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# The TOPPE<sup>1</sup> pulse programming environment for GE MRI scanners

This document applies to version 1.0 of the pulse sequence (toppev1.e).  
Tested on a GE Discovery MR750 scanner running software version DV25.1\_R01.

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This pdf is available from the TOPPE website: <https://toppemri.github.io/>.

This document is open-source. Latex code can be found in the following repository:

<https://github.com/toppeMRI/UserGuide>.

Alternatively, you can get a copy of the repository by typing the following in a Linux console:

```
git clone https://github.com/toppemri/UserGuide.
```

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<sup>1</sup>“The End Of Pulse Programming”, rearranged; pronounced “toppee”

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# Chapter 1

## Overview

### 1.1 Introduction

Implementing research pulse sequences on GE MR scanners requires EPIC programming, a time-consuming and error-prone task with a steep learning curve. Moreover, pulse sequences need to be recompiled after each scanner software upgrade, which is sometimes problematic.

This user guide describes the “toppe.e”<sup>1</sup> pulse sequence for GE scanners, which allows the entire sequence to be specified with a set of external files created with a high-level software tool such as Matlab. This makes it possible to play arbitrary sequences of RF pulses and gradient waveforms, which enables **rapid prototyping of sequences without the need for low-level EPIC programming**. With `toppev1.e`, the task of pulse programming a GE scanner becomes one of creating the various external files that define the sequence.

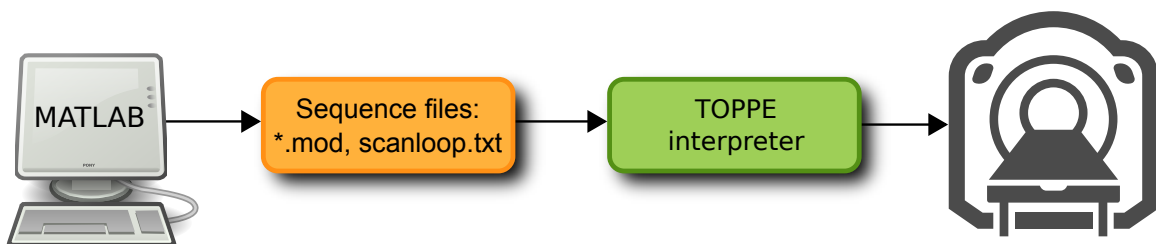


Figure 1.1: Overview of pulse sequence programming with `toppev1.e`. The TOPPE sequence files (orange) specify all details of the MR acquisition, such as RF phase cycling, gradient waveforms, and timing information. These files are created in MATLAB using the TOPPE MATLAB toolbox (<https://github.com/toppeMRI/matlab/>). The TOPPE sequence files are passed on to the TOPPE interpreter (green), a binary executable that executes the sequence on the scanner. Source code (EPIC) for the interpreter is available for download on the GE Collaboration Community site at <https://collaborate.mr.gehealthcare.com/docs/DOC-1247>. The interpreter only needs to be compiled and installed once per scanner software upgrade. With this setup, arbitrary sequences of RF and gradient pulses can be played out, which enables rapid pulse sequence prototyping without the need for EPIC programming.

`toppev1.e` was developed as a research tool at the fMRI laboratory at University of Michigan, and has to date been used in several projects including stack-of-spirals imaging, Bloch-Siebert B1+ mapping, echo-

<sup>1</sup>“The End Of Pulse Programming”, rearranged; pronounced “top dot e”

shifted RF-spoiled imaging (PRESTO), steady-state imaging with 3D tailored RF excitation, and dual-echo steady-state (DESS) imaging.

We are currently making `toppev1.e` compatible with **Pulseq**, an open file format for compactly describing MR sequences. See Chapter 4 for more information about using `toppev1.e` as a GE “interpreter module” for Pulseq files.

**Your feedback** is most welcome.

## 1.2 Required external files

In addition to the `toppe` and `toppe.psd.o` executables, which only need to be compiled and installed once for each scanner software upgrade, the following files are needed to run a particular scan (see Fig. 1.2):

### 1.2.1 \*.mod files

`toppev1.e` creates several unique “cores” (or modules), with each core/module associated with one `.mod` file (Fig. 1.2). For example, an RF excitation module may be defined by a file called `tipdown.mod` that specifies the RF amplitude and phase waveforms ( $\rho$  and  $\theta$ ) and all three gradients. Similarly, a Cartesian (spin-warp) gradient-echo readout may be defined in a file `readout.mod` that contains readout and phase-encode gradient waveforms. Finally, a spoiler gradient can be defined in a file `spoiler.mod`. Each `.mod` file is unique up to waveform scale factors and to a rotation in the logical xy-plane, and typically only a few `.mod` files are needed. Note that each `.mod` file gives rise to a separate `createseq()` call in `toppev1.e`.

### 1.2.2 modules.txt

The various `*.mod` files needed to define a scan are listed in a small text file named `modules.txt`, which simply contains a line for each `.mod` file specifying the file name, core duration, and whether it is an RF excitation module, readout module, or gradients-only module. Values are tab-separated. A `modules.txt` file for our simple spin-warp imaging example may look like this:

```
Total number of unique cores
3
wavfile_name      duration(us)      hasRF?  hasDAQ?
tipdown.mod 0      1      0
readout.mod 0      0      1
spoiler.mod 0      0      0
```

A duration of 0 means that the minimum core duration for that `.mod` file will be used.

### 1.2.3 scanloop.txt

Finally, the complete MR scan loop is specified in `scanloop.txt`, in which each line corresponds to a separate `startseq()` call in `toppev1.e`. A `scanloop.txt` file for single-slice, RF-spoiled spin-warp imaging with 256 phase-encodes might begin like this:

```

nt maxslice maxecho maxview
768 1 0 768
Core iarf iath iagx iagy iagz slice echo view dabon rot rfph recph textra freq
1 32766 32766 0 0 32766 0 0 0 0 0 0 0 0 0
2 0 0 32766 32766 -32638 1 0 1 1 0 0 0 0 0
3 0 0 0 0 32766 0 0 0 0 0 0 0 0
1 32766 32766 0 0 32766 0 0 0 0 0 21298 0 0 0
2 0 0 32766 32766 -32382 1 0 2 1 0 0 21298 0 0
3 0 0 0 0 32766 0 0 0 0 0 0 0 0
...

```

where `nt` is the total number of `startseq()` calls ( $256$  phase-encodes  $\times$   $3$  cores per TR), and `maxslice`, `maxecho`, and `maxview` correspond to `rhnslices-1`, `rhnecho-1`, and `rhnframes`, respectively, in `toppev1.e`.

**We do not recommend using the `slice=0` and `view=0` indices (“slots”)**, hence the `slice` and `view` indices both start at 1 in the above example. Each row in `scanloop.txt` specifies which module to play and with what RF and gradient amplitudes; where to store the data using `loadab()` (i.e., which slice/echo/view); whether the module is used to acquire data; in-plane (kx,ky) rotation angle; the RF and acquisition phase; a value ‘`textra`’ (in  $\mu$ s) by which the core duration is extended (see Ch. 3), and the RF/acquisition frequency in Hz. Values are tab-separated. For long scans, `scanloop.txt` can contain many tens of thousands of lines.

## 1.2.4 Legacy files

The files `legacy1.rho`, `legacy1.theta`, and `legacy2.rho` must be copied to `/usr/g/bin/` on the scanner. These files are included in subfolders of the `examples` directory in the TOPPE MATLAB repository, available at <https://github.com/toppeMRI/matlab/>.

## 1.3 Source code repositories

TOPPE is open-source and is available through the following repositories:

- Matlab scripts for creating and viewing TOPPE files, and complete sequence examples.

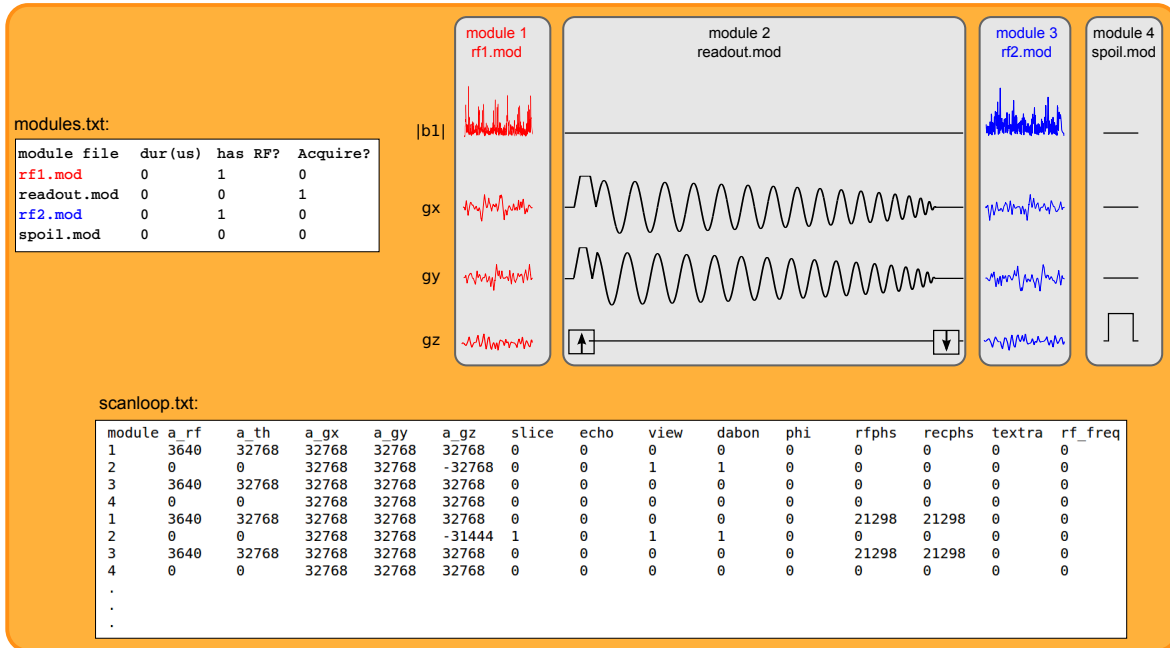


Figure 1.2: Overview of the TOPPE file structure. A TOPPE MR sequence is comprised of a (usually) small number of unique modules that are listed in the file 'modules.txt' (a). Each module contains a set of arbitrary gradient waveforms and a complex RF waveform (if applicable), and is contained within a file with extension '.mod'. These modules are unique up to waveform scale factors, and to a rotation in the logical transverse ( $k_{xy}$ ) plane. (b) Example of four different modules within an MR sequence: two 3D RF excitations, one spiral-in readout, and one gradient spoiler. (c) The file 'scanloop.txt' lists the order in which to execute the modules, and specifies all other dynamic sequence information. Each row specifies the module number as listed in modules.txt; RF and gradient waveform amplitudes; where to store the acquired data in memory ('slice/echo/view' indices). in-plane rotation angle ('phi'); transmit and receive phase; a parameter 'textra' by which to extend module duration (for dynamic TR changes); and RF transmit frequency (for slice offsets). For detailing sequence timing information, see Ch. 3.

## Chapter 2

# Using the toppe sequence

### 2.1 Creating .mod files

The TOPPE MATLAB repository (<https://github.com/toppeMRI/matlab/>) includes the Matlab script **mat2mod.m** that writes rho, theta, gx, gy, and gz waveforms for a module to a .mod file. Important notes and caveats:

- All waveforms in a module must have the same length, i.e., they must be padded with zeroes as needed.
- Even if the module is not an RF excitation module, you must create a non-zero 'dummy' RF pulse to ensure that the .mod file will be loaded correctly on the scanner (hopefully this bug will be fixed in future releases). A simple hard RF pulse of low amplitude (e.g., 0.01 Gauss) seems to work well in most cases.
- If the module is a readout module, data will be acquired every 4  $\mu$  for the entire duration of the waveforms in the .mod file. Depending on your readout trajectory, you may therefore need to discard some of the data (near the beginning and/or end of the module) before reconstructing.
- If more than one readout .mod file is used, they must all be the same length (readout windows of different widths are not permitted).
- For backward compatibility, the following must be done (this may change in future releases):
  - One of the readout .mod files must be named **readout.mod**
  - One of the RF excitation .mod files must be named **tipdown.mod**

### 2.2 Creating modules.txt

modules.txt can simply be created by hand, as specified above.



## 2.3 Creating scanloop.txt

The examples folder in the TOPPE MATLAB repository (<https://github.com/toppeMRI/matlab/>) contains several examples of how scanloop.txt can be created. Specifically, this is done in each example with the script **writeloop.m**.

We have determined empirically that to avoid data corruption, rhnslices **should be even**. In addition, for now, avoid loading the dabslice= 0 slot with data. This means that there will be an odd number of slice slots available for useful data.

## 2.4 Pre-viewing your sequence with playseq.m

We recommend displaying your sequence in Matlab using playseq.m before attempting to play it on the scanner, to verify that the correct modules are played out in the intended order. playseq.m attempts to reproduce the exact module timing seen on the scanner, using CV values in the file timing.txt. For examples of how to use playseq.m, see the readme file in the examples folder in the Matlab repository (<https://github.com/toppeMRI/matlab/>).

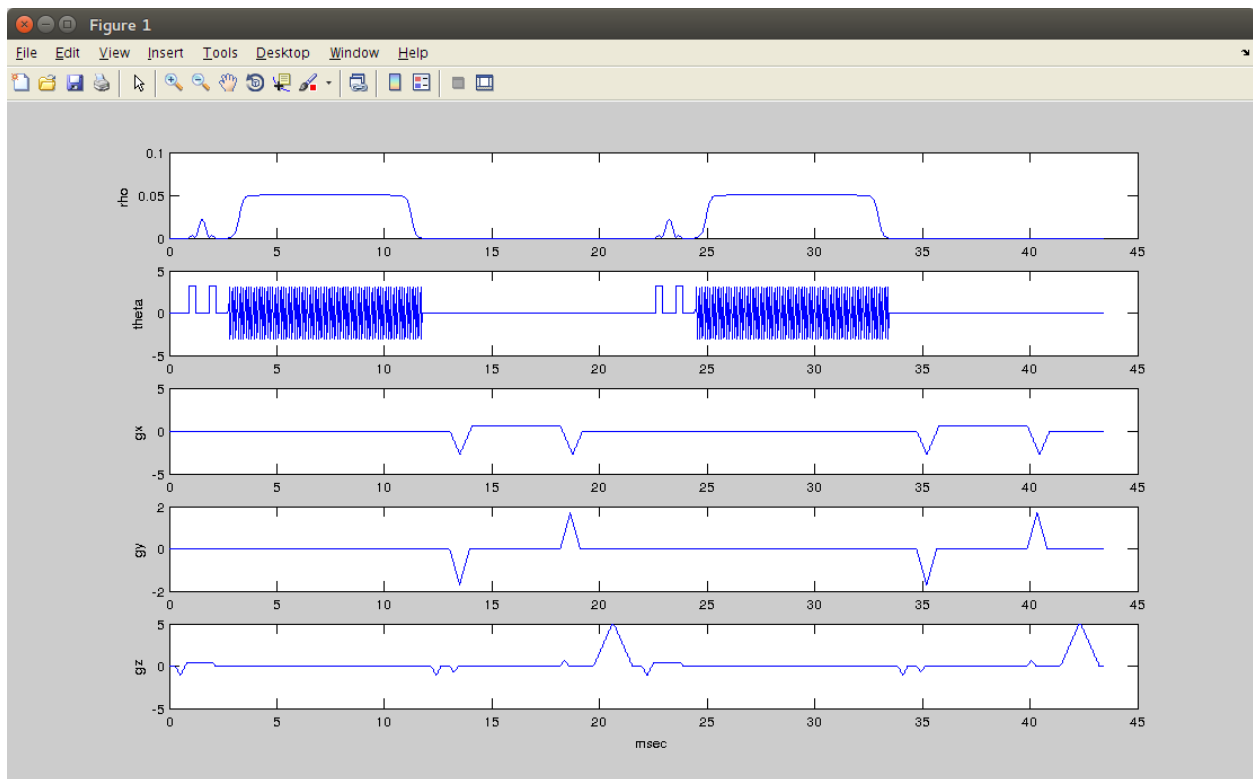


Figure 2.1: Example sequence display created with *playseq.m*. The sequence shown is a Bloch-Siebert B1 transmit mapping sequence with a 3D Cartesian readout. Like the *toppe* and *toppe.psd.o* executables on the scanner, *playseq.m* loads *modules.txt* and the .mod files listed therein, and *scanloop.txt*. In addition, *playseq.m* obtains exact sequence timing information from the file *timing.txt*.

## 2.5 Compiling the toppe pulse sequence

The current version of `toppev1.e` has been compiled for DV25, and has been tested on a GE Discovery MR750 3T scanner. The `toppev1.e` source code is in the `psd` directory.

To compile, follow the usual EPIC compilation steps. First, check compiler version:

```
which psdmake
```

With the compiler at University of Michigan, the output is

```
/ESE_DV25.0_R01/psd/bin/psdmake
```

Prepare directory for compilation and compile:

```
prep_psd_dir  
psdmake hw
```

This will create two executables: `toppev1` and `toppev1.psd.o`.

## 2.6 Step-by-step scanner instructions

Follow these steps to prescribe and run the toppe sequence:

1. Copy `toppev1`, `toppev1.psd.o`, and the legacy files to `/usr/g/bin/` on the scanner host computer (console). This only needs to be done once per scanner software upgrade.
2. Copy the legacy files to `/usr/g/bin/` on the scanner host computer (console). This is only done once per scanner software upgrade.
3. Copy `modules.txt`, `scanloop.txt`, and all `.mod` files to `/usr/g/bin/`.
4. Required files:
  - Make sure one of the readout (acquisition) `.mod` files is named `readout.mod`.
  - Make sure one of the RF excitation `.mod` files is named `tipdown.mod`.
5. Prescribe the toppe sequence:
  - Select Axial 2D pulse sequence; Family: 'Gradient Echo'; pulse: 'GRE'; PSD Name: 'toppev1'; click 'Accept'. (Fig. 2.2)
  - Prescribe a single axial slice.
  - Set shim of 'off'.
  - Other settings do not matter but must be specified. Suggested values are: Slice thickness 3, slice spacing 0, number of slices 1.
6. Save and download the sequence, and run autoprescan.
7. Click scan button. This will create a Pfile in `/usr/g/mrraw/`.

- To run a different TOPPE scan, simply overwrite modules.txt and scanloop.txt and make sure the .mod files for the next sequence exist in /usr/g/bin/. Then download the sequence (right-click) and hit Scan button. You do not need to prescribe a new sequence every time you load a new set of external files.

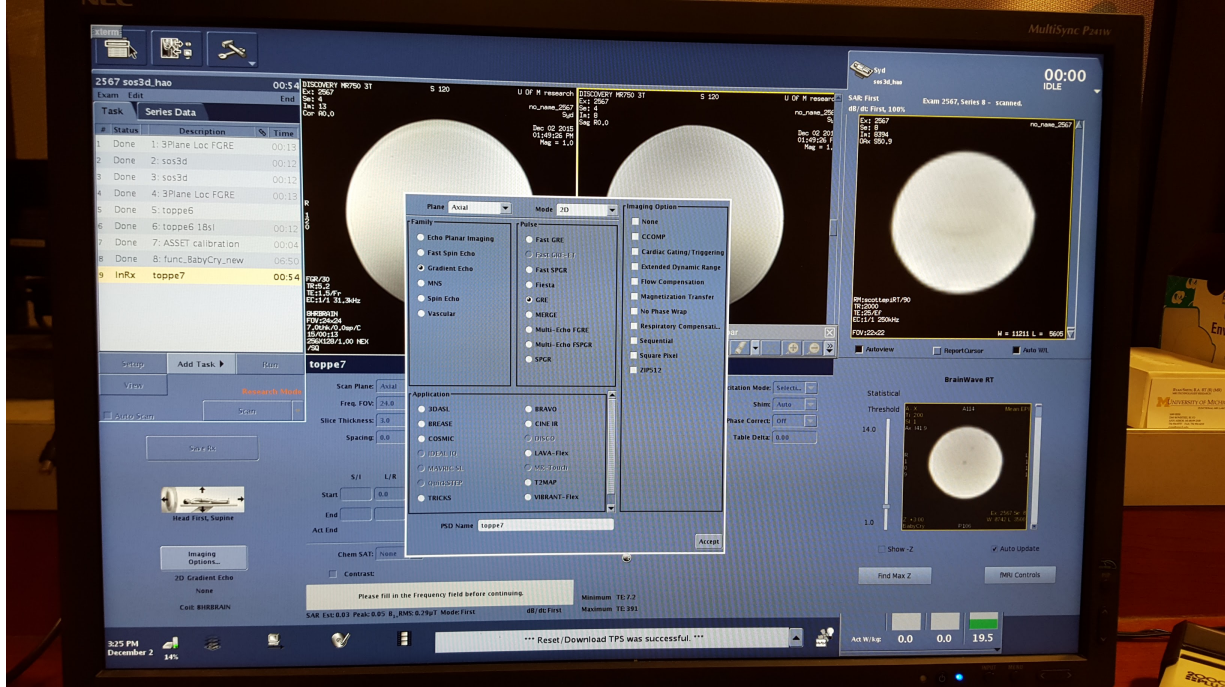


Figure 2.2: Scanner prescription, screenshot 1.

## 2.7 Checklist

Remember the following recommendations, which have been determined empirically:

- It seems that `rhnslices` should be even to avoid corrupt data.
- It seems safest to avoid storing data in the `dabslice=0` slot (in `loadadb()`), since data frames (“views”) for this slot are often flipped (reversed) with respect to the rest of the Pfile.

## 2.8 Known bugs and limitations

- Data may be saved in **reverse order** (due to `oeff` and `eeff` flags), so keep an eye out for this. Inspect your raw data.
- Auto prescan may not work, hence the use of manual prescan above.
- B1 scaling across multiple RF pulses has not been verified. May need to expand `rfpulse` struct.

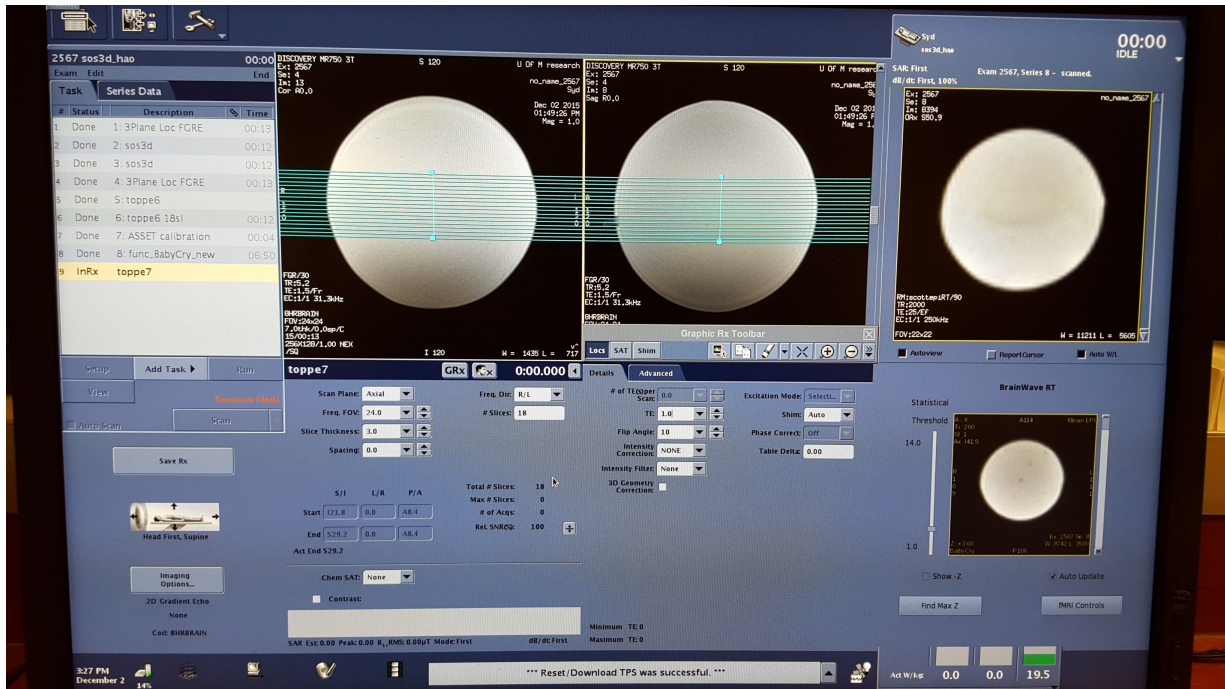


Figure 2.3: Scanner prescription, screenshot 2.

- toppev1.e does not support cardiac/respiratory gating at the moment. If other groups have a need for this we believe gating can be easily added.
- toppev1.e does not currently do any checks for SAR, PNS, or gradient heating.

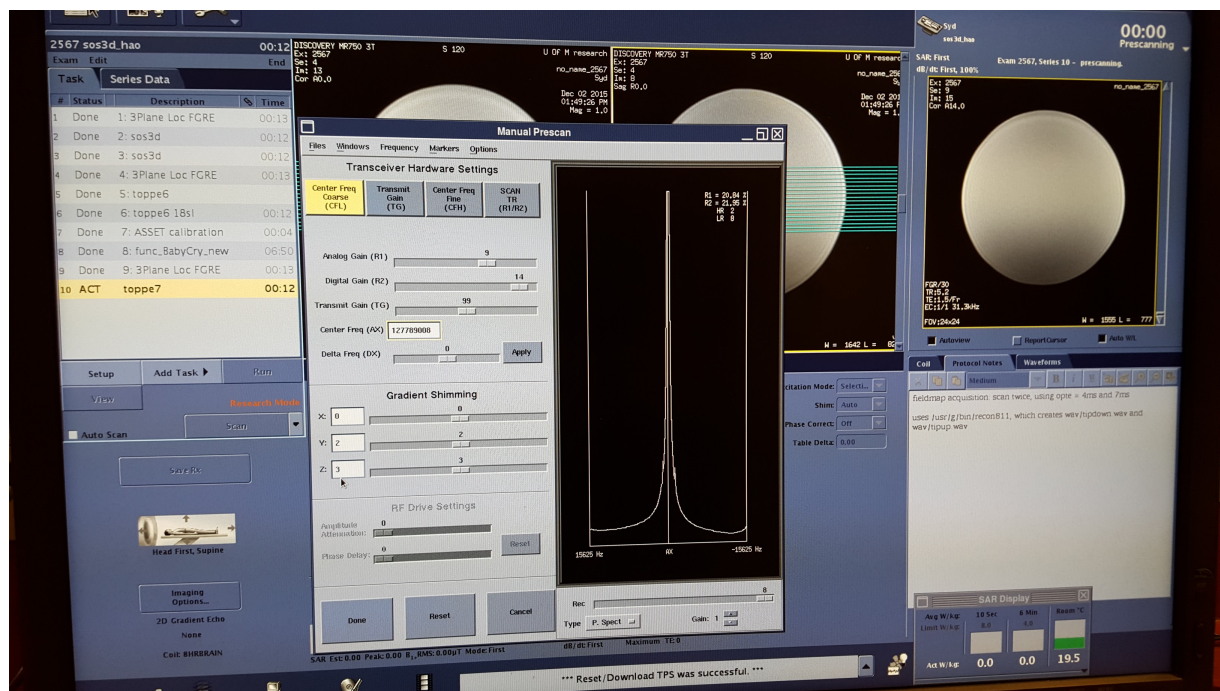


Figure 2.4: Scanner prescription, with manual prescan window.



## Chapter 3

# Controlling sequence timing

The default module duration is set to the value specified in `modules.txt`, however the duration can be extended in real-time by setting the value of the 'extra' column in `scanloop.txt` to a non-zero value. This allows the sequence timing to be controlled dynamically, e.g., for the purpose of varying TE or TR during a scan.

If the minimum module duration exceeds the prescribed duration in `modules.txt`, the minimum module duration is used (without warning). It is therefore perfectly fine to set the module duration in `modules.txt` to '0', since this guarantees that the minimum duration will be used which is often the desired behavior.

Figure 3.1 shows detailed timing information for the three module types: gradients-only, RF excitation, and data acquisition. For gradients-only modules, the minimum module duration is equal to the waveform duration plus the controls variables (CVs) 'start\_core', 'timetrwait', and 'timessi'. These have been determined empirically, and are currently set to 224us, 64us, and 100us, respectively. For RF and acquisition modules, the module duration must be extended by 'myrfdel' and 'daqdel', respectively, to account for gradient delays with respect to RF transmission and data acquisition, respectively.

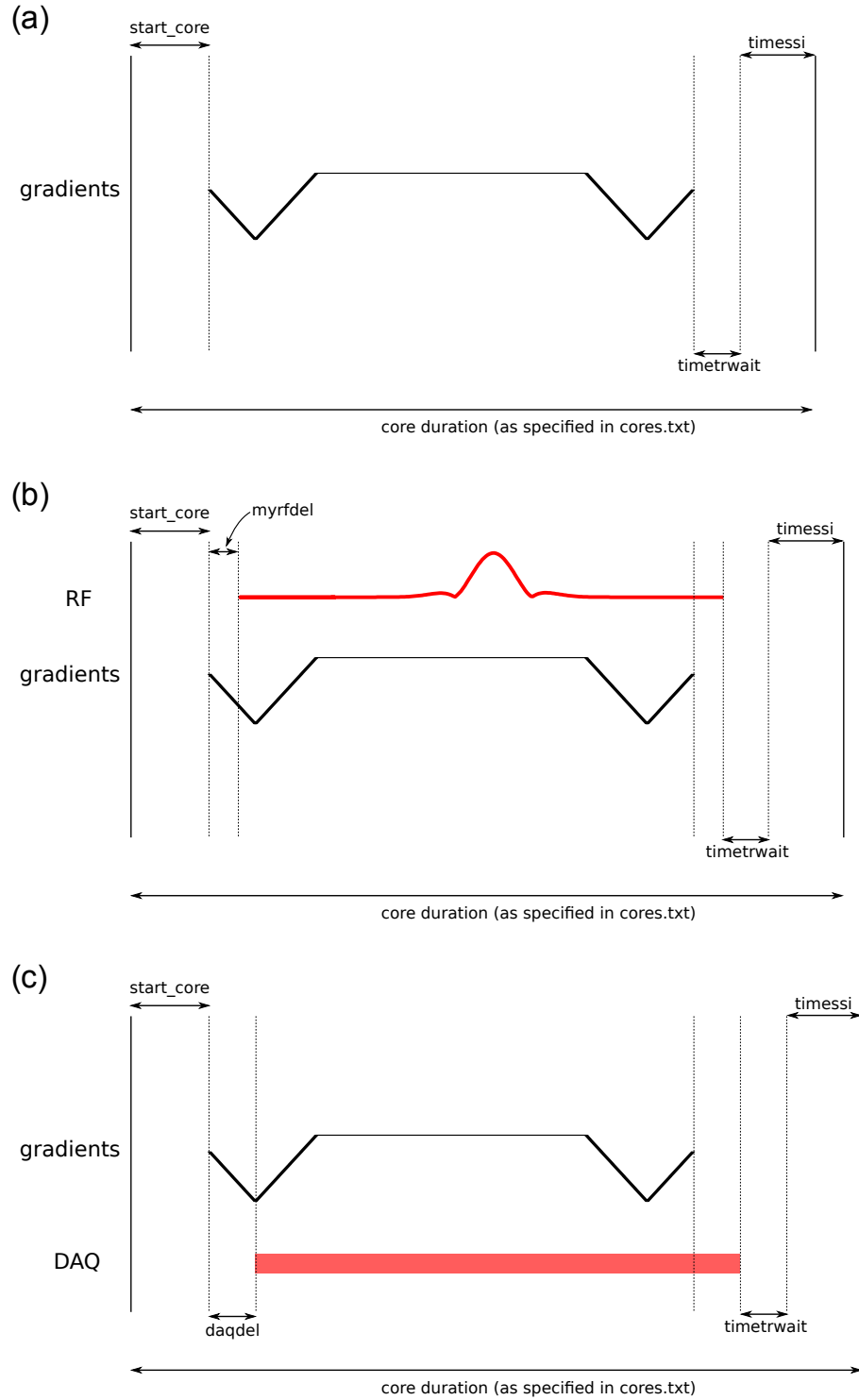


Figure 3.1: Detailed timing diagram for the three module types: (a) gradients-only, (b) RF excitation, and (c) data acquisition. The labels correspond to Control Variables (CVs) in `toppev1.e`. Note that `playseq.m` uses timing values in `timing.txt` (see sequence examples in the Matlab repository) to reproduce the precise sequence timing one should expect to observe on the scanner.

## Chapter 4

# Using `toppe.e` as an interpreter module for Pulseseq files

### 4.1 Pulseseq

An effort is currently underway to make `toppev1.e` compatible with Pulseseq, an open file format for compactly describing MR sequences. The Pulseseq file specification, along with supporting Matlab and C++ libraries, is available at

<http://pulseseq.github.io/>

Pulseseq relies on vendor-dependent “interpreter modules” to load a Pulseseq (.seq) file onto a particular scanner platform. `toppev1.e` can serve as the interpreter module for GE scanners. Interpreters currently also exist for Siemens and Bruker scanners, enabling truly platform-independent MR pulse programming. The following publication has more information about the Pulseseq platform and philosophy: <http://onlinelibrary.wiley.com/doi/10.1002/mrm.26235/abstract>.

### 4.2 Using `toppev1.e` to play .seq files

To use `toppev1.e` as a GE interpreter module for Pulseseq files, use the Matlab script **`seq2ge.m`** in the `pulseseq` directory in the beta distribution (v0.9). `seq2ge.m` takes as input a .seq file and outputs the various files needed by `toppev1.e` (`modules.txt`, `scanloop.txt`, and `.mod` files). For an example, see `main.m` in the `pulseseq` directory.



# **Appendices**

## Appendix A

# Tools for RF and gradient waveform design

### A.1 Matlab scripts included in this distribution

My own Matlab scripts for generating slice-selective RF pulses, balanced cartesian readouts, spoiler gradients, etc, are included in the `wavgen` directory in this distribution. The code is provided as-is, and is undocumented at the moment.

### A.2 John Pauly's RF pulse design code (Matlab)

John Pauly has made his Shinnar-Le Roux code available for download at

<http://rsl.stanford.edu/research/software.html>

The code included in the `wavgen/tipdown` directory in this distribution uses Pauly's code to generate SLR slice-select pulses.

### A.3 Brian Hargreaves' spiral gradient design code (Matlab)

Brian Hargreaves has made his spiral readout gradient design code available for download at

<http://mrsrl.stanford.edu/~brian/vdspiral/>

### A.4 Generating Pulseseq files

Pulseseq provides tools for waveform and sequence creation, available on the Pulseseq web page. Alternatively, sequences can be designed, simulated, and exported in Pulseseq (.seq) format using JEMRIS, available at

<http://www.jemris.org/>