

MITK Diffusion: Adapting a MITK based application to topic focused medical research

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dkfz.

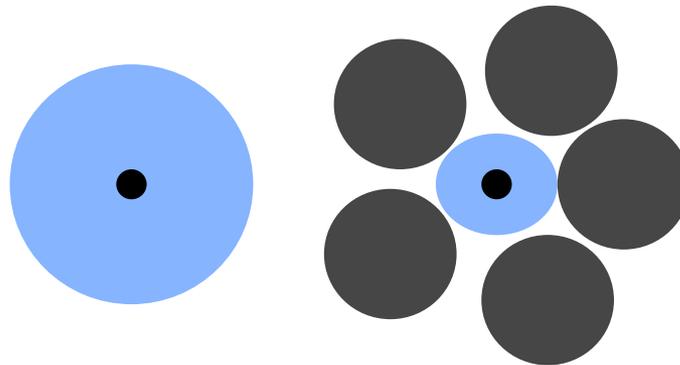
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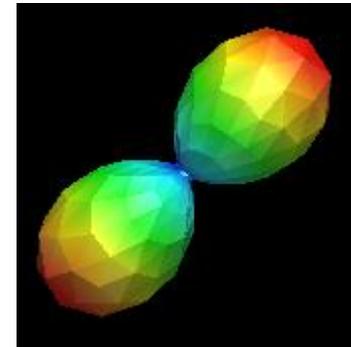
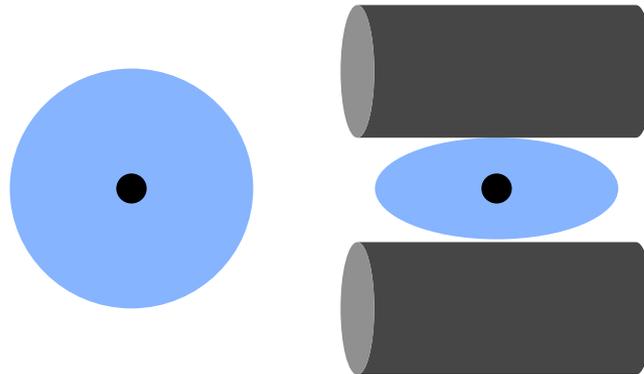
50 Years – Research for
A Life Without Cancer

A very brief description of our research

Front View:

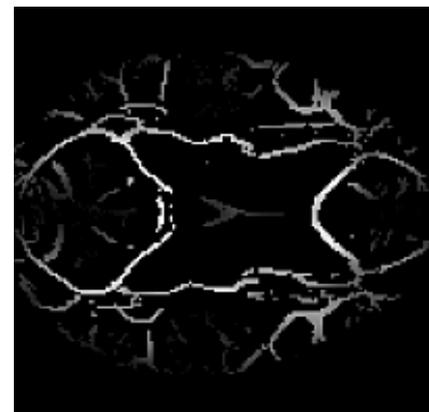
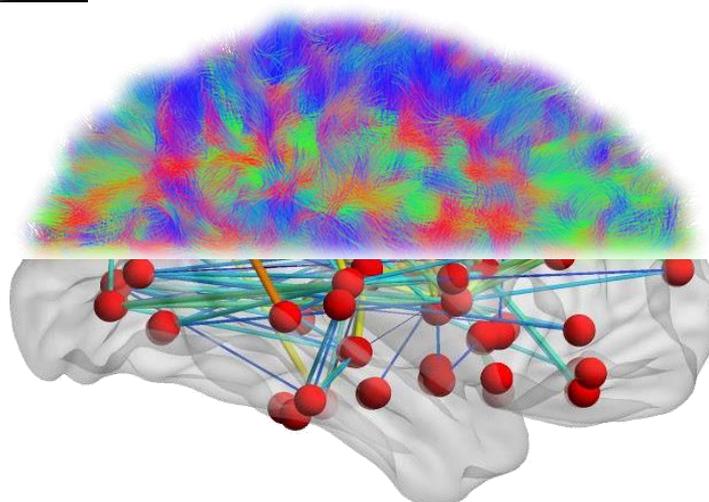
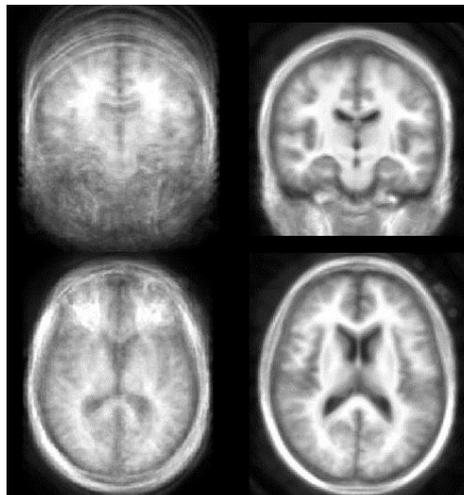
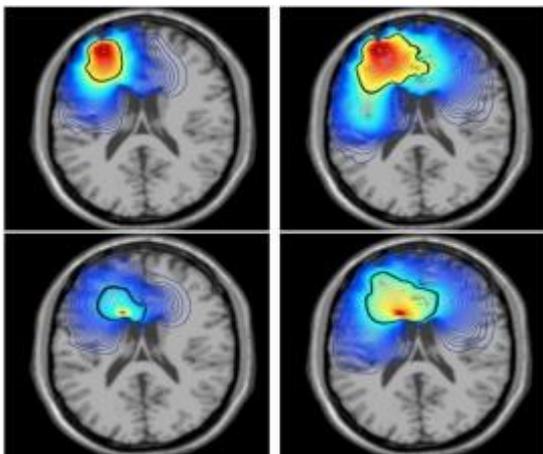


Side View:



- Diffusion restricted by anatomy
- This restricted diffusion can be measured using dMRI

A very brief description of our research – Page 2/50



Why do we want our own application?

- Own scientific topic which other researchers in our group do not work with
- Close cooperation with medical researchers in our field, provide access to our research
- Provide not only the results of our experiments, but also the methods to others world-wide

What do we want?

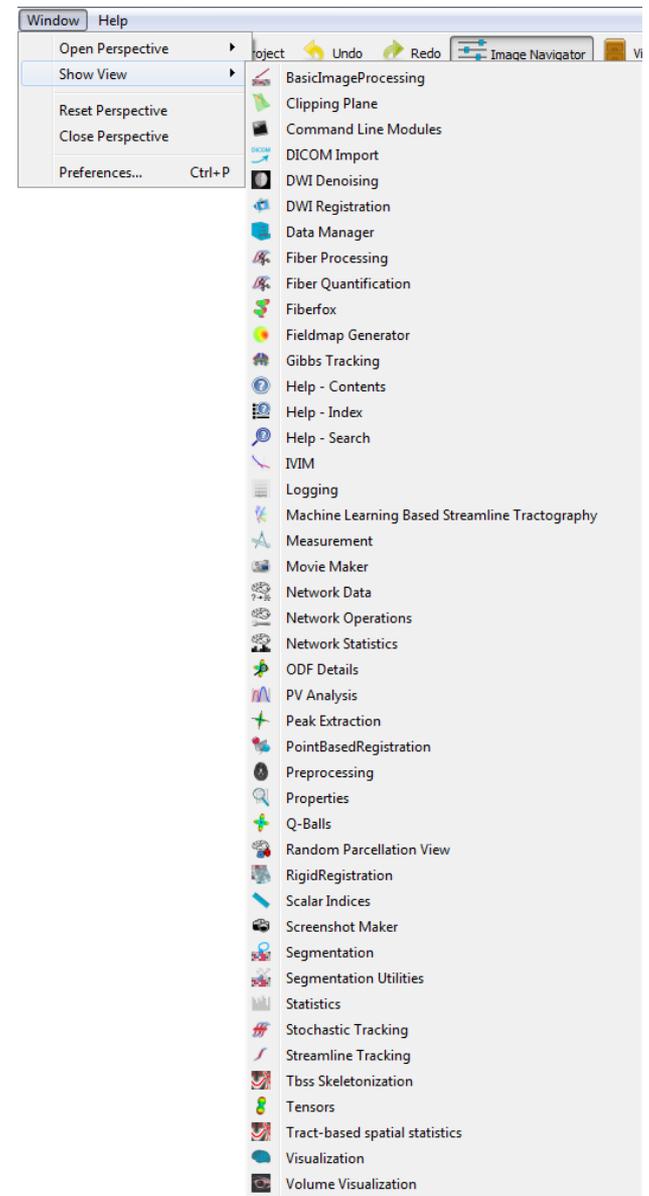
- A software that we can use to test new code/algorithms
 - Versatile and powerful
 - Easy to use
- A software that medical researchers can use without any coding experience
 - The tools needed for their work
 - Not cluttered by a lot of tools not needed for their work
 - Different Easy to use

What do we have?

- The DiffusionImaging module(s)
- The diffusionimaging plugin
- The MITK Workbench

Great let's use the workbench
and just switch on everything
we need!

Too confusing



Why create a new app?

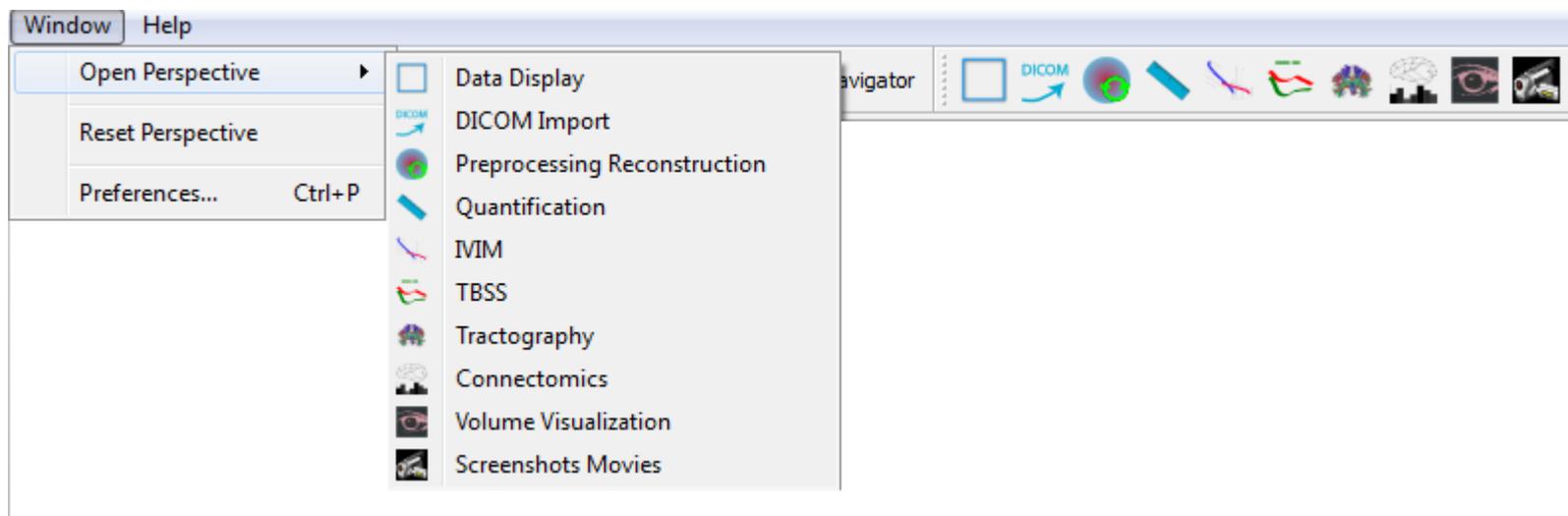
- Not possible to do everything we need within the workbench
- Own branding – useful for focusing on the community
- There is no need to synchronize everything with the workbench

What to change, how to change it?

- tleartoisn, lteartiosn, Iterations
- Several concepts where tried and changed

What to change, how to change it?

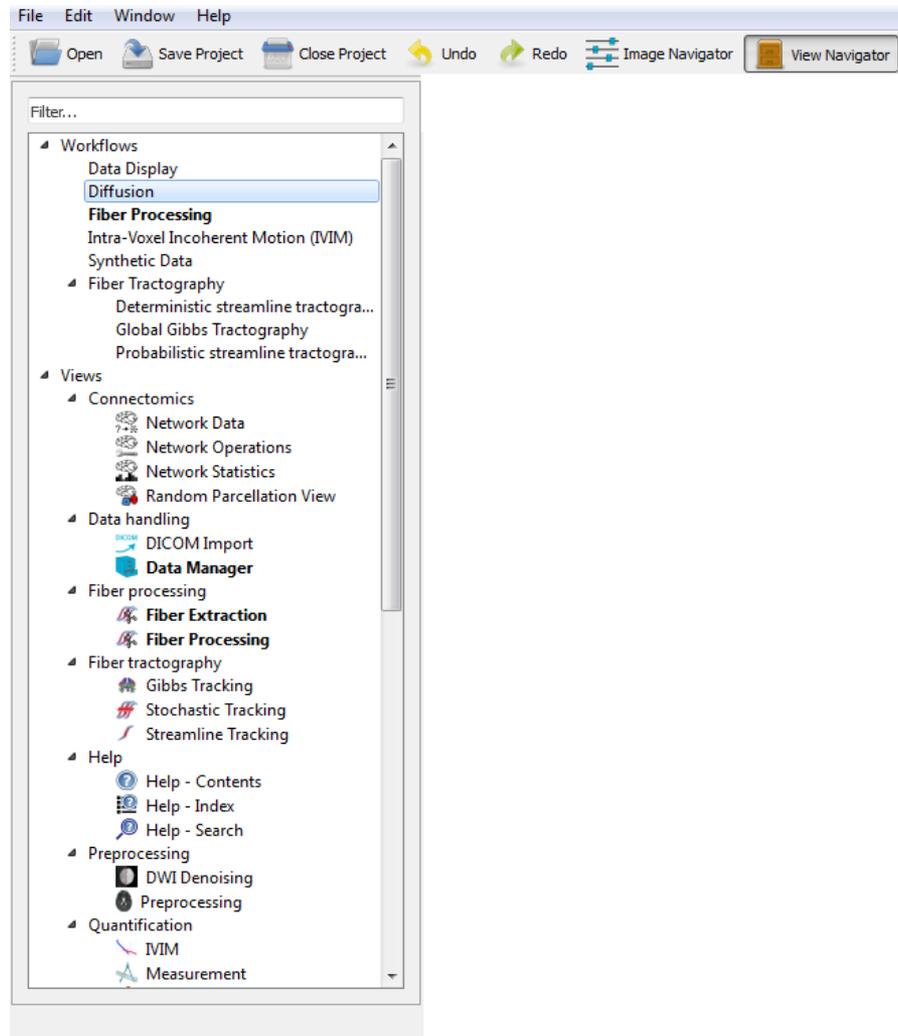
- Using only perspectives, user can not manipulate views



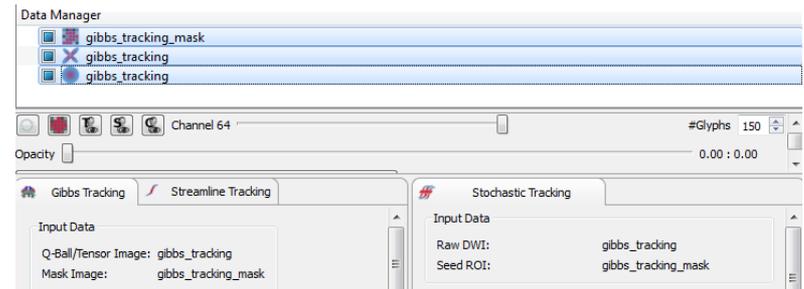
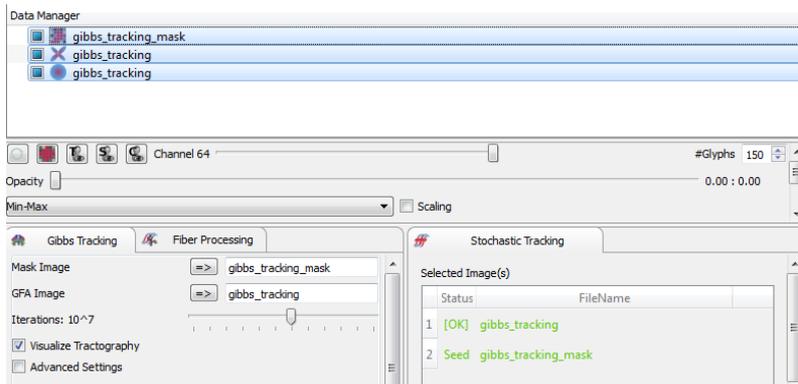
What to change, how to change it?

The screenshot displays a software interface for tractography. On the left is a control panel titled 'Data Manager' with a 'Show Welcome Screen' button. Below this are three tabs: 'Gibbs Tracking' (selected), 'Stochastic Tracking', and 'Fiber Processing'. The control panel includes fields for 'Mask Image' and 'GFA Image', both set to 'N/A'. A slider for 'Iterations' is set to 10^7 . There are checkboxes for 'Visualize Tractography' (checked) and 'Advanced Settings' (unchecked). Action buttons include 'Save Parameters', 'Load Parameters', 'Start Tractography', and 'Stop Tractography'. A status section shows 'Progress', 'Accepted Fibers', 'Connections', 'Particles', 'Proposal Acceptance Rate', and 'Tracking Time', all currently at '-'. At the bottom of the control panel are four sliders for 'Transversal', 'Sagittal', 'Coronal', and 'Time', each set to '-1'. On the right is a 3D visualization area titled 'Welcome' showing a black volume with red and blue outlines, labeled 'Transversal' and 'Coronal'.

The current perspective concept

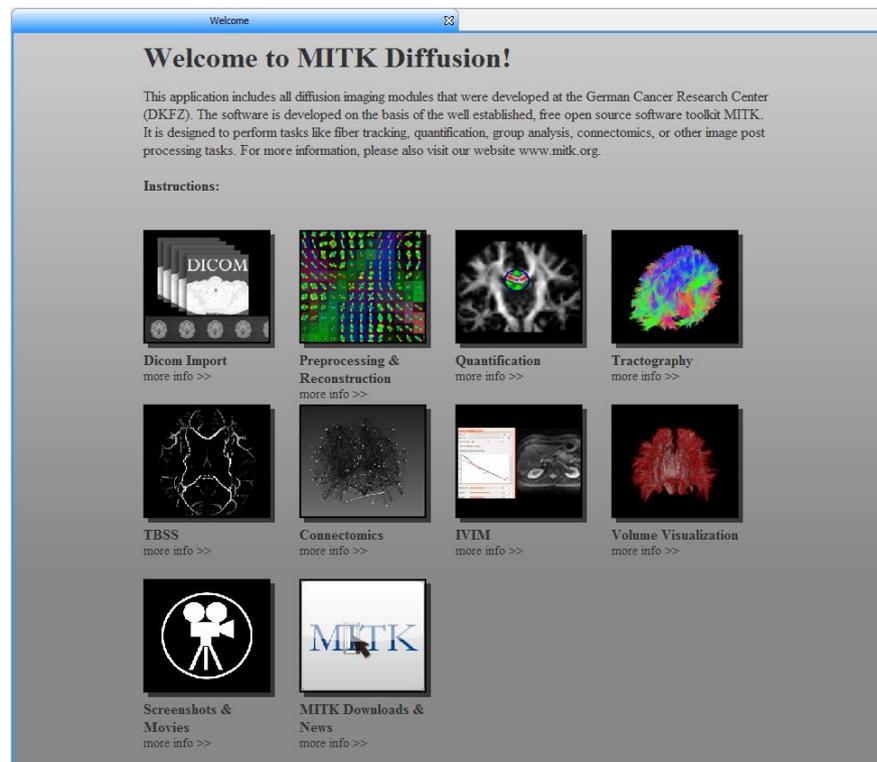


Unify input concept



What to change, how to change it?

- Own name/icon/Installer name
- More focus on the welcome screen

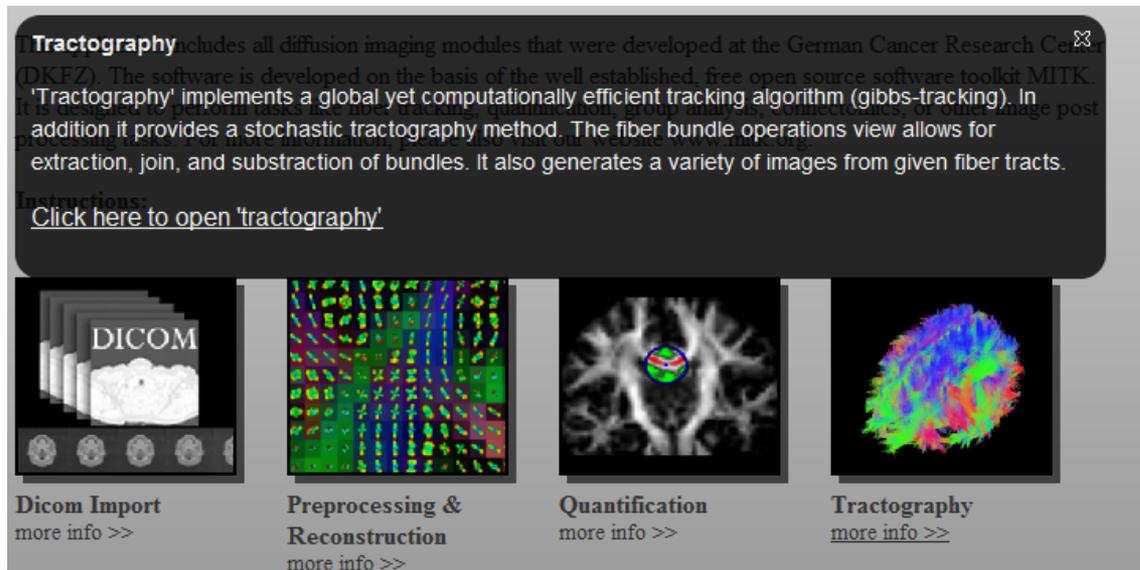


What to change, how to change it?

- Own name/icon/Installer name
- More focus on the welcome screen
- Specific workflows allow for tailored descriptions

Tractography includes all diffusion imaging modules that were developed at the German Cancer Research Center (DKFZ). The software is developed on the basis of the well established, free open source software toolkit MITK. 'Tractography' implements a global yet computationally efficient tracking algorithm (gibbs-tracking). In addition it provides a stochastic tractography method. The fiber bundle operations view allows for extraction, join, and subtraction of bundles. It also generates a variety of images from given fiber tracts.

Instructions:
[Click here to open 'tractography'](#)



The screenshot displays a software interface with a dark background. At the top, there is a text box containing a description of the Tractography software and its capabilities. Below the text box, there are four workflow steps, each represented by a small image and a label with a 'more info >>' link. The first step is 'Dicom Import' with an image of a stack of DICOM files. The second step is 'Preprocessing & Reconstruction' with an image of a colorful fiber bundle. The third step is 'Quantification' with an image of a fiber bundle with a color-coded region. The fourth step is 'Tractography' with an image of a colorful fiber bundle.

Dicom Import
more info >>

Preprocessing & Reconstruction
more info >>

Quantification
more info >>

Tractography
more info >>

What to reuse/keep?

- Many of the views of MITK workbench
- A lot of the framework logos, etc.
 - There is a limited amount of work we can use for this

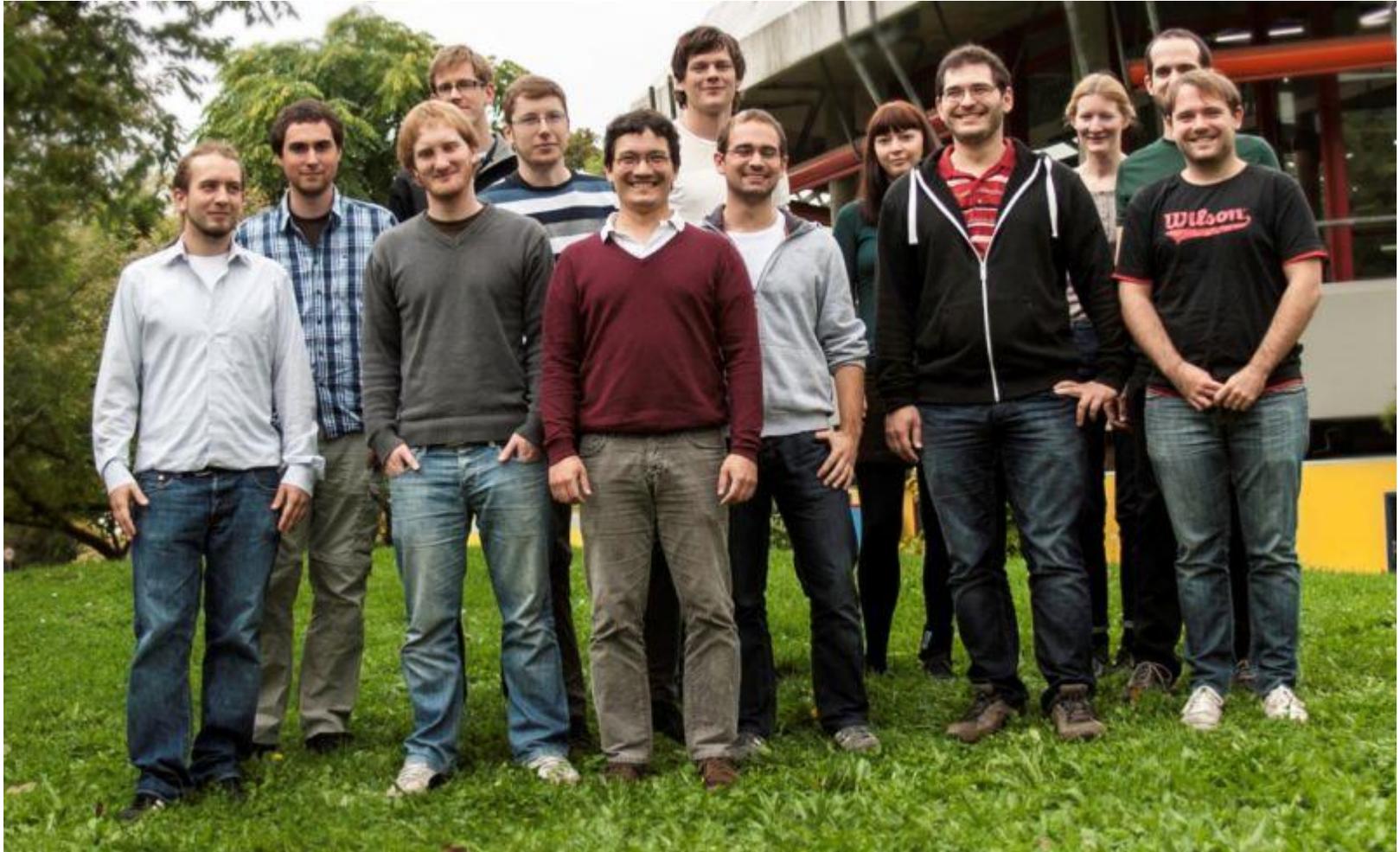
Other challenges

- Testing
- Tied to MITK release cycle

Where do we offer it?

- Flyers at conferences, perform in challenges
- Available via mitk.org
- Available via nitrc

Who is we anyway?





Thank you
for your attention!

Any questions?

dkfz.

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A Life Without Cancer