shapedDwi_Epi: A Bruker Paravision 6.0.1 pulse sequence for arbitrary diffusion encoding waveforms. Matt Budde, Medical College of Wisconsin mdbudde@mcw.edu

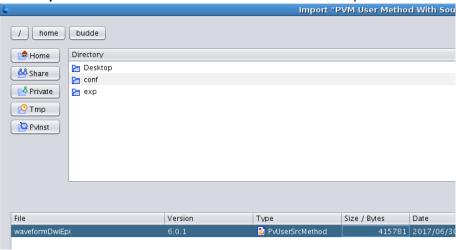
This quickstart guide describes how to install and setup a new or shared pulse sequence into the Bruker Paravision 6.0.1 environment. This one explicitly details the shapedDwiEpi sequence. This sequence allows the use of custom diffusion weighted waveforms of any shape. Everything needed to test the sequence with a default waveform is provided and can be easily installed.

(Note: the sequence is now called shapedDwi_Epi and has explicit shape names Stick, Cigar, Plane, Sphere). The images in this guide have not been updated, but the procedures are the same).

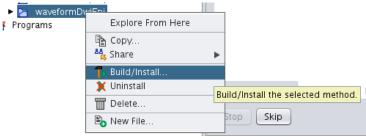
Rather than a complete protocol, it is provided as a starting point for users to develop and interface their own custom waveforms, such as oscillating gradients, qMAS rotating gradients, or some other arbitrary waveform. These decisions and creation of waveform files is left to the end-user, but details are included at the end of this document.

Installation:

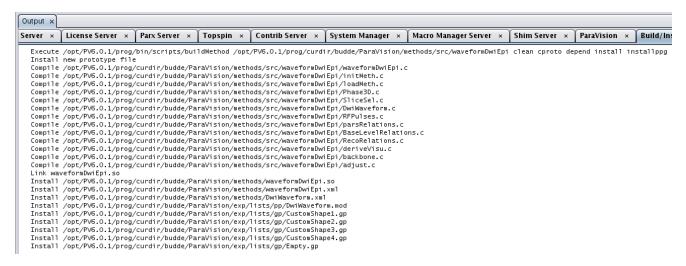
- 1. Download or copy the file shapedDwi_Epi_6.0.1.PvUserSrcMethod to your home directory folder on your Bruker scanner console
- 2. Open Paravision
- 3. File->Import->Source Method... and select the file from step 1.



- 4. Open the Workspace Explorer tab, and expand Methods Development, User Methods,
- 5. Right-click the waveformDwiEpi folder and select **Build/Install...** keeping all options selected.

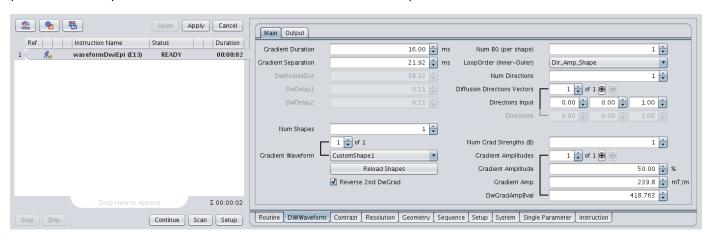


6. View the contents of the Output window to ensure there are no errors with compilation.



Scan Setup:

- 1. Open an existing exam, begin a new one, or select the Examination tab.
- 2. In the Palette, Explorer tab, select Object: AnyObject, Region: AnyRegion, Application: UserMethods.
- 3. Right-click the waveformDwiEpi protocol and Add to Scan Program.
- 4. Double click the new scan in the exam window to begin editing.
- 5. Specific to this sequence is a DWIWaveform tab with the available options.



Sequence details:

The sequence is created to allow multiple gradient shapes, amplitudes, and directions all within a single scan interface. The order of looping is controlled through the dropdown box.

Gradient shapes (waveforms): Gradient shapes are selected with the drop-down menu and include Stick, Cigar, Plane, Sphere, etc. Up to 4 different shapes can be used in a single scan. The waveforms are stored in text files contained within the source folder. As shown in the output during compilation, these get copied into the user's directory in /opt/PV6.0.1/prog/curdir/USER/ParaVision/exp/lists/gp

During the scan setup, the files are loaded from this location. However, again note that if the sequence is recompiled, it will overwrite the files in the gp directory.

The shape of the second waveform after the 180 pulse can be reversed (in time) or negated (in amplitude) using the checkboxes.

<u>Gradient amplitudes</u>: The gradient amplitude can be scaled directly and are given both in units of mT/m and % of the max system gradient. The b-value may depend on the shape so it is not directly used to scale the amplitude. However, if the waveform file contains a parameter "BFACTOR", the interface will report the expected b-value as (b-factor * G^2; units should be s/mm² to conform to other Bruker sequences). This isn't universal since the b-value depends on the gradient shape, but it does provide a means to interface the b-value and amplitude for many diffusion encoding schemes (PGSE, OGSE). Note: this feature is not correct if the gradients are not refocused. That is, it will not account for the diffusion separation (Big delta).

<u>Gradient directions:</u> The waveforms can be rotated to other axis than what is contained in the waveform file. For example if the waveform is created with a gradient along only the z(slice) axis, a direction of [0 0 1] will keep the same direction, while [1 0 0] will rotate it to the x(read) axis using rigid-body vector rotations. The user is encouraged to use the simulation tool and experimental tools to verify this feature performs as expected and the appropriate waveforms are obtained.

<u>Gradient durations</u>: The duration of the gradient waveform is taken from that parameter given in the waveform file. Waveforms should likely have a pre specified duration rather than modulating it from the interface. The sequence has not been tested with multiple durations within a single experiment. It is suggested to have the same durations for each of the shapes in a single scan.

Other notes: The waveform files are preliminarily checked to ensure they comply with the limits of the system.

- The max amplitude in the waveform file cannot be above 1 or below -1.
- Gradient time resolution (duration/npoints) must be larger than that of the system (typically 8 us per point)
- The slope between any two adjacent points in the waveform cannot exceed the maximum allowable slew rate of the system.
- An additional ramp time is internally added to the beginning/end of the waveforms to accommodate non-zero starting/ending points. For example, a trapezoid waveform can be created by a single timepoint [1.0 0.0 0.0] and system ramps will be used. A starting/ending value of 0 will still incur a ramptime at the beginning/end of each waveform.

Example waveform file header and contents:

```
##TITLE= Waveform
##JCAMP-DX= 5.00 Bruker JCAMP library
##DATA TYPE= Shape Data
##ORIGIN= Bruker Analytik GmbH
##OWNER= <nmrsu>
##DATE= xx
##TIME= xx
##MINX= 0
\# #MAXX= 1
##MINY= 0
\##MAXY= 1
##$SHAPE EXMODE= Gradient
##$SHAPE TOTROT= 0
##$SHAPE BWFAC= 0
##$SHAPE INTEGFAC= 0
##$SHAPE MODE= 0
##BFACTOR= 3640.7791
##DURATION= 0.0160
##DIRECTIONVEC= 0 0 1
##NPOINTS=1000
##XYDATA = (T X Y Z)
0.000000 0.000000 0.000000
0.048899 0.000000 0.048899
```

. .

-0.048899 0.000000 -0.048899 0.000000 0.000000 0.000000 ##END