

The IST Programme Project No. 10378

SimBio

SimBio - A Generic Environment for Bio-numerical Simulation

http://www.simbio.de



Subtask 1.1 - Image Processing

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? ?????by the SimBio Consortium

SimBio

1. Subtask 1.1 - Image Processing

The purpose of subtask 1.1 is to take a patient specific image and segment this image into appropriate anatomical segments. In subtask 1.2 a Finite Element mesh is developed on the basis of these segments. Although mesh generation is not the formal concern of subtask 1.1 the generic strategy adopted in 1.1 lends itself to the creation of patient specific meshes and the software developments represented in this release have been pursued in collaboration with subtask 1.2.

Whatever the short term requirement of SimBio, the aim must be to produce a generic approach to the problem of patient specific mesh generation. The strategy adopted in 1.1 is to segment an image through a process of image registration. Successful segmentation requires the inclusion of domain specific knowledge in the segmentation process. This is often a mixture of low-level knowledge, that segments are characterised by constant intensity (within limits) or contained within boundaries defined by intensity gradients, and problem specific knowledge about how the low level operations are strung together, but generation of an optimum segmentation can be difficult except in a few special cases. Within this release is a module (*vsegment3d*) which is optimised for intensity segmentation of brain images and this works well, but does not generalise to arbitrary images, especially the knee images used within SimBio.

With an image registration approach a previously hand segmented image is used as a reference image which can be registered to patient images. The mapping resulting from this registration is then used to map the image segments to the patient image. The domain knowledge is contained in the reference image and the segmentation and in this respect the segmentation is generic since this knowledge is distinct from the registration algorithm. The segmentation algorithms are included in this release, *vreg3d* and *vreglocal3d*. The former is optimised for rigid registration (with optimal scaling) of data from the same subject, but includes the ability to register images from different modalities. The latter is a full non-linear registration algorithm for registering images from the same modality but where one of the images is a reference image. This is accompanied by a second module, *vtransform*, which applies the mapping function produced by *vreglocal3d* either to further images (such as segments represented as binary images) or a mesh.

The aim of subtask 1.1 is to produce this segmentation, with the responsibility for meshing of this segment being that of subtask 1.2. However, an FE mesh can be generated for the reference segments, most practically using a mixture of automatic segmentation algorithms with hand editing. Again, this may be time consuming, but only needs to be done once. Following this the registration mapping can be used to map the mesh to the patient image. This does not guarantee that the mapped mesh will be ideal but smoothness constraints within the registration algorithms will give some protection against collapse of the mesh.

All modules communicate through image and other data in Vista format. The flow of data follows the following data stream



Segmentation of Head Compartments in MRI Datasets

In order to setup biomechanical and electromagnetical forward models, a finite element mesh must be provided that describes the individual object under study precisely and covers all material compartments relevant for the given problem. In addition to the intracranial compartments, white matter, grey matter and cerebrospinal fluid (CSF), the meninges have to be taken into account for biomechanical simulations. The meninges consist of a thin layer of tough skin which encapsulates the brain and separates it into mechanically partially decoupled compartments, the hemispheres and the cerebellum. This sheath is at most 1 mm thick, but relevant for a precise modelling of mass shifts in the intracranial compartment. The skull has a rather low electric conductivity and a rather high stiffness in relation to other tissues of the head. The thickness of the skull varies between 2 and 8 mm depending on the region, which is expected to influence simulation results strongly. As we are primarily interested in intracranial processes, the extracranial tissues (e.g., skin, muscles, facial bones, fat, connective tissue, nerves) are collectively given a single label.

To be able to define these compartments, T1- and PD-weighted 3D datasets must be acquired. The first processing step consists in aligning the T1-weighted dataset using the module *valign3d*. The following information has to be specified:

- 1. the position of the lower margin of the anterior commissure in the mid-sagittal plane
- 2. the position of the upper margin of the posterior commissure in the mid-sagittal plane
- 3. the misrotation angles around the ap-axis (y coordinate) and the body axis (z coordinate)

This module will also interpolate the volume dataset to an isotropical resolution of 1mm.

Next, the PD-weighted dataset is registered to the T1-weighted dataset using the module *vreg3d*. Here, the default arguments (using a cross-correlation based cost function) produce the best results. This module will also interpolate the PD-weighted dataset to an isotropical resolution of 1mm.

Then, both aligned datasets are segmented using *vsegment3d*. For T1-weighted datasets acquired on a 3T scanner using a MDEFT imaging protocol, a segmentation into 3 classes is sufficient, for datasets acquired on 1.5T scanners using flash protocols, a segmentation into 5 classes yields better results. The PD-weighted dataset is segmented into 2 classes. On output, a set of probability volumes (one per class) is produced, which is analysed further using the module *vcompseg*.

The skull is imaged best by cranial computer tomography (CCT). However, the relatively high radiation dose is prohibitive for research purposes, but may be acceptable for clinical questions. Thus for SimBio, we segment the skull from PD-weighted MR images. Due to the relatively low proton concentration of bone, this compartment has a low signal intensity. All other tissue compartments are bright. Unfortunately, a discrimination of bone and air is impossible. Thus, intracranial cavities (e.g., sinuses, cavities of the petrous bone) are segmented as "bone". For electromagnetical simulations, this may be considered as acceptable, because both bone and air have a low conductivity in comparison with all other tissue types. The systematic error introduced for biomechanical simulations must be investigated further.

The procedure for skull segmentation is sketched as follows: the intracranial tissue compartment is segmented first by computing the largest connected tissue component in class 1. This mask is dilated by 8mm and used to segment low-intensity voxels from class 0. Small cavities in the bone are closed using a morphological closing filter of 3 mm diameter. Finally, 5 iterations of a rank filter are applied to smooth outer and inner surfaces. The inner layer of the skull compartment is closed artificially (e.g., at foramen magnum).

The extracranial tissue compartment is segmented from class 1 of the PD-weighted dataset by simple thresholding. The intracranial portion is masked out using the skull mask computed above. All cavities in the extracranial portion are filled by morphological closing.

The T1-weighted dataset is used to define the white matter and grey matter compartments, which are found from the intracranial portions of class 2 (resp. 1) on the basis of a segmentation into 3 classes, and from class 3 (resp. 2) on the basis of a segmentation into 5 classes. The remaining intracranial voxels are addressed as CSF.



Figure 1: Segmentation of the example MRI dataset.

Finally, all compartments (skull, extracranial tissue, white matter, grey matter and CSF) are composed in a single volume dataset and labelled to be compliant with the material database.

In addition, the meninges may be segmented from the T1-weighted datasets. Since they are less than a 1mm thick, most parts are below the resolution limit of the scanner and indiscernible from CSF to the partial volume effect. Thus, we pursue an indirect approach for segmentation. The parts enclosing the brain are approximated as the outer layer of the intracranial brain mask. The second portion, the tentorium, separates the cerebral hemispheres from the cerebellum. Here, a segmentation of the white matter is used. A distance transform of this mask is computed. Then, the mask is cut at level of the superior colliculus of the brainstem into a portion containing both brain hemispheres and a portion containing the brainstem and the cerebellum. Both portions are moved 4 mm apart, and a

second distance transform is computed. The difference of both distance transforms is determined, and all local distance maxima below the AC-PC plane are collected in a 2D map (i.e., the xy-plane), recording the z coordinate as height information. This map is corrected for the shift applied above, smoothed using a median filter and cut with the intracranial mask. Similarly, the falx is determined from the distance transform of the cerebral hemispheres. Local maxima in the zy-plane are found within 10 mm interval on both sides of the midsagittal plane, smoothed and cut with the intracranial mask as described above. All three portions are combined in a 3D volume dataset, recovering the height information. The meninges mask may be overlaid onto the labelled compartment dataset obtained above.

The complete procedure as encapsulated in *vcomseg* needs approximately 3 minutes computation time on a typical Linux workstation.

Segmentation of Head Compartments in CT Datasets

CT datasets of the head are much easier to segment, as we are interested in discriminating soft tissue from bone only. However, the gantry and head holders should be removed for modelling, so some preprocessing is required. Finally, bone and soft tissue are labelled as specified in Deliverable 1.2b. The module *vctseg* implements this functionality.



Figure 2: Segmentation of the example CT dataset.

Segmentation of knees using the mesh template approach

The main algorithm supplied is called *Vreglocal3d*, and this code performs several sequential registrations. The function performs an affine transform as its initial registration phase. This is followed by several non-linear registration stages, which begins with a grid size of 5x5x5 nodes, and then doubles this density until it reaches the point where there are 5x5x5 pixels per element. This limit has been chosen as the densest mesh, which is most likely to be numerically stable. The reason for this multi-resolution approach is that when the image volume is split into a mesh, each element only overlaps with its adjacent neighbours. This means that for the system to behave sensibly the corresponding pixel in the target image must lie within 2 elements of the pixel in the source image. Therefore, if large deformations are necessary having a very dense mesh may not produce good results. By using this multi-resolution approach the coarse detail in the images can be matched initially, and the finer features can be resolved as the mesh density increases.

The module has the option for calculating the inverse mapping function, which may be required but is not necessary as part of the suggested procedure for Simbio, described below. The safest procedure is to always calculate the inverse mapping (the default option). However, this is time consuming, and if the user only intends to map meshes in the reverse direction (recommended) the option can be switched off. The subtlety of which transformation to use, (forward or reverse) when mapping images or meshes can be confusing, but the code is designed to be a simple as possible for the user. The definition of a forward transformation is the direction in which the registration is performed. Thus, if a patient image is registered to the template image, this is the forward direction. If the template mesh is transformed into the patient mesh the direction would now be classed as the reverse direction, being the counter direction to the registration process.

The arguments required by the function are, input and output file names, a flag to specify whether an affine registration should be used as the initial phase, a flag to specify whether to calculate the inverse transform and a smoothness constraint *lamda*. A significant amount of time has gone into making the registration process as insensitive to *lamda* as possible, and thus the default value of 1 has not required to be changed recently. However, if the value used for lamda is too large, it is still possible that the registration will be poor because the images cannot distort sufficiently due to the greater bias placed on returning a smooth solution rather than a correct one. It is anticipated that, this option will be removed at the end of the project, although it has been left in for completeness during the evaluation phase.

In addition, a function is provided to apply the mapping functions returned by the registration software to other images or meshes, *Vtransform*. It requires the user to specify a direction for the mapping. In Simbio, it has been decided that the best strategy for registering the template and patient images is to register the patient image to the template. This has the advantage that because the template image does not change a region of interest image can be generated for it that does not need to be changed.

It is suggested strongly that a region of interest image is used, which is suitable for the fixed image, covering only those features of the image which are important (e.g. the inclusion of a large amount of muscle tissue in the registration could decrease the registration accuracy of the bone regions). A general methodology for producing this is to dilate the segments for the template image to form the ROI image, and this seems to work well.

Occasionally, after a region of the image is stiffened due to collapsing elements the residual, which is the measure of registration quality, will increase. This is because the increased stiffness of the mesh pushes the image away from regions where the registration was good. This situation is not a cause for concern, as the residual does not usually increase much, and the algorithm always stores the lowest residual results which are returned regardless of the final convergence results.

Due to the inherent problems of interpolating binary volume data, and the distortion that can occur (as shown below), it has been decided that the segments should be mapped across to the patient images as surface meshes as opposed to binary volume images.



Figure 3 Image of a binary volume slice after non-linear transformation has been applied.

It is believed that the undesirable requirement to transform binary volumes as surfaces is due mainly to the large degree of anisotropy (0.35mm x 0.35mm x 2mm voxels) of the data sets collected for the knee. Assessment of how more isotropic binary volumes are mapped would have to be performed on a case by case basis, but the default method of producing a surface mesh and transforming that should always preserve the original segment details and is recommended.

<u>Summary :</u>

For the minimum compute time, and the most robust performance, it is suggested that the procedures outlined in figure 5 are followed. The registrations are performed with the default option for the –inverse and –affine (see man pages) flags.



Figure 4 Flow chart of suggested procedure for mesh template approach.

Notes:

If the user wishes to carry out any operations outside the procedure in figure 4 using the mapping function returned from Vreglocal3d, it is advised that they calculate the inverse mapping as well. The procedure in figure 4 does not require the inverse transform, and registration runtimes can be reduced significantly if the –inverse flag is set to *false*.

The registration process is only applicable to medical images of the same modality, and in the case of MRI images the same (or very similar) scan sequence.

Although it should not need to be stated explicitly, the objects in the image intended to be segmented, must be visible in the image for the registration to be reliable. This requirement seems to be self evident, but in MRI where contrast in the images falls off significantly towards the edges of the image, the segments may become unreliable if the contrast on the objects of interest no longer exists.

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1.1 brutov - converts Bruker to Vista format

SYNOPSIS

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brutov [-option ...] [infile] [outfile]

DESCRIPTION

brutov converts a group of Bruker data files into a Vista data file.

COMMAND LINE OPTIONS

brutov accepts the following options:

-help	Prints a message describing options.		
-in infile	Specifies a directory or a tar file that contains the source data.		
-out <i>outfile</i>	Specifies the output file, which will be a Vista data file.		
-white number	Specifies the percentage of voxels that will be mapped to white		
	(default 0.5%).		
-black <i>number</i>	Specifies the percentage of voxels that will be mapped to black		
	(default 10%).		
-ds 1 2	Select datasets 1, 2, etc. from an experiment.		

The keyword ``to" can be used to specify a range of indices, as in ``-ds 1 to 2". Axial and coronal slices are flipped from the radiologic convention into the natural convention, i.e. the left image side corresponds to the left body side. An attribute "convention: natural" is appended to the list to document this orientation. Note that sagittal slices are not flipped, i.e. they are found "nose left".

EXAMPLES

The following command line brutov -in WA1T961101.GB1 -out vista-file.v -rep 4 expects a directory tree with root WA1T961101.GB1 containing Bruker parameter and data files. To select only a subset of the datasets in an experiment, use brutov -in WA1T961101.GB1 -out vista-file.v -ds 4 5 7 to 14

This will convert datasets 4, 5, and 7 to 14 only.

NOTES

The attribute *convention* is always set to *natural*, and the attribute *component_interp* set to *intensity*. Conversion of diffusion tensor images is unimplemented, so the attribute *component_repn* is always set to *scalar*.

AUTHOR

Frithjof Kruggel.

1.2 dcmtov - convert DICOM to Vista format

SYNOPSIS

dcmtov [infile] [-option ...] [outfile]

DESCRIPTION

dcmtov converts a series of DICOM files into a Vista file. Input filenames are expected to be in printf format (see below), with a basename and indices ranging from first to last. On output, a Vista volume dataset is generated. Individual series within a session are represented as separate Vista image objects within the Vista file. Each image object has its own set of information regarding the patient name, image parameters etc.

COMMAND LINE OPTIONS

demtov accepts the following options:

-help	Prints a message describing options.
-in <i>infile</i>	Specifies the basename for a DICOM file series. This name should be
	given as printf format string, so that a specific filename may be generated from
	this format string and the values of first and last below.
-out <i>outfile</i>	Specifies the output file, which will be a Vista data file.
-first index	Specifies the index of the first input file, which is a DICOM file.
-last index	Specifies the index of the last input file, which is a DICOM file.

-type ubyte/ushort	Specifies the output image representation. (default ubyte).		
-white number	Specifies the percentage of voxels that will be mapped to white		
	(default 0.5%).		
-black <i>number</i>	Specifies the percentage of voxels that will be mapped to black		
	(default 10%).		

The output file can be specified on the command line or allowed to default to the standard output stream.

EXAMPLE

The following command line dcmtov -in %03d.ima -out vista-file.v -first 1 -last 203 will convert the sequence of DICOM files "001.ima" to "203.ima" into a Vista file.

AUTHOR

Frithjof Kruggel.

1.3 vtranspose3d - transpose a 3D dataset

SYNOPSIS

vtranspose3d [-option ...] [infile] [outfile]

DESCRIPTION

vtranspose3d transposes a Vista image file according to the specified co-ordinate changes and returns a re-dimensioned Vista volume dataset.

COMMAND LINE OPTIONS

vtranspose3d accepts the following options:

L	
-help	Prints a message describing options.
-in <i>infile</i>	Specifies a Vista data file containing the input images.
-out outfile	Specifies where to write the output image.
-xyz abc	Specifies the co-ordinate transpositions. Available transpositions:
	xyz (default), xzy, zyx, zxy, yxz, yzx

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

EXAMPLE

To convert a sagittal 3D Vista dataset ("nose left") into a standard axial dataset ("nose up") use: vtranspose3d -in xx.v -out xx1.v -xyz zxy

AUTHOR

Christian Uhl, Frithjof Kruggel.

1.4 vcrop3d - crop a 3D dataset

SYNOPSIS

vcrop3d [-option ...] [infile] [outfile]

DESCRIPTION

vcrop3d is used to crop a 3D dataset, given a left upper corner and an extent. Both corner point and extent are expected to be given in voxels. The corner point may have negative components. Regions of the destination volume which were not present in the input are filled with the value 0.

COMMAND LINE OPTIONS

vcrop3d accepts the following options:

1 1	
-help	Prints a message describing options.
-in <i>infile</i>	Specifies the source image dataset in Vista format.
-out <i>outfile</i>	Specifies the output file, which will be a Vista image.
-corner x y z	Specifies the left upper corner (default: 0 0 0).
-extent x y z	Specifies the extent of the destination volume (default: 0 0 0).
4 1 4 C 1	

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

AUTHOR

Frithjof Kruggel.

1.5 valign3d - align a 3D dataset with the stereotactical co-ordinate system

SYNOPSIS

valign3d [-option ...] [infile] [outfile]

DESCRIPTION

valign3d is used to align a 3D dataset with the stereotactical co-ordinate system. Relevant information, i.e., the position of the anterior (CA) and posterior commissure (CP) and the rotation angle must be specified manually.

COMMAND LINE OPTIONS

valign3d accepts the following options:

-help	Prints a message describing options.		
-in infile	Specifies the source image dataset in Vista format.		
-out outfile	Specifies the output file, which will be a Vista data file.		
-ca <i>x y z</i>	Specifies the position of the commissura anterior.		
-cp <i>x y z</i>	Specifies the position of the commissura posterior.		
-angle <i>x y z</i>	Specifies the rotation around the x, y and z axis.		
-transpose true fa	llse		
	Transpose a set of sagittal slices into axial slices before adapting		

Transpose a set of sagittal slices into axial slices before adapting the co-ordinate system.

Input and output files can be specified on the command line or allowed to default to the standard input and output streams. CA and CP position are expected in mm, measured from the left upper corner of the image volume. The convention for brain datasets denotes the x axis as parallel to the ear-to-ear direction (from left to right), the y axis to the nose-to-back direction, and the z axis to the body axis (from top to bottom). A positive y rotation (i.e. -angle 0 3 0) nods the head 3 degrees right, and a positive z rotation (i.e. -angle 0 0 3) turns the head along the body axis 3 degrees right. If CA and CP are specified, the x rotation is ignored and determined from these co-ordinates.

AUTHOR

Frithjof Kruggel.

1.6 vreg3d - register two 3D datasets

SYNOPSIS

vreg3d [-option ...] [infile] [outfile]

DESCRIPTION

vreg3d is used to register a 3D dataset with a reference dataset. Three different registration plans are implemented: one for intra-modal registration problems (such as T1-T1 registration of head datasets), one for cross-modal datasets (for registering a set of T2-weighted slices to a T1-weighted head dataset), and a "manual" plan, where the registration method, an initial rotation and translation should be specified.

COMMAND LINE OPTIONS

vreg3d accepts the following options:

-help	Prints a message describing options.
-in <i>infile</i>	Specifies the source image dataset in Vista format.
-out <i>outfile</i>	Specifies the output file, which will be a Vista data file.
-ref <i>file</i>	Specifies the reference image dataset in Vista format.
-plan <i>intra cross</i>	/ manual
	Specifies the registration plan (default: intra).
-resort <i>true false</i>	Specifies whether the stacking order of the source dataset should be
	reversed (default: false).
-scaling true false	
	Specifies whether re-scaling is allowed (default: false).
-angle <i>x y z</i>	Specifies the initial rotation angle (default: 0 0 0).
-trans x y z	Specifies the initial translation (default: 0 0 0).
-func <i>nmi cc</i>	Specifies the type of cost function: normalised mutual information
	(nmi) or correlation coefficient (cc) (default: nmi).

Input and output files can be specified on the command line or allowed to default to the standard input and output streams. For plans *intra* and *cross*, any values given for *-rt*, *-tr*, or *-method* are ignored. Note that the translation is expected to be given in mm. Typical registration problems need 10-30 min computation time on a PC equipped with a 500 MHz Intel Pentium III processor.

AUTHOR

Frithjof Kruggel.

1.7 vreglocal3d - Non-linear image registration

SYNOPSIS

vreglocal3d [-option ...] [infile] [outfile]

DESCRIPTION

vreglocal3d performs a non-linear registration of two 3D data sets. It returns the registered data set and also a mapping function which when supplied to **vtransform** will apply the mapping to an image or mesh.

COMMAND LINE OPTIONS

vreglocal3d accepts the following options:

-help	Prints a message describing options.
-in <i>infile</i>	Specifies the source image dataset in Vista format.
-out <i>outfile</i>	Specifies the output file, which will be a Vista image.

-ref reffile	Specifies the target image for registration.
-roi roifile	Specifies the region of interest image for registration. Default: +/- 10% of the
	input image dimensions on each side.
-map <i>mapfile</i>	Specifies whether to write out the mapping function.
-lamda <i>number</i>	Specifies the value of the smoothness constraint. Default: 1.
-affine logical	Specifies whether to carry out an affine transform first.
	Default: TRUE.
-inverse logical	Specifies whether to carry out the inverse mapping calculations.
_	Default: FALSE.

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

AUTHOR

Barber & Wood.

1.8 vtransform - mapping of segments

SYNOPSIS

vtransform [infile] [outfile] [mapfile]

DESCRIPTION

vtransform transforms the input data set using the mapping function provided by **vreglocal3d**. If input is a mesh, the vertices of the mesh will be transformed, nothing will be done to other components such as vertex normals. If the input is an image, an image will be returned.

COMMAND LINE OPTIONS

vtransform accepts the following options:

1		
-help	Prints a m	essage describing options.
-in <i>infile</i>	Specifies	the source image dataset in Vista format.
-out <i>outfile</i>	Specifies	the output file, which will be a Vista image.
-map <i>mapfile</i>	Specifies	whether to write out the mapping function.
-direction forward	/reverse	Specifies the direction in which the transformation is performed.
U U		Default reverse.

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

AUTHOR

Barber & Wood.

1.9 vintens3d - correct intensities a 3D dataset according to a reference

SYNOPSIS

vintens3d [-option ...] [infile] [outfile]

DESCRIPTION

vintens3d corrects image intensities a 3D dataset, given a reference image. First, intensities in both images are scaled to fit in a 256x256 joint histogram. A regression line is fitted to the joint histogram, and intensities in the input dataset are transformed according to the regression parameters. A threshold may be specified to leave out the background during the computation of the regression line.

COMMAND LINE OPTIONS

vintens3d accepts the following options:

-	÷ .
-help	Prints a message describing options.
-in infile	Specifies the source image dataset in Vista format.
-out <i>outfile</i>	Specifies the output file, which will be a Vista image.
-ref file	Specifies the reference image.

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

AUTHOR

Frithjof Kruggel.

1.10 vsegment3d - segment a 3D dataset

SYNOPSIS

vsegment3d [-option ...] [infile] [outfile]

DESCRIPTION

vsegment3d segments a 3D dataset based on intensity criteria into a set of classes. Optionally, it tries to correct for the intensity variations due to inhomogeneities of the B1 field of the MR scanner. For input data sets aligned with the stereotactical co-ordinate system, the argument -opt true specifies to correct within a minimal subvolume only, for a threefold reduction in computation time.

COMMAND LINE OPTIONS

vsegment3d accepts the following options:

0 1	
-help	Prints a message describing options.
-in <i>infile</i>	Specifies the source image dataset in Vista format.
-out <i>outfile</i>	Specifies the output file, which will be a Vista image.
-nc <i>number</i>	Specifies the number of tissue classes. Default: 3.
-cls <i>clsfile</i>	Specifies where to store the classified image.
-win number	Specifies the processing window width. Default: 8
-lim number	Specifies the intensity limit of the background class. Default: 35
-lambda1 number	Specifies the value of the first regularisation constant. Default: 20000.
-lambda2 number	Specifies the value of the second regularisation constant. Default: 200000.

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

AUTHOR

Frithjof Kruggel.

Pham DL, Prince JL (1999) An adaptive fuzzy C-means algorithm for image segmentation in the presence of intensity inhomogeneities. Pattern Recognition Letters 20, 57-68.

1.11 vcompseg - compose a head segmentation from T1 and PD-MRI 3D datasets

SYNOPSIS

vcompseg [-option ...] [infile] [outfile]

DESCRIPTION

Composes different compartments of a head (i.e., white matter, grey matter, cerebrospinal fluid, skull, meninges and extracranial tissue) on the basis of pre-segmented T1-weighted and PD-weighted MRI datasets. As input, segmented probability volumes, such as generated by *vsegment3d*, are expected. The T1-weighted dataset should be segmented using 3 classes (for MDEFT datasets on a 3T scanner) resp. 5 classes (typical FLASH protocols on 1.5T scanners). The PD-weighted dataset should be segmented in 2 classes. Both datasets are expected to be aligned with the stereotactical coordinate system, and have an isotropical spatial resolution of 1mm.

On output, a labelled image volume is produced. Labels correspond to the different material compartments as defined in the SimBio deliverable

skull	1
extracranial tissue	3
white matter	6
grey matter	7
csf	8
meninges	10

COMMAND LINE OPTIONS

vcompseg accepts the following options:

· · ·	
-help	Prints a message describing options.
-in <i>infile</i>	Specifies the T1-weighted segment class file in Vista format.
-out <i>outfile</i>	Specifies the output file, which will be a Vista image.
-pd infile	Specifies the PD-weighted segment class file in Vista format.
-threshold number	Specifies the tissue probability threshold (range 01, default 0.5).
-meninges <i>true/false</i>	Specifies if meninges are to be segmented as well.
-min_skull number	Specifies the (artificial) minimum thickness of the skull
_	(default 2mm).
-min_scalp number	Specifies the (artificial) minimum thickness of the skull
- •	(default 2mm).

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

NOTES

The meninges segmentation algorithm has undergone limited testing only.

AUTHOR

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1.12 vctseg - segment a head from CT 3D dataset

SYNOPSIS

vctseg [-option ...] [infile] [outfile]

DESCRIPTION

expects a CT dataset in isotropical spatial resolution on input. It tries to extract the head and remove parts of the gantry and head holders. It optionally segments the head into two material types, skull and soft tissue, based on automatic thresholding.

On output, a labeled image volume is produced. Labels correspond to the different material compartments as defined in the SimBio deliverable

Skull1Soft tissue2

COMMAND LINE OPTIONS

vctseg accepts the following options:-helpPrints a message describing options.-in *infile*Specifies the CT file in Vista format.-out *outfile*Specifies the output file, which will be a Vista image.-label *outfile*Specifies the labelled output file, which will be a Vista image.-op *number*Specifies the opening distance for gantry removal (range 0..10 default 4).-lim *number*Specifies the upper limit of the gantry co-ordinate (y direction).

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

EXAMPLE

The following command line produces an example segmentation of the test dataset:

vctseg -in ed1p_ct_or.v -out ed1p_head.v -lim 195 -label ed1p_seg.v

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1.13 vcolormesh – Color a surface mesh from image

SYNOPSIS

vcolormesh [-option ...] [infile] [outfile]

DESCRIPTION

uses a scalar volume data set (such as output from a simulation) and maps scalar values onto a surface mesh.

COMMAND LINE OPTIONS

vcolormesh accepts the following options:

<u> </u>	e 1
-help	Prints a message describing options.
-in <i>infile</i>	Specifies the input surface mesh required in Vista format.
-out <i>outfile</i>	The colored output surface mesh in Vista image.
-ref outfile	Specifies the scalar volume dataset in Vista format.

Input and output files can be specified on the command line or allowed to default to the standard input and output streams.

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