BME 8730

Fall 2019

Jensen’s FIELD II speckle

1. Set up a speckle image using FIELDII. Use the transducer parameters from LinearArrayExample62. Use cyst\_phantom per the script. (20)

2. Now use our “homemade” code to replicate the simulation of a Point Spread Function (“wave”). (20)

3. Use convolution of the “homemade” PSF with the phantom and verify that a similar result is obtained. Find the cyst\_phantom m-file and replicate it as a 2D regular spaced array (i.e. matching the X-Z resolution of the PSF) and insert the required modifications – i.e. 100X increased amplitude point targets with respect to speckle random scatterer level and a cyst region with no scatterers. Note that you may want to down sample your PSF if it is excessively fine in either dimension. However, please verify that your PSF is not excessively down sampled either by explaining carefully why you believe your PSF is properly sampled or by showing results with, 2X finer sampling in X and Z, and that the result is similar (not identical because it cannot be). Verify that the Std Dev/Mean is 1.9 in a uniform speckle region. You need to be sure you are analyzing the enveloped data but not the logarithmically compressed (video) data. (20)

4. An intermediate approach is to take the PSF from FIELD and do a convolution with a speckle generating phantom target. Do this. Again, be sure that your sampling is appropriate – i.e. alter either your FIELD sampling or phantom sampling or both so that they are matched. (20)

5. Repeat 1 using dynamic receive focusing. Verify that point target resolution is improved in the near field in the presence of dynamic receive focusing. Look up the field m-file for dynamic receive and use reasonable inputs. (These are derivative from xdc\_focus – requiring direction angle instead of focal point) (20)

You may not get exactly 1.9 for your SD/Mean but I do expect it to lie in range 1.8 to 2.0.