**Requirements for new File Format for storing whole study**

1. Structure
   1. Patient -> study -> series -> instance -> value
   2. Value: element/sequence
2. It must be possible to add one SOP Instance at a time
   1. Metadata
   2. Bulkdata
   3. Pixel data
3. Partial load of metadata only
   1. Retrieve all metadata for patient or study at once
   2. Selective load of bulkdata (large object)
      1. By Study
      2. By Series
      3. By Instance
      4. Pixel Data only
4. Distinguish between simple element and sequence
   1. Simple Element
      1. tag, type, value list
   2. Sequences
      1. Currently nested
      2. Would like syntax for flat sequences
         1. Id = sq.sq.sq.item.tag