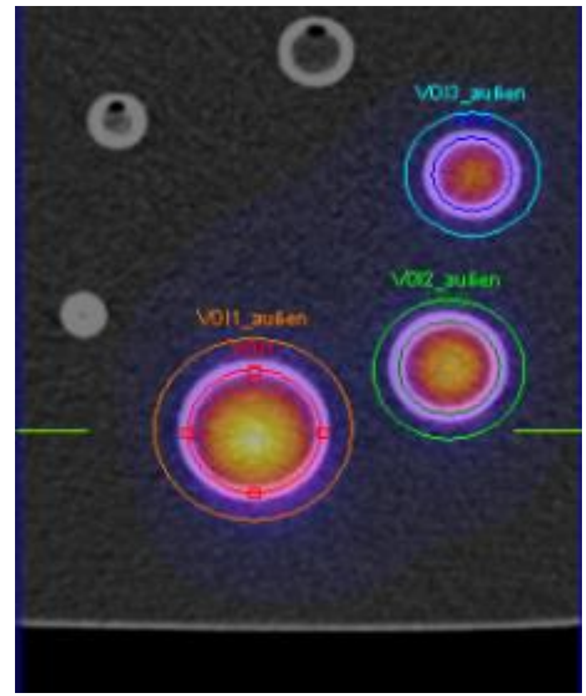


Calibration – measurement set-up

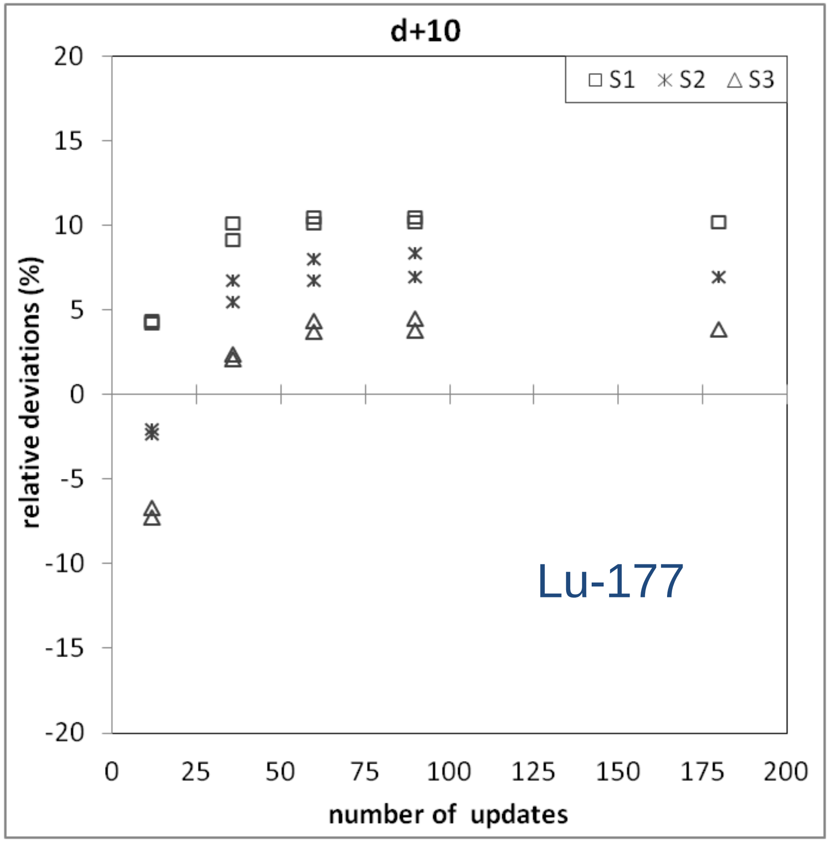
SPECT/CT: Symbia T2 (Siemens)

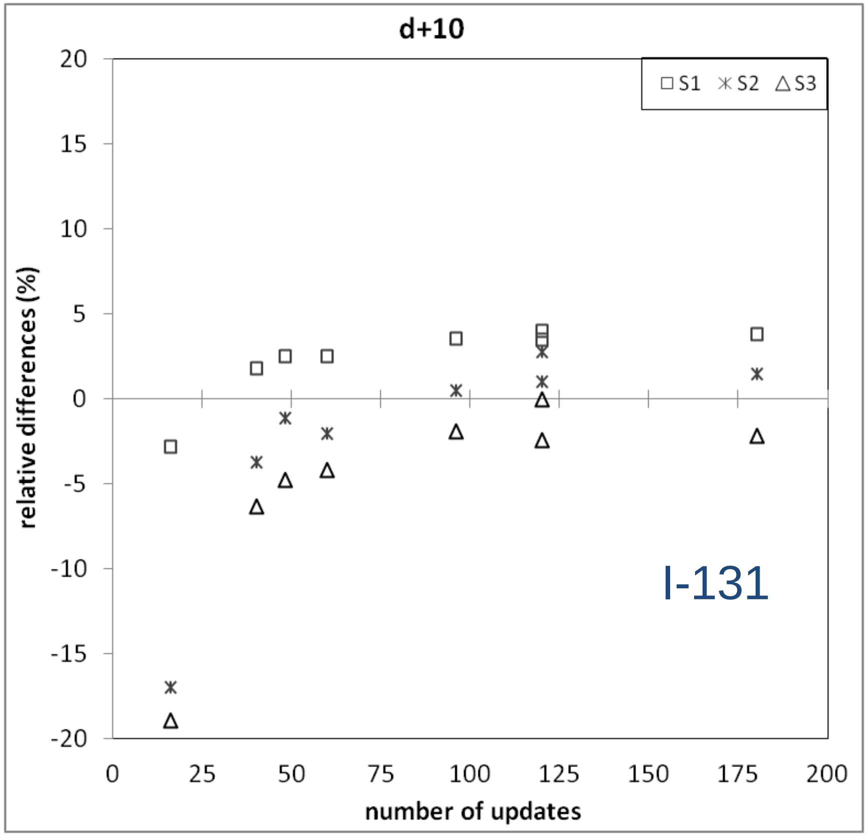
Calibration and quantification





Calibration – Reconstruction





Relative deviations as a function of the effective number of iterations for Lu-177 and I-131

Example: Application of NUKDOS in PRRT

- Case:
- Patient with meningioma
- Therapy with ^{90}Y-DOTATATE
- Pre-therapeutic dosimetry with ^{111}In -DOTATATE

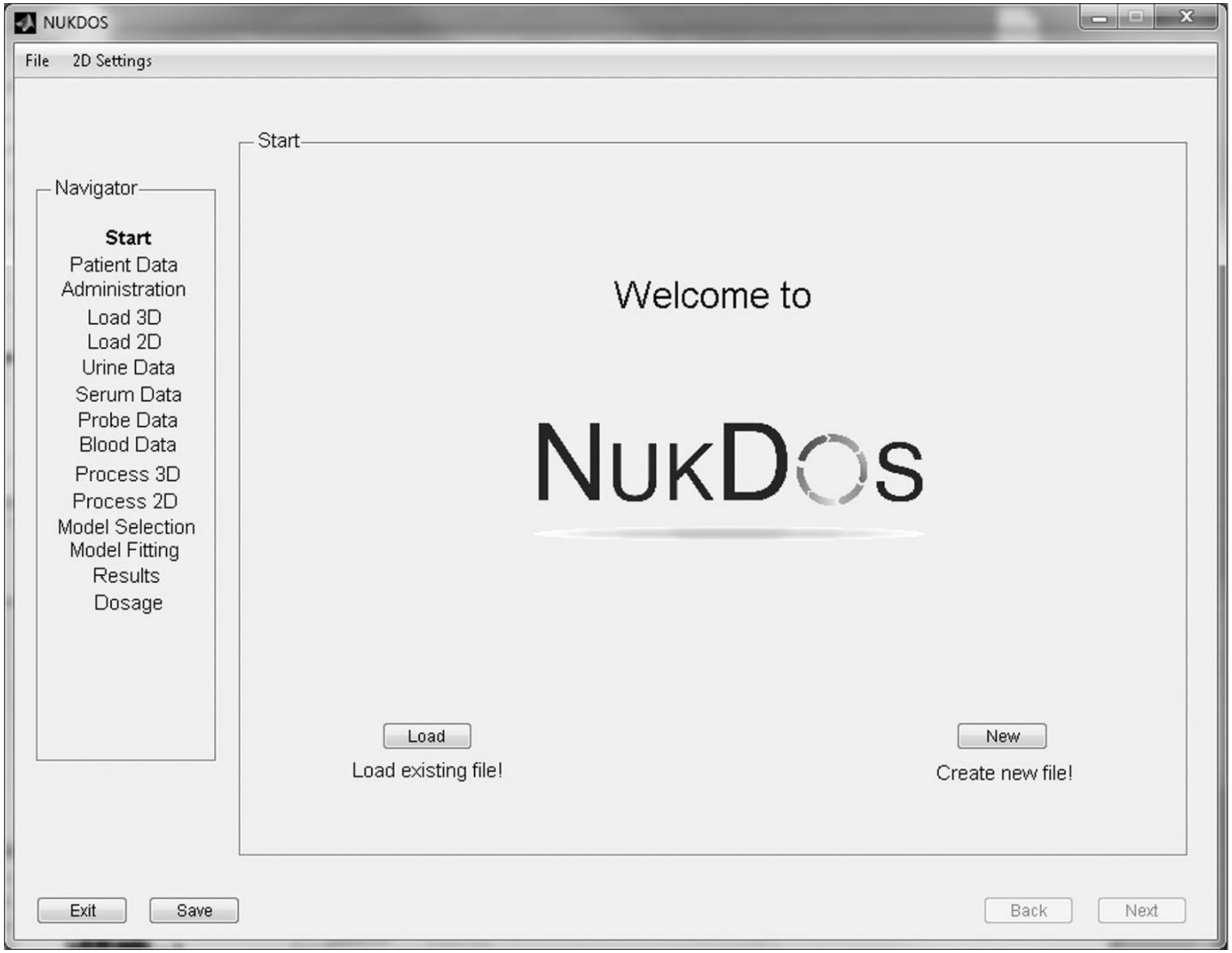
- Limit: 12 Gy to kidneys

- Activity to administer: ?
- Dose to spleen, tumour and RM: ?

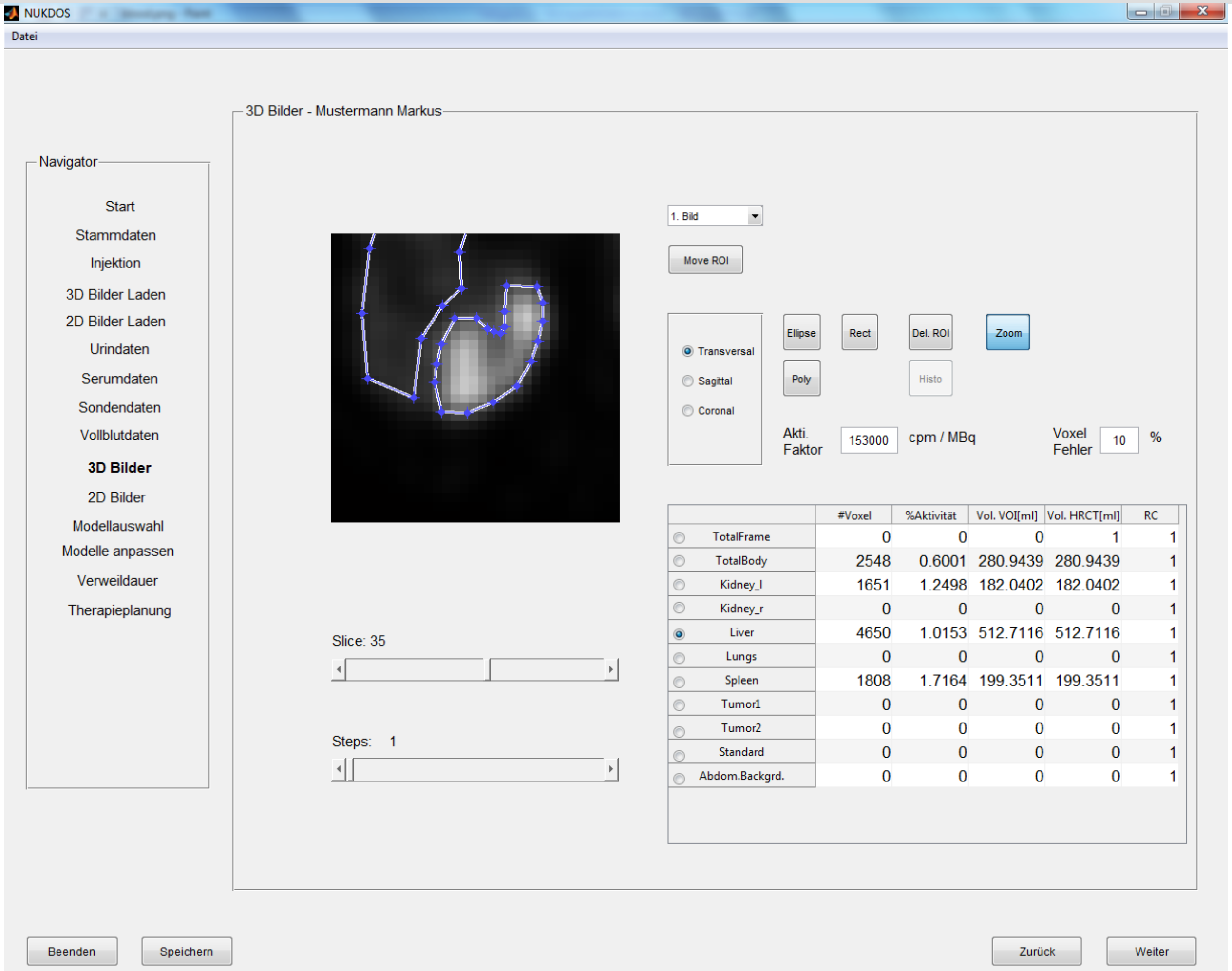
NUKDOS-Input

- Basic patient data (name, date of birth, height, weight, sex, notes)
- Administered activity (full/empty syringe, dates, times)
- 3D images (SPECT/CT)
- Gamma camera images
- External counting data
  - Blood/serum samples
  - Urine samples

Starting GUI



3D Image Processing



	#Voxel	%Aktivität	Vol. VOI[ml]	Vol. HRCT[ml]	RC
TotalFrame	0	0	0	1	1
TotalBody	2548	0.6001	280.9439	280.9439	1
Kidney_l	1651	1.2498	182.0402	182.0402	1
Kidney_r	0	0	0	0	1
Liver	4650	1.0153	512.7116	512.7116	1
Lungs	0	0	0	0	1
Spleen	1808	1.7164	199.3511	199.3511	1
Tumor1	0	0	0	0	1
Tumor2	0	0	0	0	1
Standard	0	0	0	0	1
Abdom.Backgrd.	0	0	0	0	1

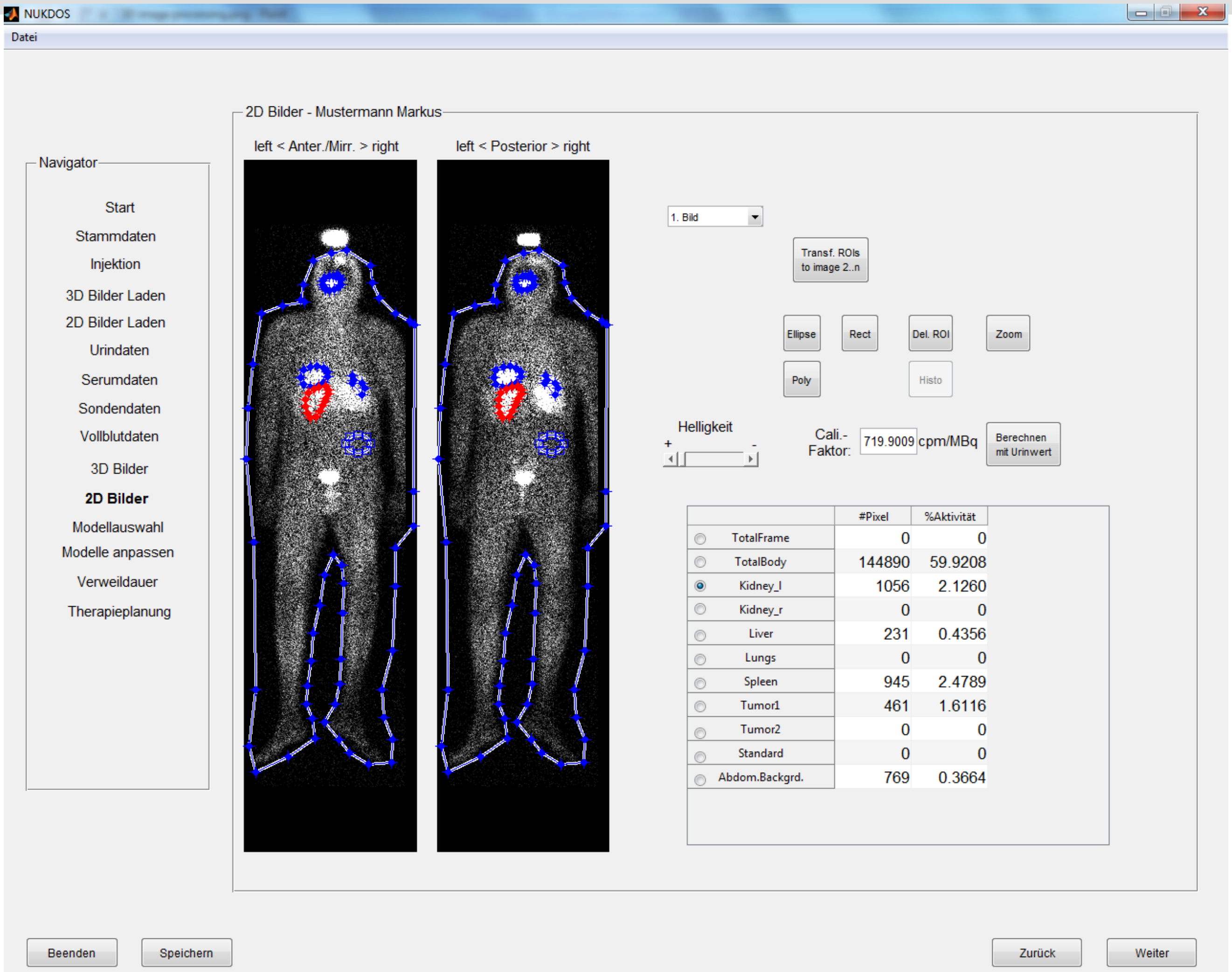
<u>CT measured</u>:

Kidney(l.):	194 ml
Spleen:	198 ml
Liver:	1811 ml
Tumour caudal:	87 ml

Total (uncertainty and bias)
Voxel error: 10%

Conditions: quantitative image

2D Image Processing



Validated using UlmDos

According to MIRD Pamphlet 16

Fitting and Model Selection

- Data error (model) specification
- Semi- or fully automated search for starting parameters
- Specification of a priori knowledge of parameter values
- Fit functions (sums of exponentials)
- Model selection using the Akaike Information Criterion (AIC)

Kletting P et al. Molecular radiotherapy: The NUKFIT software for calculating the time-integrated activity coefficient. Med Phys 2013; 40: 102504.

Molecular radiotherapy: The NUKFIT software for time-integrated activity coefficient calculation

- Provides a realistic set of functions for NM data
- Minimizes a given objective function
- Provides parameters to determine the quality of the fit
- Provides statistical criteria for choosing the best fit function
- Integrates analytically
- Determines the standard error of the result
- Validated using SAAM2 as comparison

Kletting et al, Med Phys, 2013

Molecular radiotherapy: The NUKFIT software for time-integrated activity coefficient calculation

Choice of fit functions

Kletting et al., Med Phys, 2013

$$f_1(t) = A_1 e^{-\lambda_{phys} t}$$

$$f_2(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t}$$

$$f_3(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t} + A_2 e^{-\lambda_{phys} t}$$

$$f_4(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t} + A_2 e^{-(\lambda_1 + \lambda_{phys})t}$$

$$f_5(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t} + A_2 e^{-(\lambda_2 + \lambda_{phys})t} + A_3 e^{-\lambda_{phys} t}$$

$$f_6(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t} + A_2 e^{-(\lambda_2 + \lambda_{phys})t} + A_3 e^{-(\lambda_3 + \lambda_{phys})t}$$

$$f_{4A}(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t} - A_1 e^{-(\lambda_2 + \lambda_{phys})t} = A_1 \left[e^{-\lambda_1 t} - e^{-\lambda_2 t} \right] e^{-\lambda_{phys} t}$$

$$f_{6A}(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t} + A_2 e^{-(\lambda_2 + \lambda_{phys})t} - (A_1 + A_2) e^{-(\lambda_3 + \lambda_{phys})t}$$

$$f_{4B}(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t} + (1 - A_1) e^{-(\lambda_1 + \lambda_{phys})t}$$

$$f_{6B}(t) = A_1 e^{-(\lambda_1 + \lambda_{phys})t} + A_2 e^{-(\lambda_2 + \lambda_{phys})t} + (1 - A_1 - A_2) e^{-(\lambda_3 + \lambda_{phys})t}$$

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Molecular radiotherapy: The NUKFIT software for time-integrated activity coefficient calculation

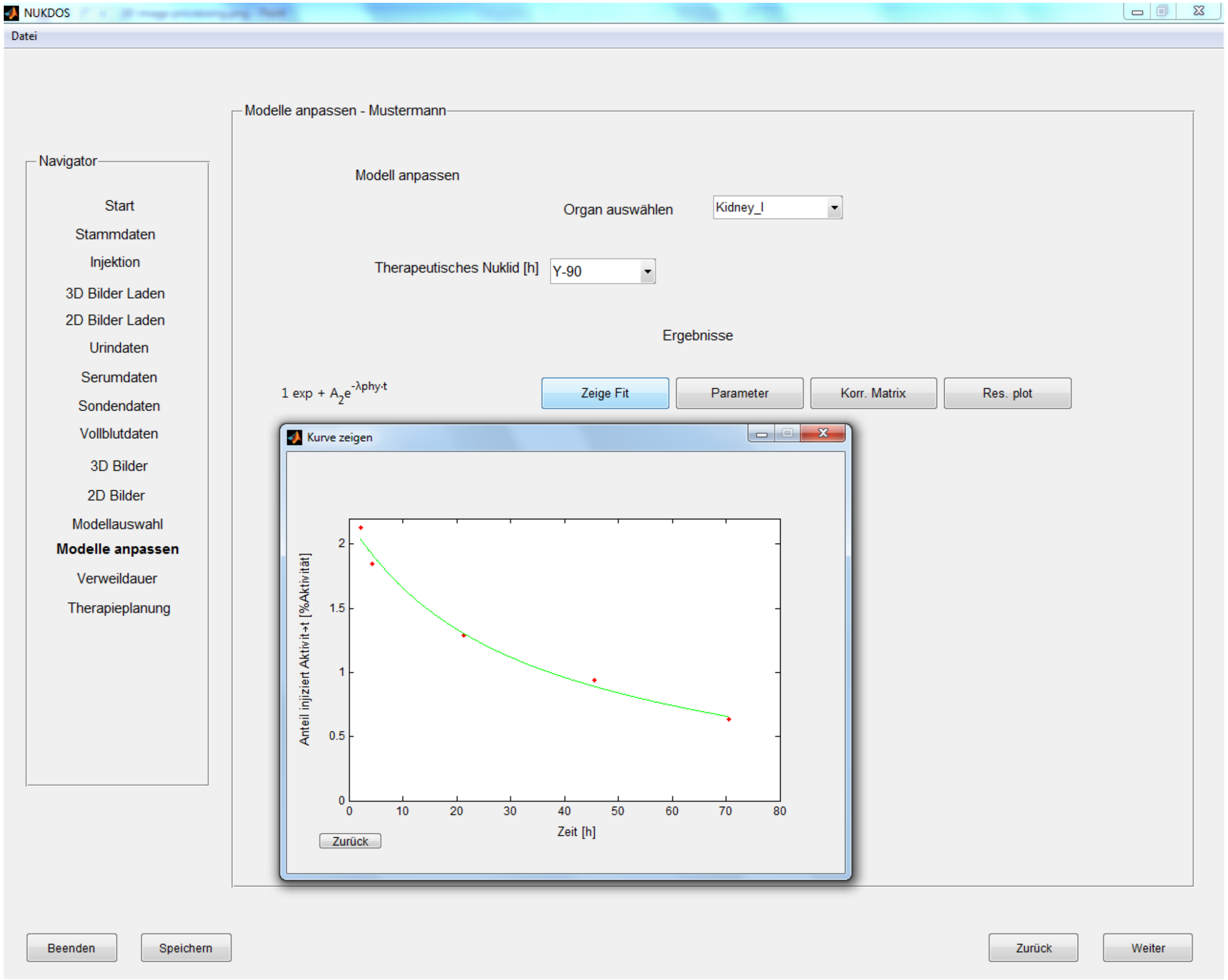
Parameters to determine the quality of the fit

Kletting et al., Med Phys, 2013

Results	Condition	Quality control
Plot	...	Visible inspection
R^2 [a]	...	Close to 1
AIC[b]	...	Compare with values of other functions
AICc[c]	J[d] $+ 2 \leq N$[e]	Compare with values of other functions
w_{AICc}[f]	All functions $J + 2 \leq N$	If $w_{AIC} > 0.01$ function is used for inference
Parameter	$J \leq N$	Plausible values
Parameter SE	$J + 1 \leq N$	CV$<$ 25% precise[g]; CV$<$50% acceptable[h]
Correlation matrix	$J + 1 \leq \mathrm{N}$	$-0.8 <$ each element < 0.8[i]
Weighted residuals	...	Random distribution

NukDos

Fitting



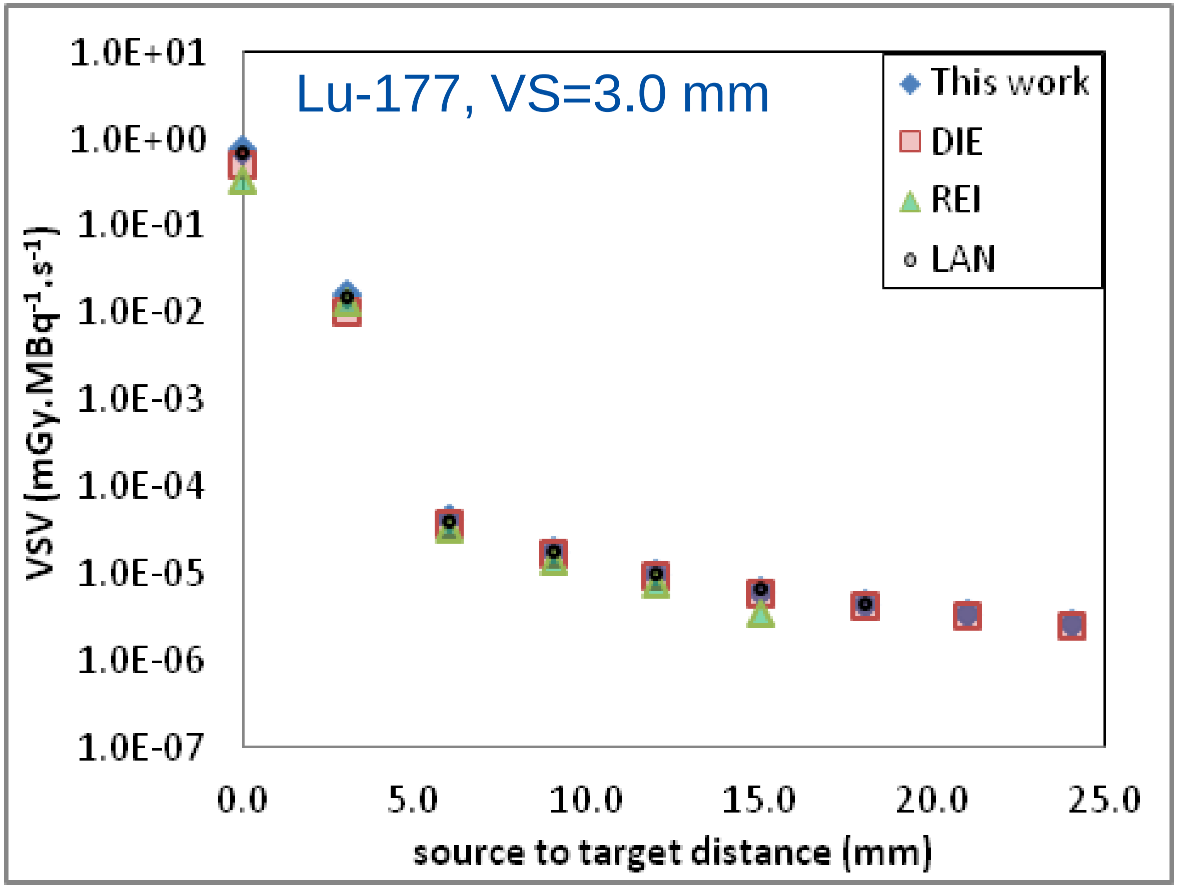
NUKDOS
Datei
Modelle anpassen - Mustermann
Navigator
Start
Stammdaten
Injektion
3D Bilder Laden
2D Bilder Laden
Urindaten
Serumdaten
Sondendaten
Vollblutdaten
3D Bilder
2D Bilder
Modellauswahl
Modelle anpassen
Verweildauer
Therapieplanung
Modell anpassen
Organ auswählen
Kidney_l
Therapeutisches Nuklid [h]
Y-90
Ergebnisse
1 exp + A2e-λphy·t
Zeige Fit
Parameter
Korr. Matrix
Res. plot
Kurve zeigen
Anteil injiziert Aktivit÷t [%Aktivität]
Zeit [h]
Zurück
Beenden
Speichern
Zurück
Weiter

Voxel S Values (VSVs)

- 3 nuclides are supported: ^{90}Y, ^{177}Lu and ^{131}I
- Images with cubical voxels of arbitrary size
- On-the-fly rescaling of pre-tabulated fine-grid Monte-Carlo simulation data obtained with MCNPX

Fernandez M et al. A fast method for rescaling voxel S values for arbitrary voxel sizes in targeted radionuclide therapy from a single Monte Carlo calculation. Med Phys 2013; 40: 082502.

Voxel S Values (VSVs)



DIE: Dieudonne et al. J. Nucl. Med. 51

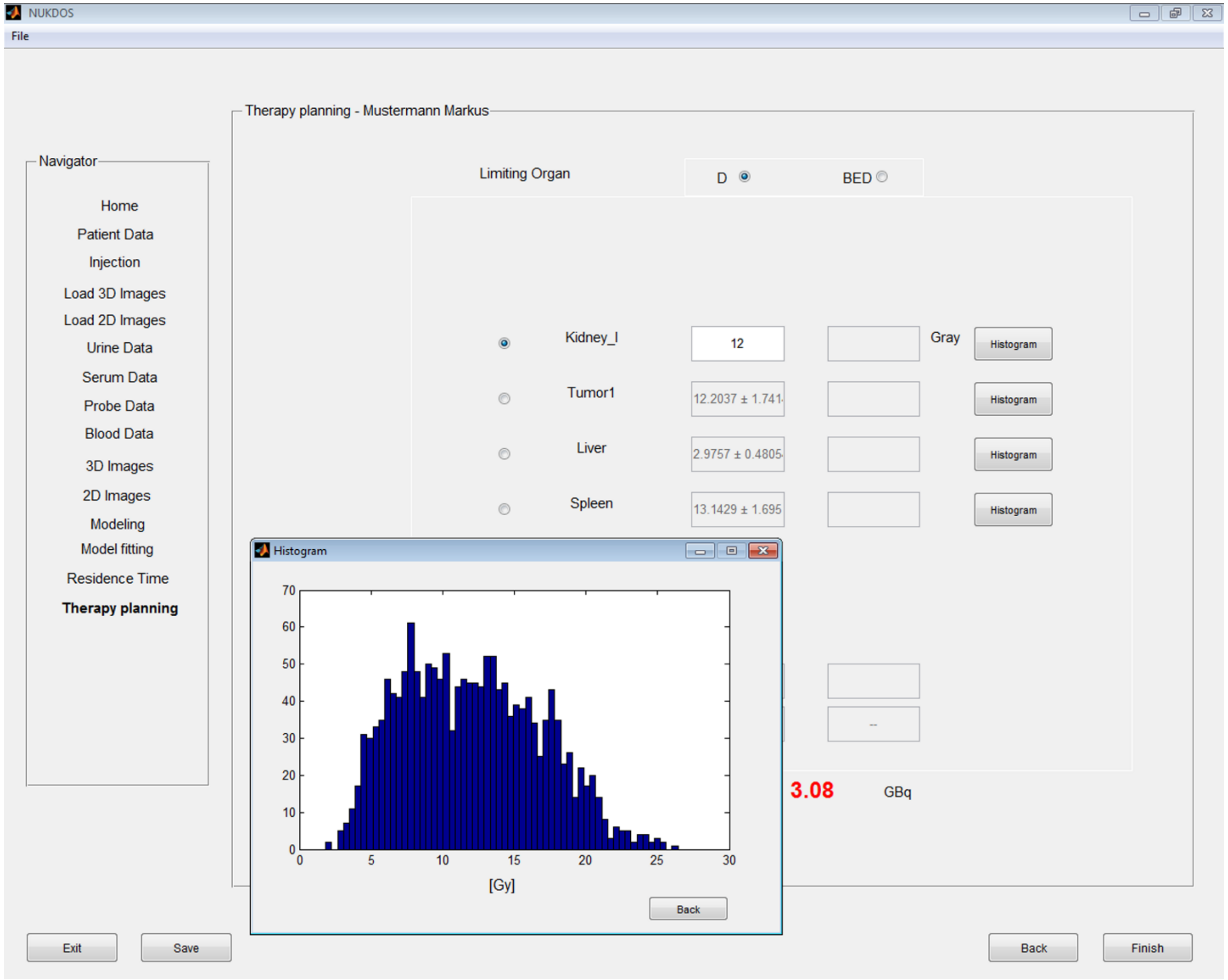
REI: Reiner et al. Med Phys 36

MIRD17: Bolch et al. J. Nucl. Med. 40

LAN: Lanconelli et al. Phys Med Biol 57

Fernandez M et al. A fast method for rescaling voxel S values for arbitrary voxel sizes in targeted radionuclide therapy from a single Monte Carlo calculation. Med Phys 2013; 40: 082502.

Therapy Planning



Validated on the organ level with OLINDA/EXM as comparison

Conclusion

- NUKDOS can be applied for Dosimetry in PRRT using a series of planar gamma camera images and one SPECT/CT. NUKDOS:
  - allows voxel-based dosimetry
  - provides an error estimate for the calculated absorbed doses
  - allows seamless workflow, no additional software is required
  - is freely available (January 2015)
- contact: peter.kletting@uniklinik-ulm.de

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