

# Welcome to the Jungle: Open-Source Software for DCE & DSC

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## Declaration of Financial Interests or Relationships

Speaker Name: Charlotte Debus

I have no financial interests or relationships to disclose with regard to the subject matter of this presentation.

# What does „open-source“ mean?

- “Generally, open source refers to a computer program in which the source code is available to the general public for use or modification from its original design” [Source: Wikipedia]
  - decentralized software development
  - source code, blueprints, and documentation freely available to the public (peer production)
  - collaborative effort: programmers improve the source code and share the changes within the community
  - software license, depending on which others may download, modify, and publish



# Why open-source?

- **Transparency**
  - What does the algorithm do exactly? (no „black-boxes“)
- **Standardization**
  - Inter-center comparability
- **Flexibility**
  - Configure to the researchers/study specific need
- **Extensibility**
  - Possibility to amend with own implementations
  - Improvement of source code via sharing changes with community



# The perfusion open-source software zoo:

## Stand-alone & plugin solutions



DATforDCEMRI: Deconvolution Analysis Tool for Dynamic Contrast Enhanced MRI  
dcemriS4: A Package for Image Analysis of DCE-MRI (S4 Implementation)



Version: 2.2

Software | Open Access



DCE@urlAB: a dynamic contrast-enhanced MRI pharmacokinetic analysis tool for preclinical data

Juan E Ortúñoz, María J Ledesma-Carbayo, Rui V Simões, Ana P Candiota, Carles Arús and Andrés Santos

BMC Bioinformatics 2013 14:316

<https://doi.org/10.1186/1471-2105-14-316> | © Ortúñoz et al.; licensee BioMed Central Ltd. 2013

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A Fast, Validated Open Source Toolkit for Dynamic Contrast Enhanced MRI Analysis

DOI 10.5281/zenodo.802969

DCEMRI DCEMRI

build passing

build passing

coverage 41%



### SOFTWARE

### Open Access



ROCKETSHIP: a flexible and modular software tool for the planning, processing and analysis of dynamic MRI studies

Samuel R. Barnes<sup>1†</sup>, Thomas S. C. Ng<sup>1,2†\*</sup>, Naomi Santa-Maria<sup>1</sup>, Axel Montagne<sup>3</sup>, Berislav V. Zlokovic<sup>3</sup> and Russell E. Jacobs<sup>1</sup>



Platform for Research in Medical Imaging (PMI)  
Steven Sourbron (s.sourbron@leeds.ac.uk)  
<https://sites.google.com/site/plaresmedima/>



Development and validation of an open source quantification tool for DSC-MRI studies

P.M. Gordaliza <sup>a, b</sup> , J.M. Mateos-Pérez <sup>a, c, 1</sup>, P. Montesinos <sup>a, b</sup>, J.A. Guzmán-de-Villoria <sup>d</sup>, M. Desco <sup>a, b, c, J.J. Vaquero <sup>a, b</sup></sup>

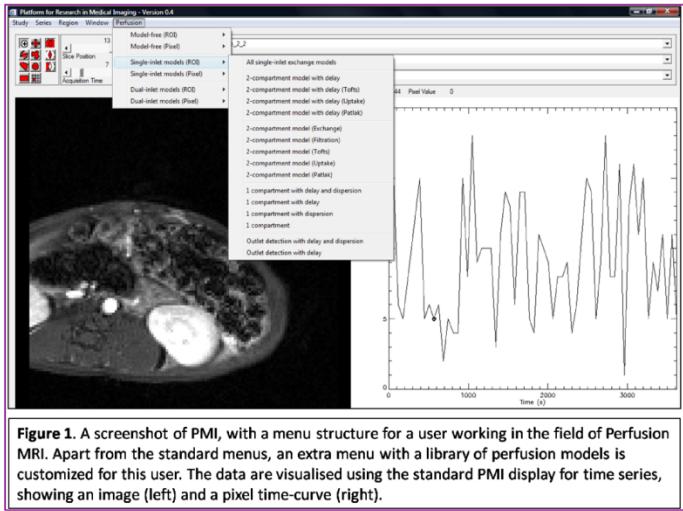


Python module for processing dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) data. Given a T1-weighted, dynamic, contrast-enhanced data set, a multilip data set, and either an AIF or blood curves, produce maps of Ktrans, ve, and vp.



# PMI – Platform for Research in Medical Imaging

Sourbron S. et al. *PMI: Platform for Research in Medical Imaging*



- IDL-based general purpose software for medical image analysis methods
- Source-code and pre-compiled binary
- <https://github.com/plaresmedima/PMI-0.4>

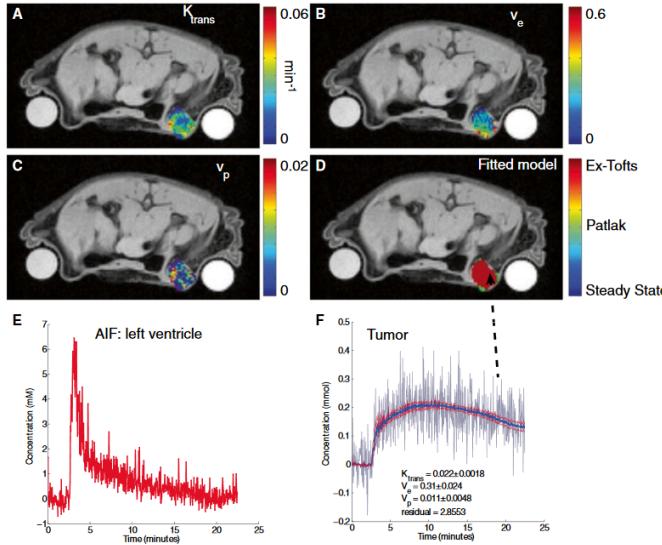
## Features

- + Segmentation and visualization
- + DICOM support
- + DCE MRI:
  - NLLS fitting with different PK models  
Uptake models, Steady-state, Patlak, Tofts, extTofts, 2CXM, 2C filtration for kidney, Dual-inlet for Liver
  - Semi-quantitative metrics Slope/Signal enhancement
- + DSC : SVD deconvolution
- + GUI available

- Commercial dependencies: IDL
- (OS-dependent)
- Poor documentation

# ROCKETSHIP

Barnes S., et al. *BMC medical imaging* 15.1 (2015): 19; doi: 10.1186/s12880-015-0062-3



## Features

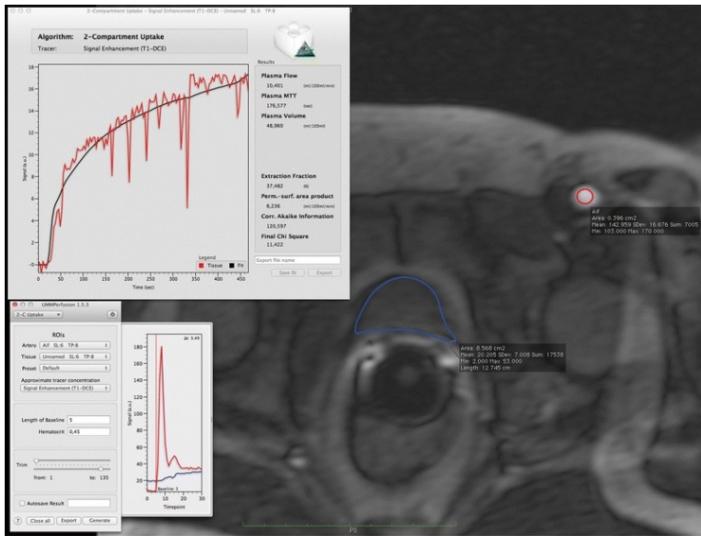
- + DICOM support
- + DCE MRI:
  - NLLS fitting with different PK models  
Tofts, eTofts, Fast Exchange Regime, 2CXM, Tissue uptake, Nested-model selection, Patlak
  - Semi-quantitative metrics AUC
- + Multi-OS

- Matlab-based Software for DCE MRI Analysis
- Source-code available via:  
<https://github.com/petmri/ROCKETSHIP>

- Matlab-based, requires toolboxes (e.g. curve fitting, Image processing, ...)
- No surrounding medical image processing ecosystem

# UMMPerfusion

zöllner, F. et al, *BMC medical imaging* 16.1 (2016): 7; doi: 10.1186/s12880-016-0109-0



## Features

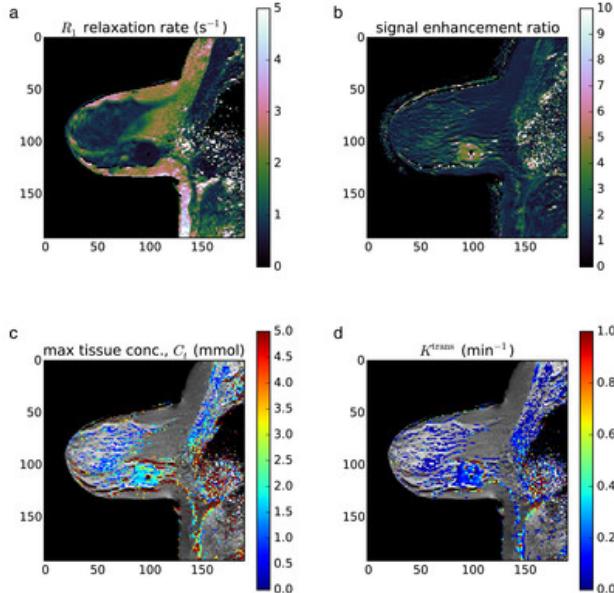
- + Surrounding medical image processing ecosystem
- + DICOM support
- + DCE MRI:
  - NLLS fitting with different PK models  
Extended Tofts, 1CP, 2CXM, 2C uptake model, two compartment filtration model (2FM)

- OsiriX Plugin for DCE MRI Analysis
- Source-code and pre-compiled binary application
- <http://www.opossumm.de/>

- Commercial dependency: OsiriX
- Available only on MacOS
- Limited automatization capability

# DCEMRI.jl

Smith, D. et al. PeerJ 3 (2015): e909; doi: 10.7717/peerj.909



- Julia- based software for DCE MRI
- Source code available  
<https://github.com/davidssmith/DCEMRI.jl>

## Features

- + Multi-OS
- + DCE MRI:
  - NLLS fitting with different PK models  
Tofts, Extended Tofts, Plasma Only
- + Validated on DROs (Tofts, eTofts)

- No direct DICOM support (supports Matlab data formats)
- No GUI
- No surrounding medical image processing ecosystem

# Ideally, open-source software for perfusion would provide ...

- Easy **data input** (DICOM support, PACS linkage)
- Graphical user interface (**GUI**), data exploration and fit visualization
- Integrated into **medical image processing ecosystems** (other necessary data evaluation steps like segmentation and registration)
- **Flexibility** in configuration (Models, Algorithms, etc.)
- Easily extendable with **own implementations** (software design concepts and reusability)
- **Automatization** supported
- **No** underlying **commercial** dependencies
- Operating-system (**OS**) **independent**
- **Standardization** and **Validation**
- **Transferable** results (general data format)





# Open-source platforms for medical image analysis



- C++ open-source software platforms for research in analysis and visualization of medical images
    - DICOM support (input/output, parametric maps)
    - Command-line interfaces, Python bindings, etc.
    - Dedicated modules/plugins for analysis and image processing: registration, segmentation, visualization, diffusion analysis, etc.
    - Modules for perfusion analysis
  - Source code and prebuild workbench application (GUI)
  - Framework structure
    - OS-independent
    - Extendible
    - no underlying commercial dependencies
    - Automatization
- Big overhead (more than just perfusion analysis)

# 3D Slicer

Fedorov, A. et al. MRI 30.9 (2012): 1323-1341;

doi:10.1016/j.mri.2012.05.001

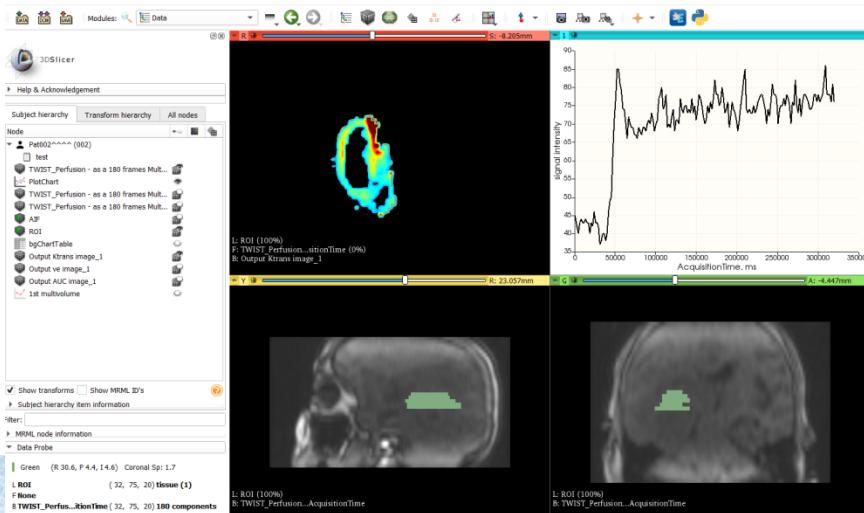
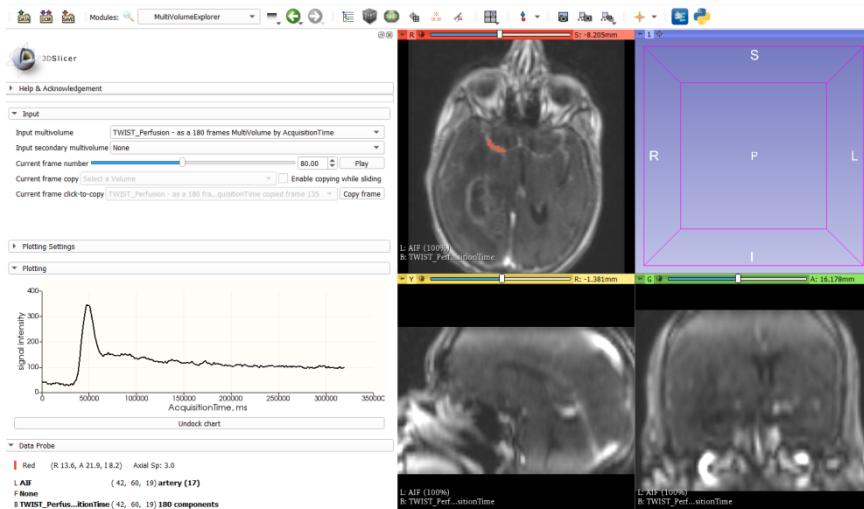
- Many command-line capabilities (Plug-in app store)
- High application flexibility
- <https://www.slicer.org/>

## + PKModelling

- Calculates quantitative parameters from DCE-MRI
- Classical Tofts and Kermode model ( $K_{trans}$  and  $v_e$ )
- Semi-quantitative metrics AUC, MaxSlope
- Interactive data visualization

## + DSCMRIAnalysis

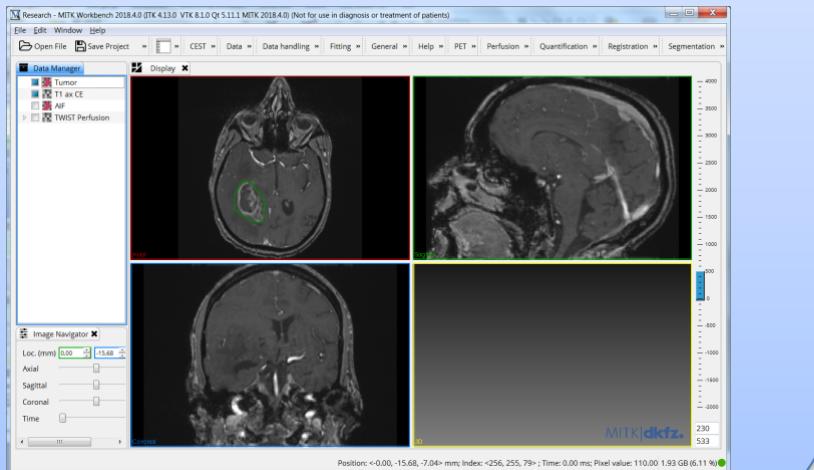
- Estimation of parameters rCBV, rCBF and MTT from DSC MRI



## Medical Imaging interaction ToolKit

Nolden, M. et al. *Int. J. Comp. Ass. Rad. Surg.* 8.4 (2013): 607-620  
doi: 10.1007/s11548-013-0840-8

- Versatile platform with high degree of modularization and interoperability
- Highly interactive medical image analysis



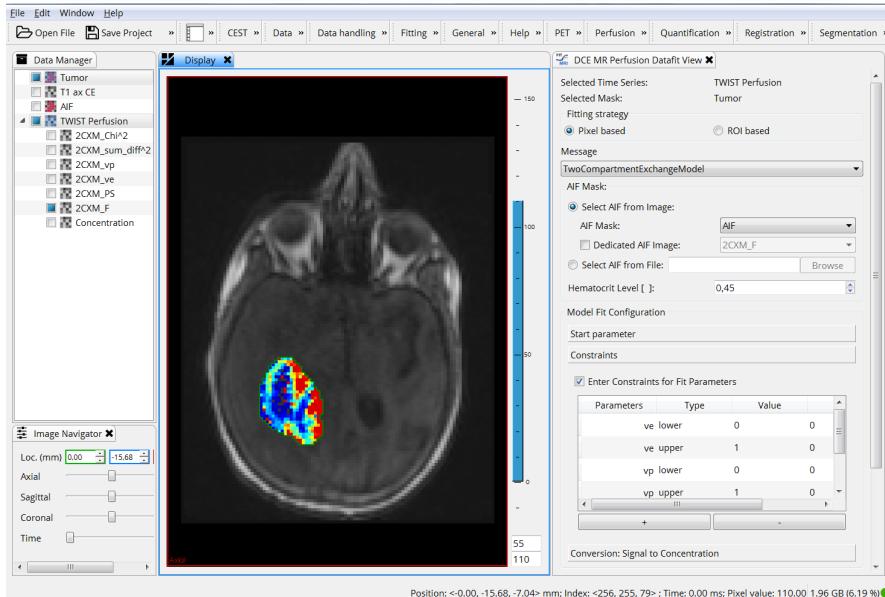
## MITK ModelFit

Debus C. and Floca R. et al. *BMC bioinformatics* 20.1 (2019): 31  
doi: 10.1186/s12859-018-2588-1.

- Open-source framework for fitting of medical image data
- <http://mitk.org/wiki/MITK-ModelFit>
- Integrated into MITK ecosystem
  - Whole analysis pipeline
  - Interactive and automatic analysis
- Modular (different data types, analysis pipelines) → Benchmarking of algorithms
- Easily extendable
- Modality independent

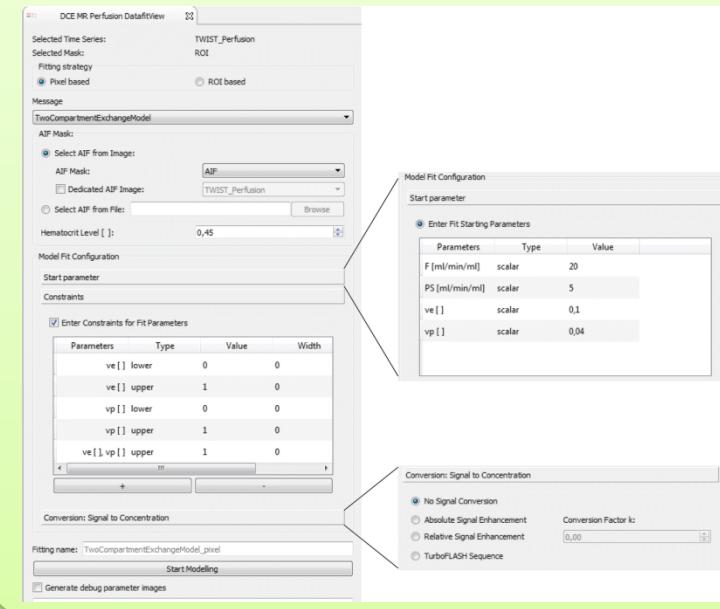
## DCE MRI:

- + PK modelling with different models  
Tofts, eTofts, 2CXM, descriptive models,... (growing)
- + Semi-quantitative metrics  
AUC, AUMC, TTP, BAT, MRT
- + Validated on DRO's

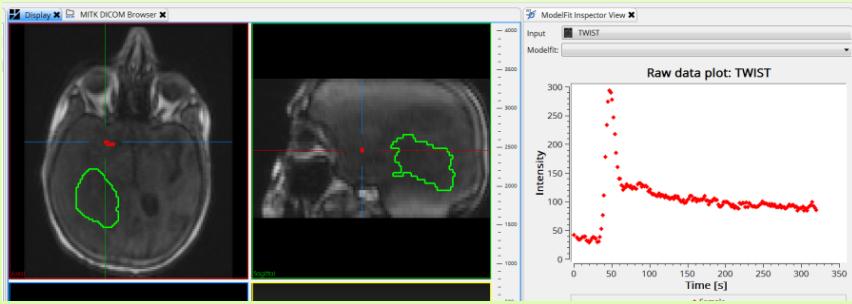
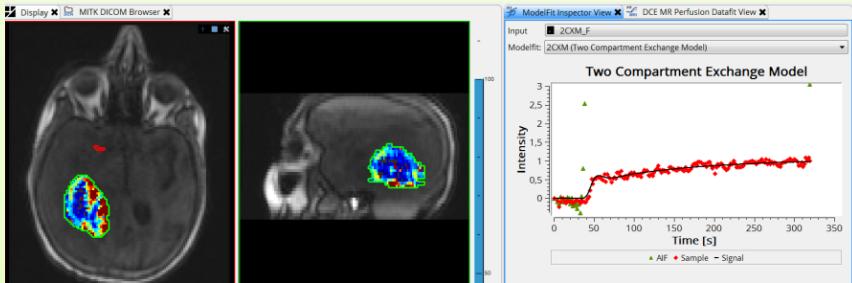


## + Custom fit configuration:

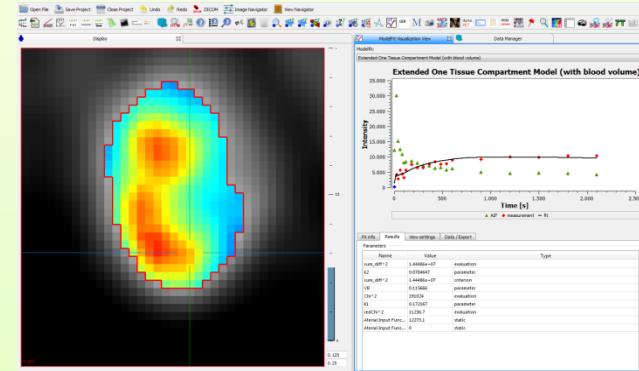
- Starting values
- Parameter constraints
- Conversion to concentration
- AIF definition



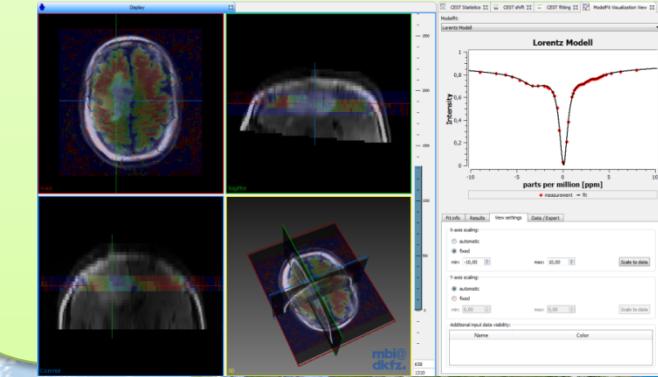
- + Interactive data and fit visualization
  - Parameter maps
  - Time curves



- + Fitting not limited to MR images  
→ e.g. dynamic PET



- + Fitting not limited to time domain  
→ e.g. CEST application



# Conclusion

- Welcome to the jungle ↔ Welcome to the desert?
  - OSIPI Perfusion Software Inventory
- There are different solutions according to different tastes (in language, flexibility, usability,...)
- Open-source is meant to be a community effort
  - Contribute!
  - Give feedback!

