WEBVTT

1 00:00:00.000 --> 00:00:08.348 Hello and welcome to a brief introduction video to D my wizard and specifically a version 1.1.

2 00:00:08.348 --> 00:00:19.300 D my wizard is a matlab based GUI aimed at the processing of 1D and 3D deuterium metabolic imaging data acquired on a number of.

3 00:00:19.300 --> 00:00:28.746 Of platforms. This video just gives you a brief walk through of the most common operation that you do within their software.

4 00:00:28.746 --> 00:00:34.613 If you have any kind of trouble or any kind of questions or require modifications.

5 00:00:34.613 --> 00:00:38.289 Please contact me directly at aerobicgraphyield.edu.

6 00:00:38.289 --> 00:00:40.880

7 00:00:40.880 --> 00:00:46.627 OK, at this point, I'm assuming that you have downloaded the my wizard software from the website.

8 00:00:46.627 --> 00:00:47.975 In this case. It is D.

9 00:00:47.975 --> 00:00:52.810 My wizard version 1.1. Zip and you can now go ahead an unzip that file.

10 00:00:52.810 --> 00:00:58.213 And normally I'd like to copy this and put it in a place where I like it to be in this case.

11 00:00:58.213 --> 00:01:01.990 Let's make a dmi directory on the C drive it will paste it there.

12 00:01:01.990 --> 00:01:04.010

13 00:01:04.010 --> 00:01:08.864 And and ideally you've also downloaded the dmi wizard data file.

14 00:01:08.864 --> 00:01:12.748 It also zip file that contains a number of Emerson.

15 00:01:12.748 --> 00:01:15.736 MRI files that you can use to practice.

16 00:01:15.736 --> 00:01:25.593 The Dmi Wizard. So far with it also zip file so go ahead and unzip that or copy that and put it again in the in the place where you

17 00:01:25.593 --> 00:01:26.640 want it to be.

18 00:01:26.640 --> 00:01:29.310

19 00:01:29.310 --> 00:01:40.174 There we go. So the first thing you typically want to do is going through the demon Wizards Directory and then go through the D my wizard settings dot text

20 00:01:40.174 --> 00:01:48.531 file. At name implies, it is a simple text file it holds some information about the colour scheme of the Demon Wizard.

21 00:01:48.531 --> 00:01:54.060 GUI's about the font name and sizes and also about the default part name.

22 00:01:54.060 --> 00:02:00.263 So you want to change this to the directory name that you have on your computer in this case.

23 00:02:00.263 --> 00:02:07.560 It's the C drive and then the dmi directory that we just made if you're happy with you can save that.

24 00:02:07.560 --> 00:02:12.549 And you can see dash already showing premade settings as well.

25 00:02:12.549 --> 00:02:15.241 That allow you to do a dark mode.

26 00:02:15.241 --> 00:02:20.210 GUI setting and you can change those as you see fit.

27 00:02:20.210 --> 00:02:28.409 OK, so normally then I would like to copy the directory name and paste it into Matlab.

28 00:02:28.409 --> 00:02:34.590 And then the GUI can be started by just typing D my Wizards in the command line.

29 00:02:34.590 --> 00:02:38.939 And then you gonna get your main window as shown here.

30 00:02:38.939 --> 00:02:43.050 The main window has basically 2 main menus.

31 00:02:43.050 --> 00:02:50.245 One is for the processing of one dimensional spectroscopy data and the other one is for the processing of 3,

32 00:02:50.245 --> 00:02:53.780 Dimensional Amar Spectroscopic Imaging data.

33 00:02:53.780 --> 00:02:57.629 So let's first quickly go truly one DM arrest data.

34 00:02:57.629 --> 00:03:05.846 And used to emphasize that this video is not an exhaustive manual to all aspects of their software that you can find in the menu.

35 00:03:05.846 --> 00:03:12.349 As I'll show later this is just a quick walk through on some of the most important features.

36 00:03:12.349 --> 00:03:16.400 So this is the menu for the one dimensional spectroscopy.

37 00:03:16.400 --> 00:03:28.824 The lines in green and boxes in green and typically related to the file loading and file handling items things in blue are spectral processing things in yellow are related

38 00:03:28.824 --> 00:03:39.442 to baseline correction integration and things in red are associated with a chemical shift referencing so the first thing you typically want to do,

39 00:03:39.442 --> 00:03:43.250 if you want to load in a data file.

40 00:03:43.250 --> 00:03:47.159 So that's where the D my wizard underscore data comes in.

41 00:03:47.159 --> 00:03:51.860 There's basically 4 different types of files there is a 3 dimensional.

42 00:03:51.860 --> 00:03:54.838 Dmi there is a one dimensional spectroscopy.

43 00:03:54.838 --> 00:03:59.802 But one average. There's a one dimensional spectroscopy with 180 averages,

44 00:03:59.802 --> 00:04:04.768 and there is 3. Dimensional MRI in this menu were interested in #2 and #3.

45 00:04:04.768 --> 00:04:12.330 So you can open that and then you can read this being brokered data you can read the FID file.

46 00:04:12.330 --> 00:04:14.782 At this point, it hasn't loaded the data.

47 00:04:14.782 --> 00:04:18.576 Yet yet just selected the file that you want to load you wanted,

48 00:04:18.576 --> 00:04:21.903 and indicate which vendor the data is from in this case,

49 00:04:21.903 --> 00:04:25.949 it is broker and then you can go ahead and load the data.

50 00:04:25.949 --> 00:04:30.786 And then the data will be displayed here in Figure 1 the time domain data.

51 00:04:30.786 --> 00:04:35.800 The red and blue on the real and imaginary aphids.

52 00:04:35.800 --> 00:04:37.310 Ann.

53 00:04:37.310 --> 00:04:44.295 In this case, these boxes here they indicate the data structure and Emmanuel have a lot of information about this.

54 00:04:44.295 --> 00:04:49.214 But basically here you have to indicate how the data structure is at the moment.

55 00:04:49.214 --> 00:04:56.230 It is just 1F ID so all of these values are one so you can go ahead and do appreciate the information.

56 00:04:56.230 --> 00:05:01.529 And there, you basically have your spectral or frequency domain over there.

57 00:05:01.529 --> 00:05:11.209 Ann. You can see it's not properly centered so you can hit this zoom out button and then you can go ahead and zoom it in.

58 00:05:11.209 --> 00:05:14.291 Closer to a manual zoom again,

59 00:05:14.291 --> 00:05:18.560 I can type in numbers here minus 0.4.

60 00:05:18.560 --> 00:05:20.829 Mine is your .5 for example,

61 00:05:20.829 --> 00:05:21.300 loops.

62 00:05:21.300 --> 00:05:23.319

63 00:05:23.319 --> 00:05:27.029 Now he can type in one.

64 00:05:27.029 --> 00:05:34.824 How to do that plus or minus buttons to to achieve the zoom that you want so the first two are zontal zoom.

65 00:05:34.824 --> 00:05:37.889 These 2 are a vertical's room.

66 00:05:37.889 --> 00:05:46.550 And then the one on the bottom is a vertical school zoom with a factor of 10 in intensity to every time you go up is a factor of 10,

67 00:05:46.550 --> 00:05:49.620 so you just make it as you see fit.

68 00:05:49.620 --> 00:05:52.213 New bit of horizontal zooming etc,

69 00:05:52.213 --> 00:05:55.173 etc. And you can always zoom out,

70 00:05:55.173 --> 00:05:59.596 then you go to the maximum spectral width and you can of course,

71 00:05:59.596 --> 00:06:01.800 zoom in again.

72 00:06:01.800 --> 00:06:07.029 And indeed 2 boundaries are set based on the cursor positions.

73 00:06:07.029 --> 00:06:12.418 An traditional spectral parameters are you can do something from line broadening your phrases 3 hers.

74 00:06:12.418 --> 00:06:18.720 Gaussian requires an additional forget transformation and you can see that the peaks become a bit broader.

75 00:06:18.720 --> 00:06:23.646 Of course, his spectrum isn't properly in phase so you need to face corrected.

76 00:06:23.646 --> 00:06:30.009 This is zero order phase and there's also a first order phase as well.

77 00:06:30.009 --> 00:06:32.637 And then you can also do baseline Correction,

78 00:06:32.637 --> 00:06:35.495 an integration. I'm going to not talk about that.

79 00:06:35.495 --> 00:06:40.807 Today I will talk about briefly about the frequency referencing so if you click this button.

80 00:06:40.807 --> 00:06:46.000 You can pick you can pick the frequency the pic that you want.

81 00:06:46.000 --> 00:06:50.339 And then if you know the chemical shift and I think this will be water.

82 00:06:50.339 --> 00:06:57.819 Then we calibrated and now the access isn't in PM so you can zoom out again and then zoom back in.

83 00:06:57.819 --> 00:07:03.019 And you can see. Now you have your beaks at the chemical shift in PM.

84 00:07:03.019 --> 00:07:06.391 Can have a quick look at the other file as well?

85 00:07:06.391 --> 00:07:09.000 Where we have 180 averages?

86 00:07:09.000 --> 00:07:14.060 If you load in the raw data that job zero file.

87 00:07:14.060 --> 00:07:20.084 You will get a lot of data you actually get 180 FI DS because they're not added together.

88 00:07:20.084 --> 00:07:28.319 Yet so if you want to see all the individual ones you have to indicate that the number of initial Fridays is other than 80.

89 00:07:28.319 --> 00:07:32.149

90 00:07:32.149 --> 00:07:41.100 Feed and reload it. You know basically show you the first F ID and if you now do a free a transformation you now have.

91 00:07:41.100 --> 00:07:44.187 180 Spectra, he will display the full spectrum,

92 00:07:44.187 --> 00:07:47.918 but you can go to the second spectrum that dirt spectrum.

93 00:07:47.918 --> 00:07:57.050 All the way to the very end and so this allows you to see how stable your data is if there's any kind of artifacts or frequency drifts in the

94 00:07:57.050 --> 00:08:00.910 data and they can also be undone with these menus over here.

95 00:08:00.910 --> 00:08:04.220

96 00:08:04.220 --> 00:08:09.120 OK, so that's where all I want to say about the one dimensional data processing.

97 00:08:09.120 --> 00:08:16.624 There's a lot more information in the manual the manual can be found in the Dmi Wizard Directory and it is right over here.

98 00:08:16.624 --> 00:08:19.199 D my wizard version 1.1 manual.

99 00:08:19.199 --> 00:08:27.009 And it has a lot of information about the spectroscopy menu and also about the 3 dimensional.

100 00:08:27.009 --> 00:08:30.831 MSI menu and we'll talk about that right now,

101 00:08:30.831 --> 00:08:35.409 so. We can go to that menu.

102 00:08:35.409 --> 00:08:48.168 Is a fairly similar appearance again things with blue are spectral parameters things in green are associated with file loading things with red in this case are amaray related things

103 00:08:48.168 --> 00:08:52.234 and things were yellow. Our metabolic mapping parameters,

104 00:08:52.234 --> 00:08:54.477 so let's do the first thing is,

105 00:08:54.477 --> 00:08:56.620 we select the dmi data.

106 00:08:56.620 --> 00:08:58.416 Can go to the data directory?

107 00:08:58.416 --> 00:09:04.465 Now it is file number one directory number one that you're interested in and this being broker data.

108 00:09:04.465 --> 00:09:07.419 You need to load the raw data dot job 0.

109 00:09:07.419 --> 00:09:10.860 Again, this only selects it's loading it.

110 00:09:10.860 --> 00:09:15.162 Gives you some parameters in the matlab window about field.

111 00:09:15.162 --> 00:09:17.097 A few number of encodings,

112 00:09:17.097 --> 00:09:22.679 etc, etc. And then it shows you one of the Fridays in this window.

113 00:09:22.679 --> 00:09:26.563 Can you have your information again after selecting for example,

114 00:09:26.563 --> 00:09:31.289 inappropriate waiting you can do a free a transformation?

115 00:09:31.289 --> 00:09:39.554 Take of course, a few seconds because it's a very large data set and then here is the spectrum from disposition disposition.

116 00:09:39.554 --> 00:09:42.001 One eight one out of a data set 2D2.

117 00:09:42.001 --> 00:09:43.125 By 2 by 2 by 16.

118 00:09:43.125 --> 00:09:50.070 So it may be completely wrong location and that's why the spectrum doesn't look very interesting.

119 00:09:50.070 --> 00:09:52.662 So of course I deal with that is,

120 00:09:52.662 --> 00:10:03.413 you want to load in an associated MRI file that can show you where the voxel location is so go ahead and go to the data directory and now it

121 00:10:03.413 --> 00:10:05.394 is directory #4, the MRI.

122 00:10:05.394 --> 00:10:07.500 He loaded F ID file.

123 00:10:07.500 --> 00:10:10.190 Launch.

124 00:10:10.190 --> 00:10:19.895 And then if we ate information and you can see how the Phantom looks like it's a number of tubes with different chemicals in each of the tube so at

125 00:10:19.895 --> 00:10:21.928 the data set of the MRI is 96.

126 00:10:21.928 --> 00:10:25.667 By 96 by 64, so let's go to the centre slides right now,

127 00:10:25.667 --> 00:10:34.311 which is 2D2. And then will also go to the center location in a dmi data set which is a 2D2.

128 00:10:34.311 --> 00:10:35.788 By 2 by 2 by 16,

129 00:10:35.788 --> 00:10:39.000 so let's go to Z slice #8 and there,

130 00:10:39.000 --> 00:10:41.432 you can see the Red Square.

131 00:10:41.432 --> 00:10:46.789 That indicates the voxel location at position one in X.

132 00:10:46.789 --> 00:10:48.330 8 in Y an 8 Ng.

133 00:10:48.330 --> 00:10:51.408 It is the true plane dimension,

134 00:10:51.408 --> 00:10:57.279 so if you move the red volume to a more interesting location.

135 00:10:57.279 --> 00:11:02.000

136 00:11:02.000 --> 00:11:07.648 There we have a spectrum and so he began zoom in similar to the one dimensional menu.

137 00:11:07.648 --> 00:11:12.909 So that we can see all of the peaks and we can walk through the data.

138 00:11:12.909 --> 00:11:20.629 And. As such. Right they have different chemicals in different locations.

139 00:11:20.629 --> 00:11:24.019 OK, we can also display the data.

140 00:11:24.019 --> 00:11:28.230 By hitting this Emirates I button there.

141 00:11:28.230 --> 00:11:34.009 Will take a few seconds because it's it's quite a large data set to the 2 actually 2 bye?

142 00:11:34.009 --> 00:11:37.460 1024 data point I believe.

143 00:11:37.460 --> 00:11:39.120 With after a few seconds,

144 00:11:39.120 --> 00:11:49.399 he will show you, your 2 dimensional grids on this particular Z slides and you can see you have signal where the tubes are and there's basically no signal where

145 00:11:49.399 --> 00:11:59.105 there are no tubes. Now there are certain spectral that are in red an spectrum that are not in red there in blue now that difference is if a particular

146 00:11:59.105 --> 00:12:04.750 virtual location. The signal in that location is it above the threshold or not.

147 00:12:04.750 --> 00:12:08.785 In this case, these are in red there above the threshold,

148 00:12:08.785 --> 00:12:12.544 the ones in blue or not so by lowering the threshold.

149 00:12:12.544 --> 00:12:20.059 Let's say to 5%. We can change that and if we now show the spectroscopic image again.

150 00:12:20.059 --> 00:12:22.950 Then you will see that you have more red Spectra.

151 00:12:22.950 --> 00:12:27.500

152 00:12:27.500 --> 00:12:36.051 There we go, she's now pretty much everything that we want everything that we want to have signal has signal now?

153 00:12:36.051 --> 00:12:42.503 Why is it important that is important because some operations like linear prediction.

154 00:12:42.503 --> 00:12:49.553 They only work on spectral that are in red and that his basement done just to save some time.

155 00:12:49.553 --> 00:12:58.169 There will be an awful lot of data that have no signal and it will be wasteful to do complicated math on.

156 00:12:58.169 --> 00:13:00.590 Virtual location that have no signal.

157 00:13:00.590 --> 00:13:03.690 Charlottes quickly talk about linear prediction.

158 00:13:03.690 --> 00:13:10.460 As you can see if you load it in the dmi data.

159 00:13:10.460 --> 00:13:13.880 That if it is. Typically,

160 00:13:13.880 --> 00:13:22.152 the way they did my data is acquired it is basically a pulse acquire sequence with the phase encoding gradient in it.

161 00:13:22.152 --> 00:13:29.020 The presence of the phase encoding gradients basically delaye simple acquisition by a little bit,

162 00:13:29.020 --> 00:13:33.086 for this particular scene because it is 0.6 milliseconds.

163 00:13:33.086 --> 00:13:35.119 The spectral width is 2 1/2.

164 00:13:35.119 --> 00:13:36.941 KH making the dwell time,

165 00:13:36.941 --> 00:13:43.740 400 microseconds. So there is about a one and a half data point of delaye between the excitation.

166 00:13:43.740 --> 00:13:46.014 And the first point of acquisition,

167 00:13:46.014 --> 00:13:56.028 let's make that tool. There's two data points that are missing now linear prediction allows you to back calculate those 2 missing data points.

168 00:13:56.028 --> 00:13:59.397 So if you type in here 2 and hit linear prediction.

169 00:13:59.397 --> 00:14:05.149 You basically have to indicate the part of the spectrum that contained signal.

170 00:14:05.149 --> 00:14:08.844 And then you can see here it will do the calculation for 2500.

171 00:14:08.844 --> 00:14:11.249 Spectra that's already a lot of Spectra,

172 00:14:11.249 --> 00:14:13.125 but it goes fairly fairly fast.

173 00:14:13.125 --> 00:14:18.039 But if you didn't have to threshold if we would do it for all Spectra.

174 00:14:18.039 --> 00:14:24.879 Which would be 16,000 so you've definitely improved on the speed?

175 00:14:24.879 --> 00:14:29.120 So if you give it a second you will see that all of this process is done.

176 00:14:29.120 --> 00:14:33.059 All of the signals will be in face never we up and positive.

177 00:14:33.059 --> 00:14:40.250 At the moment, there, not as you can see because of that 2 points data gap.

178 00:14:40.250 --> 00:14:42.000 Cable almost done here.

179 00:14:42.000 --> 00:14:52.250

180 00:14:52.250 --> 00:14:57.460 And there, we are so now we have to display it.

181 00:14:57.460 --> 00:14:59.640 There we are so now if we now work,

182 00:14:59.640 --> 00:15:01.519 a little bit through the data.

183 00:15:01.519 --> 00:15:07.460 You can see that pretty much the picture up M positive if we go down a little bit here.

184 00:15:07.460 --> 00:15:11.245 Go to a different volume see all of the peaks are up and positive.

185 00:15:11.245 --> 00:15:20.057 Now there is important for the final step that I want to talk about which is the parameter mapping parameter mapping allows you to make an image of a given

186 00:15:20.057 --> 00:15:27.330 peak so for example, if we click here parameter map and we select the center peak right over there.

187 00:15:27.330 --> 00:15:34.677 He basically generate an image it integrates this part of the spectrum between the 2 lines and then displays,

188 00:15:34.677 --> 00:15:38.885 it at and as an image but that is a phase sensitive operation.

189 00:15:38.885 --> 00:15:46.610 The signals have to be up in positive if the sequence are out of phase you may end up with zero integral.

190 00:15:46.610 --> 00:15:49.166 You got to do that for other peaks as well,

191 00:15:49.166 --> 00:15:57.700 and you will see you get in a different spatial distribution because the chemical content of these different tubes is different.

192 00:15:57.700 --> 00:16:00.860 OK let's go back to the 3rd Speaker looked a little more interesting.

193 00:16:00.860 --> 00:16:03.850

194 00:16:03.850 --> 00:16:13.700 So we can also do is you can overlay this on an MRI and MRI is really loaded so if we click this button over here.

195 00:16:13.700 --> 00:16:15.881 And we do the parameter net again,

196 00:16:15.881 --> 00:16:20.350 then you can see that you can overlay it with an MRI image.

197 00:16:20.350 --> 00:16:21.443 And so you can see,

198 00:16:21.443 --> 00:16:23.630 there are images now in the background.

199 00:16:23.630 --> 00:16:28.224 But maybe it's not bright enough So what we can do is we can make the transparency.

200 00:16:28.224 --> 00:16:33.909 A little bit lower on the metabolic image and so you can see the MRI a little bit better.

201 00:16:33.909 --> 00:16:35.409 And so there gonna have it,

202 00:16:35.409 --> 00:16:38.570 he MRI in the Emirates Ioannou overlapping with each other.

203 00:16:38.570 --> 00:16:40.679

204 00:16:40.679 --> 00:16:47.076 We can also do an interpolation which that is more like a visual trick,

205 00:16:47.076 --> 00:16:51.253 but it can sometimes look look more appealing.

206 00:16:51.253 --> 00:16:56.761 If you will then you can have you have 3 types of images one?

207 00:16:56.761 --> 00:16:59.695 Is the native Amazon resolution.

208 00:16:59.695 --> 00:17:10.890 One is an interpolation based on FT and one is based on like convolution convolution typically gives the best results and the.

209 00:17:10.890 --> 00:17:18.579 This number 3 basically tells you how much smoothening has been done.

210 00:17:18.579 --> 00:17:20.950

211 00:17:20.950 --> 00:17:27.368 Final thing I would like to remark is sometimes you're not interested in all the signals.

212 00:17:27.368 --> 00:17:29.651 So you can draw an ROI as well.

213 00:17:29.651 --> 00:17:32.859 And so let's say that we drawn ROI over here.

214 00:17:32.859 --> 00:17:38.410

215 00:17:38.410 --> 00:17:41.589 Headsets if we now do the parameter map again.

216 00:17:41.589 --> 00:17:44.089

217 00:17:44.089 --> 00:17:50.204 You will see that. Now he only overlays a map multiplied with the ROI answer.

218 00:17:50.204 --> 00:17:52.159 This could be a good option.

219 00:17:52.159 --> 00:17:56.250 If you want to have a brain only ROI for example.

220 00:17:56.250 --> 00:18:01.619 Now this is an early version of the email is it in the next version.

221 00:18:01.619 --> 00:18:13.153 And is mapping these mapping options will be a lot more sophisticated way you can do multiplication of Maps and a bunch of other of other things as well.

222 00:18:13.153 --> 00:18:19.970 So I encourage you to check the website frequently for newer versions of Dmi Wizard again.

223 00:18:19.970 --> 00:18:22.291 This is only a quick overview.

224 00:18:22.291 --> 00:18:27.009 If you want to have more details you can find it in the manual.

225 00:18:27.009 --> 00:18:29.874 But this is all I wanted to say about it.

226 00:18:29.874 --> 00:18:35.883 Thank you for using the my widget and let me know if you encounter any problems.