## Options to adapt the inhomogeneity correction procedure in BrainVoyager

This is no official Brain Innovation support document. For any questions or remarks contact heinecke(at)brainvoyager(dot)com

BrainVoyager version used. BVQX 2.84 (Windows7, 64bit)

Dataset used: Getting Started Guide (CG) anatomy

For many advanced anatomical data processing steps in BrainVoyager it is crucial to correct the inhomogeneity within the VMR project created on the basis of the 3D anatomical data. Depending on the scanner and aquisition details, there are different types and "strenghts" of inhomogeneity in the data.

The standard automatic intensity based inhomogeneity correction is usually sufficient for many purposes, but depending on the types of final analysis you have in mind for your anatomical data, more adaptive inhomogeneity correction steps are advised. At least when one wants to create proper surface reconstructions (esp. "flat map" representations), run the cortex-based alignment or a cortical thickness analysis, this is a highly advised.

This document describes a usually quite effective adaptation of the automatic inhomogeneity correction procedure in BrainVoyager.

## 1. Automatic inhomogeneity correction

We load the first version of the VMR.



We open the V16 dialog from the Volumes menu.



This dialog is based on the automatically created and linked V16 file.

This contains the original intensities of the data, while the VMR contains only the truncated 8bit version of the data (this stores the voxel intensities in 226 greyscale values. In case this dialog should appear greyed out (not functional), there is either no V16 available or the names of the VMR and V16 file differ (this will never be the case for the first projects created by BrainVoyager.

We start the automatic inhomogeneity correction via the "GO" button.

patial transformations		Intensity inhomogeneity correction (II (C)				
Export .V16	Tal Scale .V16	No. of cycles: 2 A	uto-IIHC: GO			
Iso-Voxel To SAG		Include mask generation (or all EXe				
Trilinear interpolation	Cubic spline interpolation	Save resulting IIH corrected .V16 data to	o disk			
) Sinc interpolation	R: 3 🕏	Tissue range threshold: 0,25 🜩 Intensity threshold: 0,30 🜩	Detect WM			
Apply mask	Del	Multiplicative model Addi Visualize fit (bias field) in secondary VMR Order of polynom for fit: 3	tive model			
		Presegmentation-based ("blue" WM):	Correct IIH			
hift data set		Mirror data set along axis				
Shift X		TAL axes convention     O BV axes convention	Flip X Axis			
Shift Y			Flip Y Axis			
Shift Z	Step size: 1 🜩		Flip Z Axis			

The procedure include an automatic extraction of the brain. The results are stored as \_IIHC.vmr and IIHC.v16 file.



Two intensity histogram show the distribution of intensities after the first and second correction cycle.

For standard usage of the VMR, one could stop the inhomogeneity correction now and proceed e.g. with normalising the data into Talairach space.

## 2. Additional manual correction

When one has some more advanced anatomical processing steps in mind, a manual inhomogeneity correction can be added.

To do so, we have to first create a manual selection of the white matter (so called "presegmentation"). We can best obtain this goal by using the tools of the "Segmentation" tab on the 3D volume tools.

3D Coords	Con	egistration	Spatial Transf	Talairach	Segmentation		
Value rang	e	Boundi	ng box	2	Op	tions	Autom. Segm.
Min: 10	00 🗘	x: 0	191 🗘	Show	d	ean	1
Max: 2	55 🗘	y: 0	255 🗘	Load	Ra	nge	Grow Region
New: 24	40 🗘	z: 0	255 🗘	Save	Fill	Box	Expand
Filter, smoo	othing —			-	Border		Reload
Gaussi	ian	FWHM: 2	,0 🗘 Cycles:	1	Dilate		Marked
					Smooth		Non-Marked
Sigm	a	Range: 2	0		🗌 Flip FG /	BG	Reload All
Draw with	mouse -				Reconstructio	n	
		🗌 Enab	le 💿 2D (in-pl	ane)	Prepare		
	1993						

To start, we best use the "Grow Region" button. The procedure selects all voxel (spreading out from the the current mouse position) within a specified intensity range.

Because we already performed the automatic inhomogeneity correction, we can select the Min: and Max: values of the Value range quite easily. Very often a starting range of about 150 to 190 leads to satisfying results. One has to click within the white matter to properly start the procedure. If the intensity of the selected seed voxel is for some reason outside the selected value range, no voxel will be demarcated.



After clicking the "Grow Region" button, a good part of the white matter is selected. But there are still some white matter voxels with values either below the selected minimum or above the selected maximum value. The best option to proceed is to use the "Expand" function. This just marks neighbours of already selected voxels.

We expand the "Max" value to 225 (the maximal intensity value) and click the "Expand" button.

3D Coords	Coregistra	ation	Spatia	al Transf	Talairach	Segmentation	
Value range	E	Bounding	g box —	12	21	Optic	Autom. Segm.
Min: 150	<b>)</b>	x: 0	•	191 🖨	Show	Clea	in
Max: 22	5 ≑	y: 0	•	255 🗘	Load	Ban	Crow Persion
New: 240	) 😫	z: 0	*	255 🖨	Save	Fill B	ox <u>E</u> xpand
Filter, smoot	hing				-	Border	Reload
Gaussia	n FWH	IM: 2,0	)	Cycles:	1 🗘	Dilate	Marked
						Smooth	Non-Marked
Sigma	Rang	ge: 20	<b>÷</b>			Elip FG / B	G Reload All
Draw with m	iouse					Reconstruction	<u></u>
		Enable	۲	) 2D (in-p	lane)	Prepare	

The "Expand" button can be used multiple times (based on the fact that each neighbouring voxel has again new neighbours). In some cases, it may also be necessary to reduce the Min: value

<b>a</b>	BrainVoyager QX	- Ø ×
Audio ( ) (the Worker Worke	Diamitologiager QX         Image: Diamitologiager QX	- 0 4 9 9 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
R Voet: x = 155 y = 50 y = 73 intensity = 0	ι	

To start the manual inhomogeneity correction, we open the V16 tool and use the "Correct IIH" button.

Export .V16	Tal Scale .V16	No. of cycles: 2	-IIHC: GO			
Iso-Voxel To SAG		Map GM and WM peaks to standard VMR values				
Trilinear interpolation	Cubic spline interpolation	Save resulting IIH corrected .V16 data to dis	k			
) Sinc interpolation	R: 3	Tissue range threshold: 0,25 🜩 Intensity threshold: 0,30 🜩	Detect WM			
Apply mask Mask.vmr	Del	<ul> <li>✓ Multiplicative model</li> <li>△ Additive</li> <li>✓ Visualize fit (bias field) in secondary VMR</li> <li>Order of polynom for fit: 3 ◆</li> <li>Presegmentation-based ("blue" WM):</li> </ul>	Correct IIH			
hift data set		Mirror data set along axis				
Shift X		TAL axes convention     BV axes convention	Flip X Axis			
Shift Y			Flip Y Axis			
Shift Z	Step size: 1		Flip Z Axis			

It is important to note that the manual correction does NOT automatically save the VMR or V16 file. So we have to save both files manually. I usually add another part the end of the name, this way the last created file is easier to find.

Dateiname: CG_IIHO	4C_IC_v16	
Dateityp: Anatom	mical 16 bit 3D MRI files (*.v16)	
	CG2 3DT1EL SINCA TAL ymr	
Dateiname:	: CG_IIHC_IC	
Dateityp:	Anatomical 3D MRI Files (*.vmr)	

The manual inhomogeneity correction procedure can be repeated multiple times. Each time, a new white matter selection has to be performed.

## 3. First running the manual inhomogeneity correction

As an alternative approach to the procedure described in section 1 and 2, one can also run the manual inhomogeneity correction first. This is based on the idea that the automatic

inhomogeneity correction may introduce a bias in the intensity distribution and thus running the first correction on an improved sample of the white matter can lead to improved results.

The main problem is to get a proper selection of the white matter – this would be a problem using the inhomogeneous VMR as the starting point. Quite often one is either selecting too few white matter or too many grey matter voxels in this case.

So we use a trick and basically utilize the result of the automatic inhomogeneity correction to then select the white matter with a simple range of intensities.

We run the steps described in section 1 and 2 up to the level of white matter selection (before pressing the "Correct IIH" button).

3D Coord	ds	Core	gistration		Spatia	Trans	sf	Talairach	Segmen	tation	
Value ra	nge –		Boun	ding b	oox —		-			Options	Autom. Segm.
Min:	150	\$	x:	0	\$	191	*	Show		Class	
Max:	225	•	у:	0	•	255	\$	Load		Range	Grow Region
New:	240	•	z:	0	*	255	•	Save		Fill Box	Expand
Filter, sr	noothi	ng —							Border -		Reload
Gau	ussian		FWHM:	2,0	•	Cycles	: 1	•	D	ilate	Marked
			1000000000		0.00		000		Sr	nooth	Non-Marked
Si	gma		Range:	20	-				🗌 Flip	FG / BG	Reload All
Draw wi	th mo	use –						-	Reconst	ruction —	
			🗌 Ena	ble	۲	) 2D (i	in-pla	ine)	Pr	epare	
	-	S			0	1 70 (	-				Terror and any second second

We open the "Options" of the "Segmentation" tab.

Call I	Masking	Operations	Settings			
Mark-	Based Region	n-Of-Interest De	efinition	bi dge Rem	noval	
Mark	color: 240	•	Define VOI		Remove	Bridges
Brain	peeling					
✔ G	et high-pass	filtered result	Cha	nge size of resul	ting brain mask:	0 🛊
G	et result with	labeled (blue) i	mask 🔿 Apply	only high-pass	filter Segme	ent Brain
Volum	etry					
Mark	color: 240	÷.	N	of voxels:		Count

We click the "Define VOI" button. It is usually a good idea to add the name of the subject into the VOI name. In some cases, VOIs of different subjects are combined and this way there are no problem regarding the assignment of regions to subjects.

Defi	ne Volume	e-Of-Int	erest (V	0I) <b>?</b>	×
Propert	es of new VOI	I.			
Name:	CG_WM				
Color:					
			Cancel		ок

At this point it is also advised to save the VOI file itself, which is not done automatically.

CG_WM	Show VOIs	Add
	Hide VOIs	Remove
	Show time course	
	In new window	
	a AND b	
	a OR b	
	NOT a	
	Delete	
how "VOIs x Subjects" view 🛛 🕚	Edit	

We open the first (uncorrected) version of the VMR project.

We open the region of interest analysis tool and load the white matter voi file which has been stored before.



We click on the VOI and use the "Show VOIs" button.

Project Waard New Project Open Save Files Pane Log Pane Info P	Pane Preferences PullScreen User's Guide				* 3D Volume Tools
					System coords Close X: 120  Full Dialog > Y: an
			Volume-Of-Interest Analysis	12	Zi 304 0 Surf Module
		Volumes-Of-Enterest list	e course (VTC	) fies	
		CG_WM	Show VOIs	Add	
A A A A A A A A A A A A A A A A A A A	PR	1 L	Hide VOTe	Remove	đ
			Show time course		4
			Significant voxels		4
			a AND b		
			a OR b		٥
			NOT a		a
	19-24		Delete		<u>.</u>
		Show "VOIs x Subjects" vie	rw Q Q Edit		9
	TRA	VOI file: CGWM.voi Load	Add Save Bn Ne	v Options Close	~
	and a state				
		<b>N</b>			
	1 For V For				
	P				
	A STAR				
		9/			
		//			
		y			
	CIL.	y			

The visualisation of the VOI will depend on the selected color of the VOI (which can be changed via the "Edit" button and the transparency of the VOI (which can be changed via the "VOI Functions" tab of the VOI Options.

Access Options	VOI GLM	ANCOVA	VTC Data	Transformations	VOI Functions	3	
VOI -> Draw in Convert	VMR	Flip left / right Flip	X Axis	VOI consistency Verify VO	Voxels v	vith map values VOI Details	VOI transparency Value: 1,0
VOI -> Surface Create	clusters	Overview table	e with VOIs co VOIs	enter of gravity O Across subje	cts	Table	Table
Expand selected	d VOIs	Create MSK file	e from VOIs ed VOIs	Use all VOI:	s Reso	olution: 3 🗘	Create MSK
Probability maps	5	Multi-VOI even	t-related ave	eraging plot	Browse	Generate Plot	VOIs with map values

Before we can start the manually driven inhomogeneity correction, we have to turn the VOI into a voxel demarcation. We can do this via the "Convert" button on the VOI Functions tab.

ccess options VOI GEM	ANCOVA VTC Data	Transformations	VOI Functions	
VOI -> Draw in VMR Convert	Flip left / right Flip X Axis	VOI consistency Verify VOI	Voxels with map values	VOI transparency Value: 1,0
VOI -> Surface clusters Create	Overview table with VOIs <ul> <li>Individual VOIs</li> </ul>	center of gravity	s Table	VOI map peak voxels Table
Expand selected VOIs Dilate	Create MSK file from VOIs	Use all VOIs	Resolution: 3	Create MSK
Probability maps Create	Multi-VOI event-related av	veraging plot	Generate Plot	VOIs with map values

The next screenshot shows the VOI after pressing the "Convert" button and clicking "Hide VOIs".



To start the manually driven inhomogeneity correction, we open the V16 tools dialog and click the "Correct IIH" button.

A 16.8	Bit 3D Tools ? ×
Spatial transformations         Export .V16         Tal Scale .V16         Iso-Voxel         To SAG         Trilinear interpolation         Sinc interpolation         R:         Apply mask         Mask.vmr            Del	Intensity inhomogeneity correction (IIHC)         No. of cycles:       2         Include mask generation (brain extraction)         ✓ Map GM and WM peaks to standard VMR values         ✓ Save resulting IIH corrected .V16 data to disk         Tissue range threshold:       0,25         Intensity threshold:       0,30         ✓ Multiplicative model       Additive model
Clean Mask size: <ul> <li>Extract Brain</li> </ul> Shift data set   Shift X   Shift Y   Shift Z   Load .V16      VMR -> V16	Image: Secondary With Secondary With Correct IIH         Order of polynom for fit:         Image: Secondary With Correct IIH         Mirror data set along axis         Image: TAL axes convention         Image: BV axes convention         Flip X Axis         Flip Y Axis         Flip Z Axis         Clear V16 Mem         Brightness         Close
	BrainVoyager OX

After the manual procedure, we again have to save the result (V16 and VMR file) manually. The brain extraction can be performed via the "Volumes" menu.



It is advised to save the resulting VMR with a new name.



The results of the different inhomogeneity correction procedures can be compared in different ways. A simple option would be to load both VMR (automatic and manually driven result) and use the Tile mode in the Window menu.



Afterwards, one can best use the Link VMRs checkmark in the 3D Volume tools. This makes sure that the same position is represented in all loaded VMRs. The right side of the next screenshot shows the manually corrected VMR.

