# **Sequence Installation**

- 1. Copy the file 'multiBandsEPI\_6.0.1.PvUserBinMethod' to the disk of your Bruker system. Open the ParaVision 6.0.1 and click 'File'->'Import'->'Binary Method' and select 'multiBandsEPI\_6.0.1.PvUserBinMethod' on the path where you put.
- **2.** Copy all the RF Waveforms (\*.exc files) to the **ParaVision** system. The wave folder path is '....->**PV6.0.1->exp->stan->nmr->lists->wave**'.

## **Scanning parameters**

## 1. MB Mode

Change the 'MB Mode' to select MB Factors (MBF), e.g. the 'Bi-Bands' is for an MBF=2 experiment; the 'Tri-Bands' is for an MBF=3 experiment.

Echo Time		15.000 🖨 m	s Slice Packa	ge 🖵 1 🖨 of 1 🔾 🖨		
Repetition Time		1000.000 🖨 m	ns Slic	es		1 🛊
Averages		10 🖨	Slice Orientati	on	○ Coronal	
Repetitions		5 🛊	Read Orientati	on Le-Rt OV-DOR	lo-Cd	
Scan Time	0h0m50s0ms		Slice Thickne	ss		0.400 🖨 mm
			Image S	ze 80	60	
Segments		1 🛊	Field of Vi	ew 20.000	15.000	mm
Signal Type	Fid  Spin Echo			✓ CAIPIRINHA Mode		
Bandwidth		300000.0 🖨 н	z	✓ Reference Scan		
Band Spacing Factor		1.00		Sine Readout		
MB Mode	Bi-Bands	•	View Mo	de 💿 Regular 🔾 Revers	se 🔾 Alternate	
Routine Contrast	Resolution Reference RF	Geometry Se	quence Setup	System   Single Parameter	Instruction	

#### 2. View Mode

For some cases TOPUP distortion correction is required. The 'View Mode' is the way of EPI echo train phase encoding. The 'Regular' is blipping up; The 'Reverse' is blipping down; The 'Alternate' is blipping up for even # frames and blipping down for odd # frames.

#### 3. Sine Readout

To reduce acoustic noise of EPI scanning, select 'Sine Readout' to change the trapezoid readout gradient waveforms to be sinuous.

#### 4. CAPIRINHA Mode

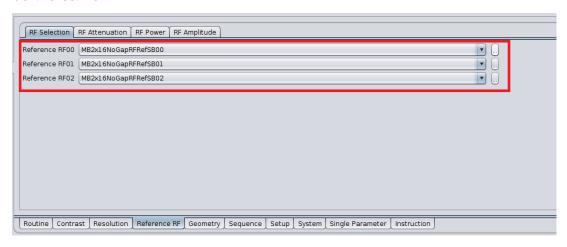
Phase chopping MB slices obtained to reduce g-factors. It is strongly recommended to keep selecting **CAPIRINHA Mode** always.

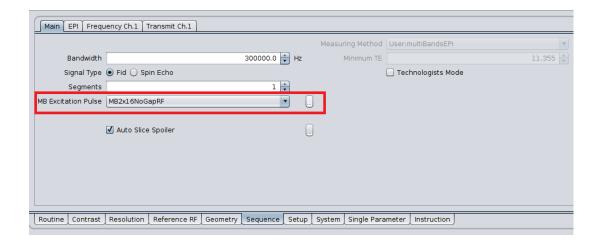
### 5. Reference Scan

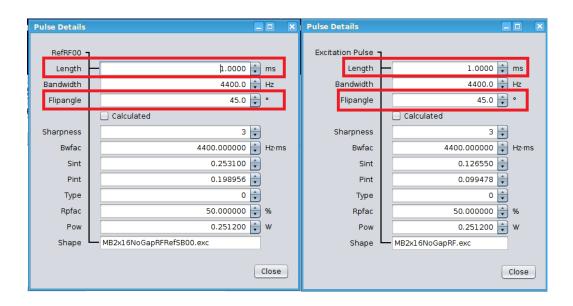
Switch on the 'Reference Scan' is for a reference scan; switch off the 'Reference Scan' is for an fmri scan. The reference scan data is required for any fmri scan data reconstruction. All the scanning parameters should be the same.

#### 6. RF Waveforms

All RF waveforms have to be designed, made and manually set by user. Technically, the RF waveform is unable to be dynamically generated yet. The MB Factor, MB slice number and slice gap ratio must consistent with the MB RF waveforms used. Slice thickness and gap can be adjusted. If MBF = N, it is required to set N+2 RF waveforms (1 MB RF and N+1 SB Reference RF). The pulse length and flip angle of all RF waveforms should be the same.







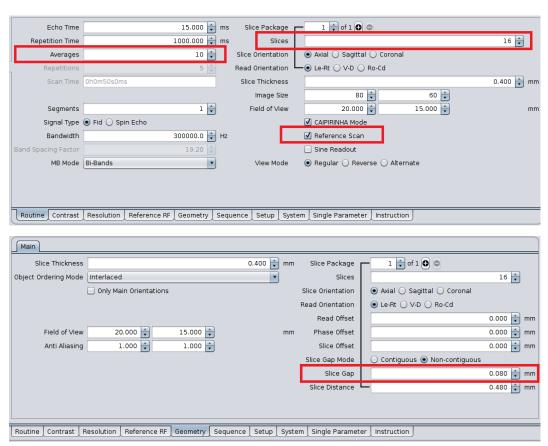
# Scanning Example

An example was shown below: MB RF waveform parameters were used MBF =2, slice number = 32, slice gap ratio = 0.2.

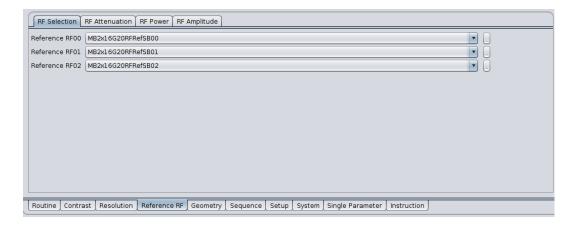
## 1. Reference scan

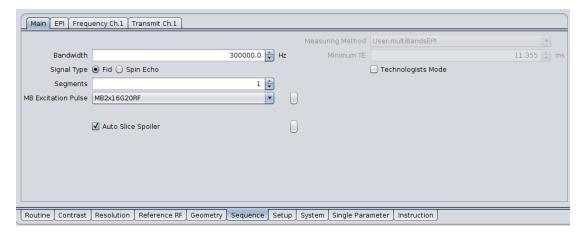
Switch on 'Reference Scan', set all scanning parameter e.g. TR/TE Bandwidth, FOV, Matrix resolution, Shimming and under sampling parameters (e.g. Zero Filling, Partial Fourier or phase encoding GRAPPA), The 'Repetition #' is fixed for reference scan. For the reference scan, it is strongly recommended to add the signal averaging # to improve reconstruction quality. In this example, we set the average # to be 10. For MBF =2, slice number = 32, the slice number is set to be 16 (Slice

number/MBF). If the slice thickness is 0.4 mm, set the slice gap to be 0.08 mm (slice thickness×slice gap ratio).



Set all RF waveforms, for MBF = 2, 1 MB RF and 3 SB reference RF are required to be set. The pulse length and flip angle of all RF waveforms should be the same.

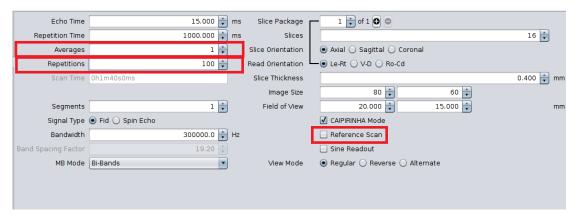




When all is prepared, finish the scan.

#### 2. FMRI Scan

Duplicate the scan and switch off the 'Reference Scan', change the 'Repetition #' and 'Averages #'. Finish the scan.



Something about 'View Mode': The **Regular View Mode** Reference scan can only support the **Regular View Mode** Fmri data reconstruction; The **Reverse View Mode** Reference scan can only support the **Reverse View Mode** Fmri data reconstruction; The **Alternate View Mode** Reference scan can support all of the three 'View Mode' Fmri data reconstruction.

## Reconstruction

The reconstruction tools can be run on Microsoft Windows system.

 Click the 'MBParallelReconVxxx.exe', if it cannot open please click the 'vc\_redist.x86.exe' to install Microsoft Visual C++ Runtime libs.

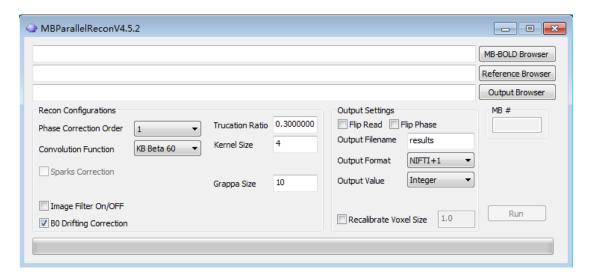
### 2. Instructions of some parameters

Output Format: select a results data format. 'No Format'-- a binary file like as Bruker's '2dseq'; 'Analyze 7.5'-- output as NIFTI1 format (\*.hdr+\*.img); 'NIFTI+1' -- output as NIFTI+1 format (\*.nii).

Recalibrate Voxel Size: When the 'Output Format' is selected as 'Analyze 7.5' or 'NIFTI+1'. The output voxel size can be recalibrated by change the zooming value.

Image Filter On/Off: Switch on the 'Image Filter On/OFF' and set the 'Filter Width' value to filter image results. SNR can be improved but also get blurring.

It is recommended that not change other recon parameters unless it is necessary.



## 3. Run the tools.

Click the 'MB-BOLD Browser' to select a folder containing FMRI data.

Click the 'Reference Browser' to select a folder containing reference scan data.

Click the 'Output Browser' to select a path for exporting results.

Choose the 'Output name', 'Output Format'. Set the 'Recalibrate Voxel Size' if it needs.

Click the 'Run' button and wait till it is done.