QIBA VOL-CT Group 1A Update WebEx
February 19, 2009
12 PM CDT
Call Summary

In attendance:

Nicholas Petrick, PhD (Chair)
Kristin Borradaile
Charles Fenimore, PhD
Mario Gavrielides, PhD
Lisa Kinnard, PhD
Binsheng Zhao, PhD

RSNA
Susan Anderson
Joe Koudelik

General Discussion
Kristin Borradaile of RadPharm to provide protocol feedback to Dr Petrick from reader perspective

Filter (Detail vs. Medium)
Proceed with detailed filter (typical filter used for lung nodules)

Three size tools agreed upon
- 1-D measurement
- Bi-directional measurement
- Volume measurement
- Spiculated, lobulated or ovoid, spherical
- Reasonable approximations possible with lobulated/ovoid shapes

Location indicator at top of nodule to avoid bias?
- Control over nodule slice identification needed - where to set the 1st slice?
    - Nodule itself will be identified - generally, only one lesion per image provided to readers
        - No confusing merge of lesions for readers
    - Do not want to bias reader to central slice by providing too much information (i.e. providing reader with central slice ID)
    - Provide top or bottom nodule slice identification only proposed
        - Selecting the top or bottom slice might create a partial volume bias – bad
    - Readers need to determine the central slice on their own
    - xyz can be provided per case
    - Pilot study will tell if lesion location issues exist

Window / level variable or fixed
- Fixed or clinician adjustable (variable)
- Default to "lung-setting" or "lung-level" perhaps
- Need to record a variable window level also
- Density of nodules (used in dataset) close to 0 HU (+100 and –10 HU)
- Stick with FIXED window in pilot study – can be changed later

Size measurements in sets of 10 - randomization process
- Need to randomize the reads

- Lesions not done with all tools in the same session
- Two datasets (20 nodules each)
    - Sets A and B
    - Slice thickness at 0.8 and 5 mm (perhaps even 10 mm)
    - α and β by density (-10 and +100)
    - Group by sets of 10 to use same tool for many lesions
- Reading Session
    - Read with same tool 10 cases in a row
    - Density of 5 cases
    - Not completely randomized though
    - Latin Squares – variation would be in clusters of 5 cases
    - 2nd session – simply reverse the read process
    - Idea here is to control bias
- Pilot to be with 2 readers only studying 10 nodules only
- Both readers in pilot can read again in full study
- Dr. Petrick sent list of pilot study read cases to Kristin Borradaile at RadPharm for review and comment
- Dr. Petrick to post general outline? on the Wiki

Additional output formats for segmented data

- Should Siemen's output be converted into other formats?
- Is the DICOM format general enough?
- Feedback concerning output format needed

Other issues

- Triangular facets could produce refined pictures of nodule surfaces
    - Can be read by multiple scanners
    - PLY readers out there
    - 2-D contouring in 3-D programs may have new usage to determine volumes
    - PLY file – all readers should look the same and software should be consistent
    - Is DICOM more consistent?

Next Steps:

- Dr. Kinnard to look into nuances of the Siemens analysis package to determine output format and need for conversion?
- Dr. Petrick requests feedback concerning the protocol posted on the QIBA Wiki
    - http://qibawiki.rsna.org/index.php?title=VolCT_-_Group_1A
- Pilot scheduled for next week – depending on RadPharm schedule
    - Readers will only see files in Table 1 (pilot study)
    - Table 2 (full study) not sent to RadPharm yet