Herbert Y. Kressel, MD  Hi. This is Herb Kressel. Welcome to this month’s Radiology podcast. Today I’m delighted to be joined by Dr. Vikas Gulani, Associate Professor of Radiology Biomedical Engineering and Urology at Case Western Reserve Medical School. Dr. Gulani is the Director of the MR at Case Western. Welcome Dr. Gulani.

Vikas Gulani, MD, PhD Thank you. Thank you very much for having me.

H.Y.K. I attended the last years ISMRN meeting and the buzz everywhere was about this new incredibly interesting technique MR fingerprinting and I was delighted to see a paper submitted by you and your group on MR fingerprinting in the abdomen. I suspect many of the people who are hearing or viewing the podcast may not be familiar with MR fingerprinting. Can you tell us exactly what is MR fingerprinting?

V.G. MR fingerprinting is a technology that we developed to provide very accurate and efficient methods for quantifying multiple parameters simultaneously in MRI.

H.Y.K. So it’s a way of getting rapid quantitative MR data?

V.G. Yes

H.Y.K. How does it actually work? It seems very complicated and sort of science fictiony.

V.G. It’s a very interesting method. What we do is that instead of modeling our images as some sort of exponential decay or exponential recovery, what we say is okay we’ll let the signal in MR vary in ways that we would never have tolerated previously. And so we generate very complex looking signal time courses very, very fast and then what we do is we go back to our knowledge of physics and we build a dictionary of all possible time courses that we can conceive of based on a possible range of the parameters that we could be measuring. And then once we have this dictionary we simply match the time course in each pixel to the best corresponding entry in the dictionary. When you match it, the numbers that went into creating that dictionary entry are the numbers that we’re after, for example T1 or T2. With doing this, we end up with very accurate, very fast maps and (inaudible) efficient and with much better than we had ever even hoped to go.

H.Y.K. The parameters that you’re varying are those like TR and TE and...

V.G. Yes, we can vary TR, TE flip angle basically anything that would have been previously thought of as a user controlled parameter. This can be varied in an MR fingerprinting sequence.

H.Y.K. With these dictionaries that you’ve developed it sounds like theoretically you’ve covered the range of all possible signal patterns, but is there a benefit to kind of keep adding to data based on knowledge of sort of this is the range for colon liver metastasis for example?

V.G. Yes, right now the way that we’re building the dictionaries, we’re taking a fairly general approach. That is that we say okay the T1 could range from a very, very small number to a very large number and we’ll vary the T1s possible through that entire range. This allows us to
stay general if you don’t encounter unexpected differen-
tes in your dictionary. In the future it should be possible
to build dictionaries that are more disease specific and
that is something that we’re definitely thinking about.

H.Y.K.  Good. Now it sounds sort of, I mentioned it
sounds science fiction, how computer intensive is this?
Do you need sort of all of the NSA’s computers to process
this?

V.G. Actually it’s surprisingly forgiving on the comput-
ing side. The hard work, the heavy lifting, is creating the
dictionary. But this is done once and you save it on your
apposition computer and then it’s there forever. Once
you’ve created this dictionary the process of matching
the patterns, the obtain time courses against the diction-
ary entries, this is actually very fast. It’s a very simple
task.

H.Y.K. Can I do it on my laptop?

V.G. Yeah you could actually. It would be a little slower
than what we would do on the apposition computer but
you could do it on your laptop.

H.Y.K. And speaking about slower how long does it take
to process the data? In this study that we’ll be speaking
about you had sort of 2D data that you were looking at.

V.G. Right. Since we have the dictionary stored, it just
takes a couple of minutes per slice.

H.Y.K. Okay. Now getting to your… I beg your pardon.

V.G. I meant a couple minutes for the whole cassette.

H.Y.K. Okay. The paper that we’re publishing in Radiol-
ogy is about applying the technique in the abdomen and
as I read it apparently in trying to use this technique in
the abdomen the variability in the B1 and B0 magnetic
fields caused a problem presumably because a signal in-
consistently varied across the field of view and over time.
How did you actually go about solving this problem?

V.G. B1 inhomogeneities are a known problem for ab-
dominal imaging particularly at high fields such as 3T or
I guess now-a-days intermediate field at 3T. These in-
homogeneities we expected to encounter. This was not
surprising to us, but when you have this problem then if
you have a signal time course that you’re modeling the
signal time course without including these B1 inhomoge-
neities, you know that your signal time courses are not
going to correspond to the actual (inaudible) that you’re
going to encounter. So we knew we needed to take care
of this. The way that we went about taking care of it we
said okay we could either build B1 inhomogeneities into
every dictionary entry as our variable or we could simply
measure our B1 and then add that to the dictionary for
each pixel. Pixel-wise add that to our matching process.
That’s the approach we took because we can get a B1
map in two seconds. So if we’re doing a breath hold total
of say 18 seconds, 2 seconds of that is spent on the B1
mapping and the rest on the MR fingerprinting acquisi-
tions that we’re after.

H.Y.K. Very interesting. Could you now tell us specifi-
cally about the study that is being published in Radiolo-
gy? What did you do? What did you find? How did you
actually validate the T1 and T2 values that you derived?

V.G. Right. What we did can be followed from figure
2. This is instruct, it shows a flow diagram of the work
flow. What we have and entries into the dictionary are
T1s, T2s and B1 values TRs and flip angles to basically
model a higher signal time course. The B1 can be derived
from the block sievert measurement that we took. Using
the block equations and this B1 map, then you have the
dictionary plus the B1 map; and then you acquire the sig-
nal. This is the signal evolution from the MR fingerprint-
ing experiment. The signal in each pixel is then matched
against this giant dictionary and then once you have this
matching process done the closest matched signal time
course from the dictionary, the T1 and T2 that we went into
creating that entry is the T1 and T2 that we’re after.
Those are the properties that we mapped out and that’s
what the technique spits out at the end. That’s figure
2 and if you go to figure 4 this then shows this process
in image format. Figure A or subfigure A in figure 4 is
a typical image from an MR fingerprinting experiment.
As you can see, it looks pretty bad and this is not some-
ting anyone ever used for any diagnostic purpose. This
is what the images are after but philosophically MR fin-
gerprinting says we are not after individual images, we’re
after the map so why bother trying to make our images
look really pretty, we’re (inaudible skips) maps. Then in
B you see a block sievert acquired map for this subject.
In C, D, and E you see MR fingerprinting maps that have
no B1 correction. In F, G, and H you see fingerprinting
maps that do have the B1 correction. In I, J, and K we
show the subtraction of these maps so J for example is
a subtraction T2 map, and T2 is where we see the max-
imum error from the B1 inhomogeneities. And you see
the B1 inhomogeneity contributions to those maps from
the difference image.

H.Y.K. I see. T1 and T2 mapping could potentially be
quite useful. I know for example in the heart T1 mapping
now is all the rage. What specific avenues of application
do you envision in the torso?

V.G. I see two huge directions that we would like to
take this in. One is that we in our group are trying to
go after a completely quantitative characterization of
lesions and that is that if I can create based on quantita-
tive acquisitions a space that includes T1, T2 diffusion,
profusion quantitatively. So you can have a multi-dimen-
sional space with which two quantitatively character-
ized lesions and could that lead to more definitive, less
variable characterization of lesions less dependent on
the skill of the reader and more dependent on objective
data? This could go to where it’s identifying types of lesions. The other major direction that we see ourselves going in, a huge direction for us, is the idea of response to treatment. Quantitatively, and before seeing size differences, assess response to treatment, again using a multi-dimensional space. This is sort of a holy grail for imaging in some senses because we’re all used to reading our CT scans that come two, three months down the road; and two-three months down the road we’re telling them well this one got bigger, this one got smaller, and A we’re not able to give really a proper response as to what is happening biologically in this tissue. And secondly, two or three months later the patient has been – if the treatment is unsuccessful, here she has been going through unnecessary treatment for that long and there’s could we get to an earlier tailoring of the treatment using quantitative approaches in imaging. That’s a big issue for us.

H.Y.K. Very, very interesting. It sounds like “beam me up, Scotty” work here, sort of like very, very spaceship. In the real world, where are we? Is this ready for prime time? Is this something that I could expect in a software release soon or is there a whole bunch of further development before people who are listening and viewing this will be able to use it?

V.G. We are using it quite a bit on our patients on a research basis. We hope that it is ready for prime time very soon. We’re working to get it out so that people can use it all out there. It’s around the corner.

H.Y.K. So around the corner in the next year or so or around the corner…

V.G. Yeah, hopefully the next year or so but we have to wait to see. These things take some time to iron out.

H.Y.K. I think this is fantastic work. It’s certainly a glimpse into the future. I’m delighted that you’re able to share the work with us and thanks so much for sharing your thoughts.

V.G. Thank you.

#### Dealing with Uncertainty in CT Images
Radiology 2016; 279:5–10
Joel G. Fletcher, MD • Shuai Leng, MD • Lifeng Yu, MD • Cynthia H. McCollough, MD

#### Virtual Monochromatic Images from Dual-Energy Multidetector CT: Variance in CT Numbers from the Same Lesion between Single-Source Projection-based and Dual-Source Image-based Implementations
Radiology 2016; 279:269–277
Achille Mileto, MD • Andrew Barina, MD • Daniele Marin, MD • Sandra S. Stinnett, PhD • Kingshuk Roy Choudhury, PhD • Joshua M. Wilson, PhD • Rendon C. Nelson, MD

#### Quantitative Features of Liver Lesions, Lung Nodules, and Renal Stones at Multi-Detector Row CT Examinations: Dependency on Radiation Dose and Reconstruction Algorithm
Radiology 2016; 279:185–194
Justin Solomon, MS • Achille Mileto, MD • Rendon C. Nelson, MD • Kingshuk Roy Choudhury, PhD • Ehsan Samei, PhD

**Herbert Y. Kressel, MD**

Hi. This is Herb Kressel and welcome to the April Radiology podcast. This month we have a rather special panel discussion with the authors of three related articles published in the April issue of Radiology and as these came across my desk I was reminded of a point in my radiology fellowship at UCSF where we were working with the GE Company on an early version of a CT scanner. We were having a lot of problems with clip artifacts and one of the physicists developed some software that he called rubout that would effectively remove both the clip and the artifact and give you a pristine image and everyone was so scared about altering the fidelity of the image that that program never saw the light of day. Now, we’re into very advanced image processing techniques that affect dose reduction and visualization and people have started looking at the effect on the quantitative fidelity of the underlying information as depicted on CT scans. And so today we’re joined by Drs. Samei and Solomon from Duke. Dr. Samei is Professor of Radiology and Chief Physicist in the Department of Radiology at Duke and Justin Solomon; we’re giving him the benefit of the doubt. He’s a PhD graduate student and Dr. Samei assures us that by the time the issue is published, he will in fact be Dr. Solomon. So welcome Dr. Samei and Solomon. Joining them, also authors on the paper by Drs. Solomon and Samei, are doctors Mileto and Nelson from the Department of Radiology at Duke. Dr. Mileto is an imaging research fellow in the abdominal imaging section. And Dr. Rendon Nelson of course is Professor of Radiology and Vice Chair for Research at Duke. And rounding out our panel is Dr. J.G. Fletcher who I asked to kind of look at these papers and try to make some sense of them and give us a rationale of how we might go forward. So let’s get into the nitty gritty here and I’d like to start with Dr. Samei and the paper that you’ll be discussing is “Quantitative Features of Liver Lesions, Lung Nodules, and Renal Stones in Multi-detector CT Examinations: Dependency on Radiation Dose and Reconstruction Algorithm.” Dr. Samei what was really the rationale for doing this study? Was this a matter
of sort of theoretical concerns or was there a practical, clinical issue that had been raised?

Ehsan Samei, PhD It’s rather a practical one actually built upon the experience that you relayed to us earlier. As I look at the CT, one of the major hallmarks of the CT has been the fact that it is somewhat quantitative and very precise compared to a lot of other imaging modality that we have out there. At the same time we do recognize that there are a great enough quantitative information that can be extracted for medical images and in the case of CT of course the precision of the CT would be of tremendous value in that regard. However, your experience you relayed to the fact that we have had concerns in the past that we don’t want to alter the appearance of the images because we are concerned that that might impact the precision and reliability of the quantitative information that we gain from the CT images. In the last few years we have seen significant changes in CT. Two major developments have been the development of iterative reconstructions which aim to provide a more high-quality rendition of CT images. At the same time there has been a great push to reduce radiation dose. We ask ourselves a question, if the we moving on to dose reductions to implement iterative reconstructions clinically and to reduce radiation dose aggressively, what would be the impact of that in the precision of the images that you would be expecting from CT, especially in the context of biomarkers. When we talk about biomarkers we should also ask the question what biomarkers. There is not only one biomarker. We essentially set to look at a series of biomarkers related to the morphology and the texture and the accumulation attributes of lesions of interest in lungs and kidney and liver and to see how those attributes are reflected differently as we change to iterative reconstructions and as we reduce radiation dose.

H.Y.K. I see. Thank you. Dr. Nelson the study that you all did, Virtual Monochromatic Images from a Dual Energy MDCT Acquisition Variance in CT Numbers from the Same Lesion between Single-Source, Projection-based, and Dual-Source Image-based Implementations looked at the specific issue of CT numbers and the monochromatic images that can be derived. You choose to do a phantom study and what was kind of the rationale for looking at this and looking at it that way?

Justin Solomon, MS Sure. We had this nice data base of images, locations that had known lesions, three different lesion types. We looked at liver lesions, lung nodules, and kidney stones. We had images at two dose levels, 100% dose and 50% dose, compared to standard clinical dose; and then three different reconstruction algorithms; traditional FBP and the ASIR reconstruction algorithm and model-based iterative reconstruction as well MBIR.
We took all these known lesions, we took the images and we did a series of quantitative assessments on them so we extracted a total of 23 different quantitative features and we drew upon the radiomics literature to decide what features we wanted to look at. They described things like the size and the shape, the attenuates and the edge blurring properties, the distribution of pixel values and the texture features. So we extracted all of those features and did some statistical analysis to look at how reducing radiation dose or changing the reconstruction algorithm affected those quantities. Essentially we were kind of overwhelmed with the number of different results we had. There was a lot of stuff going on in the paper, but to kind of summarize, we found that both dose and reconstruction algorithm affected the quantitative measurements of various different features. But overall kind of the largest effect we saw was from some MBIR affected the greatest number of different features.

**H.Y.K.** Okay. What was some of the magnitude and the differences in the size of lung nodules, renal stones, or CT number or texture differences? Give us an idea of the scale of these changes.

**J.S.** Sure, so for example we saw that with lung nodules and renal stones they were about, the volumes for example were on the order of 10% lower when you used MBIR versus filtered back projection. When we looked at the texture features there was kind of a wide range on how they were impacted, but on the order of 15% to 30% differences depending on which reconstruction algorithms we used.

**H.Y.K.** Those seem like pretty sizable differences. They’re not sort of in the noise I would say. In this case I guess they were in the noise, but in conventional parlance. Anyway, what were some of the key findings of your study Dr. Mileto?

**A.M.** Basically we applied a multivariate aggression analysis to our data both polychromatic and monochromatic. And basically we saw that with changing variable with the same changing variable under the same condition basically, so the two scanners were responding in a different way when they were operating in single energy or in dual energy modes. Of note, when the two scanners were operating in a single energy, polychromatic base mode, what was happening is that of course there were differences between the two scanners in (inaudible) or for example the KDP. But when we associated this variable to the scanner style basically there was no significant effect of this variable on the differences in polychromatic CT number between the two scanners. As opposed to that, with monochromatic imaging we saw that when we change the same variable with different scanner, that scanner will respond differently to the changing variable. Of note, we saw that there was a 30% difference in monochromatic CT numbers as a function of the iodine content and the energy level. In particular these changes were most pronounced at the low KV and with the low or higher concentration investigated which was .8 mg (inaudible).

**H.Y.K.** Dr. Nelson were you surprised?

**R.C.N.** Well I expected it to be some differences but it was more than I expected. It’s a tough issue because as you know and J.G. knows I really believe that to a certain extent interpretation of CT is an art more than a science and maybe it’s less than a science than I’d like to believe. I don’t know I’m struggling with that.

**H.Y.K.** You know I don’t know if you saw, but we recently published a special report I can’t remember the exact title but it was something like CT images are more than images they’re data. It was whole idea of the -omics revolution and kind of looking at these features and then if these features are evanescent they’re sort of data minus it seems like. So Dr. Fletcher with all of this in mind I called upon you a rational mind from the Mayo Clinic who has sort of thought and written about these issues quite a bit and I thought that the editorial you did with your colleagues at Mayo was wonderful. How should we make sense of this?

**J.G. Fletcher** I was on a scanner this morning and the first two cases are always outside cases. They look a lot different than what I’m used to looking at. We’ve known for a long time that CT numbers and some truth it’s really dependent on the x-ray spectra, the detector, the patient. If you do a CT scan on a different system it’s going to look different. As I’ve looked at these things I’ve kind of thought well there’s two aspects. There’s the visual interpretation that I’m doing and then there’s the quantitative aspect with Dr. Solomon and Samei did. When I’m looking at a scan for the first time my main job is to detect what’s abnormal. So I really want to do whatever I can to maximize the detection of that abnormality. That might be (inaudible) imaging, it might be dual energy imaging. I’m aware that the images look a little different when I use iterative reconstruction or when I get a monochromatic image. But if I can only give a small amount of contrast for example or if I’m looking at a hyper-attenuating lesion like an HCC, I’m going to use everything in my arsenal. I’m not going to worry about you know because a patient hasn’t been imaged before. I’m going to use whatever I can at the moment. I think that when you get into follow-up scans then you do want to try to use the same technology or if you did a multi phase scan you’re going to want to try to do the same type of scan. We do that in clinical practice. But I think that there is a divergence when we get to using iterative reconstruction in terms of those quantitative parameters that people need to be aware of and that you know if you look at for example the paper by Dr. Solomon and Samei that there wasn’t so much textural features that were changing when they kept the filtered back projection at the lower dose. I think that over time there is going to be more of a divergence between what we need to look at visually so that we can see the difference versus what we would look at textur-
ally where the textural features are actually teaching us something that we cannot perceive.

H.Y.K. But there is this interface where you’re measuring a lung nodule over time, someone with a screening CT and they come to you and you have to measure the lung lesion and people are already struggling to figure out how much of a change is a real change or with adrenal lesions you’re looking at CT number changes all the time. Yeah, I think you’re right. I love the way you conceptualize it but there’s already more of an interface between the quantitative and the morphologic I think. Doctors Nelson and Mileto where do you think we are with this? How are you going to use this information in your own practice?

A.M. That’s a very tough question. For sure I think radiologists, I mean especially radiologists who are really interested to join a dual energy and (inaudible) program should watch out when we, so basically when they look at the same lesion in longitudinal study with different platform. Because we believe these differences might be due to differences in the CT and it might be deceiving attributed to changes in that (inaudible.) I mean for example in renal lesion imaging where the radiologist are accustomed to use CT images with some defined threshold that might be a problem.

H.Y.K. Dr. Nelson I’m not sure, but I suspect, that there are people who are going to be watching and listening to this who already have a dual energy CT or they have a single energy monochromatic capability and a department that has other scanners that don’t have that and I bet that’s the case at your institution. How are you planning on doing your work?

R.N. First of all, I think the changes that represent size are probably more important to me. I think we rely more on size reproducibility than we do on attenuation reproducibility. We assume that there are going to be differences. Most of the time when we look at something as attenuation we’re not really comparing with attenuation previously, we’re looking more at its attenuation relative to a pre-contrast or something like that. I think we generally don’t rely on those differences from different time points as much because we haven’t been able to over the years. So I don’t know if that will really change. I’m more bothered by the fact that there’s differences in size relative to what Dr. Samei and Dr. Solomon found.

H.Y.K. Dr. Samei what do you think we should be doing with this? Are we in a spiral we’re not going to get out of or is there some way to think about this so that we can have a bit more consistency?

E.S. This is an enlightening discussion. I’m very happy that we’re doing this. To me I think there are two ways to take this. One would be taking it more of a perspective approach and the other one is taking more of a retrospective approach. But prospectively, I’m talking about how we can adjust the way we do patient imaging so that we can take more of a quantitative information, more relevant and consistent quantitative information from patient images. In that regard I think we need to first of all realize as we adjust various attributes of image acquisitions such as dose, we need to realize what is at stake, what is what we’re potentially compromising in that regard, number one; and number two where we should put our priorities. For example, I was surprised by the fact that the impact of the constructions on the features that we were extracting from the images were larger at the impact of dose. I would have expected the other way. If we are putting our priorities or interests, our funding, our attention, to reduce optimization, perhaps a larger fraction of that priority should also be given to other attributes. That’s more of a sort of prospectively adjusting things to make it better. But the other way to also take this on is to think about retrospectively what we can do and hope we have already acquired images with whatever program you have, what are you going to do. If you could understand the sort of dependency of space there might be a situation which you can take the data from one algorithm or scanner and adjust it 30% up or 30% down and say okay we’ve got the level of calibration are we being able to relate numbers that are acquired from different protocols?

H.Y.K. That’s a very interesting idea. The other podcast in this month’s issue relates to MR fingerprinting and there they’re actually looking at the signal intensities against what they call a dictionary which is basically a library of pre-modeled signalate patterns from a variety of quantitative MR parameters and then you make an image by fitting the signal you have into the library that you’ve gathered. So that’s a very interesting idea. Dr. Fletcher the other thing that you covered that I think has really struck me is the implications for research particularly multi-center research and as I was thinking about it in this discussion today, we’re hearing a lot about big data and the people who are skeptics saying there are two things you can say about it, it’s big and it’s data, but if you have in all these inconsistencies that may or may not be well modeled, I think it could get very tough to understand how do you kind of put this, you know if you have a well controlled study and you know the scanners and you know this is one thing, but if you’re looking at kind of the pooled data from 200,000 people that have undergone a CT scan, it’s hard to image that you can just assume that it’s all going to sort of come out in the wash without accounting for it as a confounder. How do you think we should think about multi-center research in this context?

J.G.F. Well I think it’s going to be a lot more complicated and it’s going to involve phantom experiments to make sure that the things that you’re testing are reproducible because otherwise you are going to have a hot mess and what you can come out with are only those preserved features across your dose and reconstruction levels.

H.Y.K. Right.
J.G.F. I’d like to, and I go back to another point which I think is the dose issue that was raised. I think that iterative reconstruction as we know is the spatial resolution is contrast dependent. You can lose low contrast size as you go to very low dose. We’ve seen that with renal stones clinically and things like that and it’s interesting to me that with the Remy-Jardin paper they – you know I struggle with why do they come up with the same answers with a dose reduction and iterative reconstruction, whereas with the liver and kidney things were not.

H.Y.K. I think it’s the high versus the low contrast issue.

J.G.F. Yes and I ask Norbert Pelc at RSNA about some lung nodules, we had a very low dose study we did with lung nodules, and they were getting smaller. I asked him why that was and he says it’s because you’ve taken a high contrast test and made it a low contrast test by doing it at such a low dose. I think that if someone has metastasis or we’re looking for metastasis let’s not worry about a 50% dose reduction. We don’t need to worry about that and we can keep it at high dose and still throw on the iterative reconstruction and we keep it at a high contrast task. But I do see outside studies where people are doing things at such a low dose and they’ve thrown on the MBIR or the sapphire and it’s a hot mess.

H.Y.K. Dr. Nelson what do we do about research?

R.C.N. I think there’s more room for quantitative studies but this is a real problem. We not only have a lot of data and we’re not sure what to do with it. The whole other thing that’s involved here is not just the attenuation but you can measure iodine concentrations on material decomposed data sets and water concentrations and we’d like to think that those were quantitative as well but we don’t really know. I think we need to stick with the Hounsfield units and figure that out before we start moving to another complete different paradigm.

H.Y.K. You know there’s this huge push and in our journal we see it all the time for these biomarkers that are image based biomarkers that are diagnostic and prognostic. The results are actually quite encouraging but the concern is that as we get more and more use with these techniques and less and less control over the variability that they’re introducing we’re going to sort of undermine the integrity of the biomarkers and the biomarkers have a process for being qualified as a biomarker, but the qualification may be done on a group of instruments or settings that are not appropriate for the way it’s used subsequently in research. This really seems like something that our organized professions, societies, and manufacturers need to kind of deal with. Personally, I don’t think we’ll do ourselves a service if we just go back to being pure morphologists and ignore all the data that’s actually imbedded in these, but we’re not going to do ourselves a service if we start spewing forth numbers that really air bars are bigger than the effect size.

E.S. If I can add to this, essentially, I think talking about quantitative imaging we don’t have an understanding of the size of the air bars becomes meaningless.

H.Y.K. Right. Well on that merry note, Dr. Fletcher you always have a way of putting a nice spin on things, you want to have the last word?

J.G.F. One thing that this brought to mind is about a year and a half ago we started, Jeff Fidler did a study looking at bone strength from CT colonography scans we’ve repeated that with enterography, and before we implemented it we thought well you know we turned KV selection on, we have iterative reconstruction, how are we going to know we’re going to get the same numbers. It really wasn’t, I have to say I thought it would be a big deal, it took about a month. We only scan people a certain number of ways. We did every kernel, this iterative reconstruction, that iterative reconstruction, gave every thing to the company that does this and they came back with very reproducible numbers. We have to do the due diligence but it may not be as terrible as it sounds.

H.Y.K. I want to thank you all because I think you’ve raised a very, very important issue. Obviously we can’t address it at this point but I think by understanding what the issues are and sort of working together to get a path forward, hopefully we’ll be able to be able to have the benefit of the quantitative reproducible data. Thank you all for participating.