Thank you Dr. Sunil and can you project my slides?
So it is quite interesting that now we are talking about digital path in almost all the
specialties of the pathology and it is becoming integrated part of the directing diagnosis
and that is why we must admit that digital path and AI is the future or the fourth revolution
in the diagnostic environment, Teriam and how it is different from the conventional pathology
rather than seeing the slides or everything working under the microscope.
Now we get the opportunity to work on the computer screens similar to the radiologist
and this AI assisted tools also helps to give the more precise diagnosis and assisted diagnosis.
So is it, are we ready to sell our microscope?
This is a question which every pathologist asks or are we going to lose our jobs to these
AI tools they are also questionable.
So there are a lot of applications of this tool but the major it has started with the
education research but now many applications are coming to the clinical use or for the primary
diagnosis.
So the good thing is the many research activities they are moving towards the clinical use and
there are immense benefits of this technology because it not only improved the quality
but also increased the productivity of the pathologist and we can give the more dedicated
time to the specialized field.
A specialist called, pertaining to the oncovatology, the AI and digital pathology help to bridge
all the various modality on a single platform and it can have a diagnostic, diagnostic,
predictive and prognostic rule.
So not all the field of the diagnostic and the mentarium can be taken care if you use
the digital AI tools in the routine practice.
So this has been observed across various tumor types and across their various application
right from the survival prediction, mutation prediction and response predictions but the
development of these tools, we have to just understand they are various, these algorithms
are either at the cell level, tissue level or even patient levels and then the more futuristic
rule is to bridge all these applications together so that we do not have to go looking
for the single single application at one time.
So this was just a background, rest of the talk I will focus for mainly for the lung
and how it is helping the digital path and AI fields are helping in the lung cancer because
this is a lung dedicated lung cancer sessions.
So it can have a various application right from the counting of the tumor quantification,
segmentation and classification of the tumor to the predicting the genetic profile and even
the outcome.

So just to start with the diagnosis, we make a diagnosis using at the morphological pattern,
use some ISCs and then offer a diagnosis of adenocarcinoma, squamous or small cell carcinoma
and then tissue is usually subjected to the molecular testing but how AI can help based
on these models, they can even on the biopsy resection or even on the frozen sections, you
can predict whether the tumor is adenocarcinoma versus the squamous carcinoma but the level
of confidence is still between the 7 to 2 in 90% and this is improving day by day with
the more advancement.
So once if the level of confidence increase or improved beyond 90% it can be used in
the clinical practice.
The second application which AI can or these tools can help is the tumor quantification
which is essential part for people who are going for any molecular testing.
So what these tools do, they segment or identify the tumor focus from the background stroma
or necrosis or inflammation and it help to give the more precise and quantification of
the tumor area which is very much essential for the molecular testing.
So if once you have a case and upfront we have information which is more precise as compared to the interobservant variability and in addition to these tools they can also
measure these tumor area.
So we have a more precise help can be offered to the molecular diagnostic assay but at the
same time we have to be careful for some false positive or false negative like macrophages
or the normal mucosa which can be also sometime misdiagnosed.
So the training of the algorithm is very important for that.
Another application which is called as a 3D digital path because why I am talking about
this especially in the lung cancer because we are more and more interested to push that
issue for the molecular diagnosis.
So what these tools do, so they scan the paraffin blocks similar to what is done by the routine
CT scan or the imaging technology and they create a virtual image so without cutting
any slides or the blocks you can get the information about the tumor content present
in the blocks.
So it can upfront help to identify which particular block is to be used without wasting any time.
Another application for even at the site time of the biopsy procedures like instant digital
pathology.
There are some coming application which can even create the image on the fresh tissue
so like this is an instrument called viva scope so it can help to even at the time of
the biopsy.
So there is a you can try the tissue directly for the molecular diagnosis and it was also
showed by that the block or the tissue course which have a more of the tumor

content or
significant tumor content can directly move towards the molecular testing.
So even so it can be very exciting to get the molecular reports like a GFR or those even on the same day as that of the procedure.
So this technology was it the paper was present in one of the conference where on the same
day using this and idealize a platform for EGF, the report was available to the clinician
on the single day.
Another important thing which we do as a pattern identification of the tumor and here
also AI applications can be of help because they can there are models which can predict
the which patterns of the tumor is present on the biopsy or even on the resection specimens
which but the problem is that when we develop these models there is a lot of inter observer
variability and there is you can see this paper has come which in which involved around 18
pathologist and there is some variability in establishing the ground truth.
So we have to be very careful when we adopt these models but it has immense potential
at least it can grade the tumors as per ICLC and high grade patterns like micro papillaries
solid they can be easily predicted.
Another application is about the identification of lymph node metastasis which can be used
across various types but it also has some challenges especially or the confounding factors
especially in the long granum metastasis inflammation can be can cause a problem and in Indian context
and thoracotic frequency.
So the algorithm which are developed in western population might not be applicable here and
there are a couple of other problems and in lymph node metastasis the prediction of the
metastasis focus can be variable but with now with the new application that even these
algorithms can help to predict even micrometasis.
So just this is one of the models which we are using in our labs what they do first they identify the lymph node and then identify the tumor focus and it gives the tumor area
as a heat map.
So it is very easy for the pathologist to reconform whether the metastasis is present or not.
Another next application is about predicting the mutation profile and which is also of
very keen interest.
So even if on HE images if you can get a information about the EGFR or the common alteration it
can be a very good help and it can also help to try the patients like these patients
should be must be tested for these alterations and we are also doing a couple of these studies
and both also on the imaging that is Dr. Abhishek has published this paper based only on the
imaging and also on the on the on the tissue which is another.
Next application is about the predicting the response of the of the tumor or how the tumor

is going to behave based on the HE image.
So this is called as a word like a HE 2.0 that means you can predict the behavior of the
tumor only on the base at the baseline information it can be very useful application.
So all these application how they are beneficial to the clinician the major benefit to the
clinician is it can reduce the time and very significantly and they as a pathologist we
can try the samples and use these new diagnostic modality very more carefully.
So this was about the various AI application.
So another application of AI is about the quantification of immunostains especially they
help to give the very objective scoring of of of the tumor like just to give the example
of KI 67 which is a use used very commonly in the neuroendocrine tumors.
So these applications can help to give you as they are more very reproducible reliably
we can use and earlier we used to use this as a bigger snapshot of this and count positive
or negative images but they now they can be very easily counted by using these software.
But one thing we have to be very careful when you are using especially for the KI 67 it
is not very strong or dark looking brown cells we have to take into account but also various
variable intensity.
So whenever anyone you start using these technologies we have to be very careful what
the algorithm is trained for and not to miss any weak positive cells.
Another problem which a person can face when we are using them as a whole slide imaging
there should not be any false false positive areas which are which are detected by the
algorithm like just to give you example here the lymph node in this is a metastatic
tumor in the lymph node and even the algorithm is counting the normal lymph node.
So the selection of the area of the region of the interest is also very careful briefly
about PDL1 we know that PDL1 is one of the very promising biomarker but it it has some
concerns related to the interpretation and the scoring.
So AI applications are in process of development but they are not very well established as
compared to the HART2 which is a HART2 ERPR in the in the breast.
The main reason is about the challenge is the algorithm do not have to only count the tumor
but also need to segregate the the the background immune cells or the stromal cells which can
also show the shows the expression.
So that is why the the PDL1 interpretation is little challenging especially in the lung
cancer.
So the but in future this will also come into the practice because many researchers are working
to address these common challenges about the PDL1 and there are multiple multitude studies
where it has been demonstrated that the level of confidence is improving day by day and
the high level of confidence was seen with the Wenton ISP 263 because the staining

is
more bright.
So anything which is more bright crisp is easy for the algorithm so to interpret.
The future is hope is that these all algorithms will come as integrated with the routine workflow
on our computer screen and even for the other biomarker for the immunotherape we know that
it is not only PDL1 but we need or need also to quantify the immune micro environment and
which will not be possible using the single ISC.
So we need to use the multiplex ISC is more and more in future and so but the quantification
of them is challenging and towards the end we are moving towards the world of a generative
AI where all these application are integrated into it and these are the couple of the models
which came in last couple of years which say that region language that means based on the
whole slide these algorithms will not give you information about any specific type but
also completely generate a report which can be a little dangerous for the pathologist
because there is a fear that we might lose our job.
So this is one of the model is you can see on the whole side images the auto generators
the reports are auto generated and the various parameters are coming up.
But whenever we include a human in this along with this algorithm the interpretation is
and the output of these algorithms improve a lot.
So towards the end we have to use these all applications as a multi and it provides a
good opportunity to discuss in the multi issued disciplinary way and so the finally in the
lung cancer we have lot of potentials like tumor detection classification and micro environment
analysis and these applications will increase day by day and the AI applications will become
a routine part of the routine of the diagnostics.
So with this I thank our digital path team and we have to move away from the microscope
to the computer screens in future.
Thank you.
Thank you Dr. Rajee for the excellent talk we can take one or two questions.
Yes.
You presented a data kachnoma slides with it within a spatter of the digital side.
Yes.
Is it the new observation or previous view also you have been observing the technology.
So this is not a new observation but these are the various patterns and out of them the
certain patterns have high chances of like aggressive behavior like solid growth pattern
microbapillary growth.
So but the quantification is based on the just eyeballing by the pathologist.
So it is even in the resection specimen we have to quantify and give the percentage of
each component.
So that is as per the recommended.
But now AI algorithm can help to identify these patterns.

That was the second part of question whether you know you think AI algorithms are helping
you to pick the rare admixture of the cells and patterns in more efficient manner.
Yes.
So it will definitely help because you will not it even if there is a small component
even 5 or 10 percent which can be missed by the routine observation can be picked up.
But at till date we have to reconform as a pathologist whatever the algorithm is picking
is right or wrong.
So if you do say the right term we can identify each.
If our weather is exon 19 or 20 10 but can we be able to go deeper with the rehabilitation.
So these algorithms has not matured enough.
So right now they are just based on the because they are trying to analyze site new mainly
nuclear features and further going deep into the cells to identify especially for the molecular
profiles.
So right now they can just predict it is present or absent and rather than going but in future
it might be possible.
And that needs more large data set of various other different type of alterations.
Like you need a large data set of common mutations and even including the rare mutations
then only it can help.
So basically it is a probability as of now suppose if there is no EGFR or no targeted
mutation identified by AI at least you can put the patient straight away on chemotherapy
without wasting without anticipating for that thing to occur.
And even if if algorithms say that it is likely to do that case immediately for rather than
testing.
So it will help to try your cases which rather than putting them in a queue it is better
to push those cases upfront for the testing to the molecular lab which are likely to show
the rotation.
But that is with the belief that you only get funds for the negative but there can be
positive also.
Yes so that is when we need a definite confirmation.
So molecular right now it will not go.
If you just like negative then you can push it to be much happy it may not be right.
Yes I still need to test them because this may be false negative actually and you may
still find an EGFR organization.
Then such time these become the robust like I play this game with myself every time.
Whether this will be a false game this will be EGFR positive.
And I check that.
So it is possible on my form J2 really you know like I will say with 50% success to predict
that this will be EGFR and for loss because that can also go overlapping.
But that is what I wanted to say that the eye can still be positive.
Yeah so only this is evolving field so we will come to know about how much.

People should not go over with that belief that if we are saying negative.
Yes yes.
So a great talk actually and any role in FNAIs so can they read the FNAIs for you.
So FNAIs see even for the digital they are always challenging because they are not at
the one plane.
So even the scanning or digitalizing them was challenging but now they are more advanced
digital scanners has come which has started to pick up identify those nuclear features.
But cytology is more challenging as compared to the tissue because the cells are not at
the same level.
So as compared to the conventional FNAIs people especially for the cervical cytology for
the capsule where LBCs are used.
So that can that is being used as a very common tool for the screening of to pick up the LBCs
and those.
So LBCs has an advantage but conventional cytology is still challenging for these AI
algorithms because cells come at the one level.
Yeah.
And the features like neuro cells, micro-vesculine and cities also see can be also be different
based on using different types.
Yeah so all these whatever issues which we face for the routine diagnosis or the background
or the cell or micro environment they can well be a study but we need a different application
separate application of the models which are trained to us.
So that is why the generative AI which is it is trying to bring all the information together
using various applications like even counting mitosis, necrosis, timber area.
So these foundation models which are came up in last one to two years they try to bridge
all these individual applications so that at towards the end we get all integrated and
comprehensive reports rather than going for different application software for analysis.
And do you foresee that there will be a universal application for all these technologies or will
it be the tumor types actually?
No so it is because primarily you look for mitosis you look for the same characteristics
of grading so will it be universal or not?
No it can't be universal.
No because the tumors do not read the books so wherever there is a very crisp boundaries
these AI applications work well but where there are grey zone areas it will be difficult.
No there are certain features they take into account the optical density of nuclei and cytoplasm
the regularity of the margin the thickness of the nuclear envelope and the cytoplasmic granularity
the alignment of the nucleus with the surface is it moving the longest direction is moving
at 30 degree 40 degree or is it at 90 degree.
So there are several.

No no they they they they they they they.
No the cell boundaries defined the nuclear envelope thickness is defined in a section unless it unless
there is one tumor which is syncycial even if it is syncycial it will still have a cell margin
probably the digital scanning can identify those cellular margin so there are several common
features of malignancy which the AI platforms can identify.
So you must stop of the nuclear storage.
Specific to the histology.
Yes.
So just one last question you mentioned that with the large data you can train a good AI.
How large your data set needs to be.
No so now this is a common challenge which people also feel so it is a so why we need a large
data set because we know want a model to be more and more more robust.
But sometime it is practically not possible so in addition to the large data set if you
have a different very data set from the different geographic zones that is also important.
So it is not only the number but also the diversity of the data set that is also crucial.
So that is why you need the algorithm which is developed in US or Europe and even if it
is FD approved might not be really reliable for us.
And people has tried TCGA as a database but the image qualities were not used and once
they tried these models in the TCGA data set they work well but when we start using so
even the EGA firm model which we are validating it worked well for the TCGA but not didn't
work well for us.
So there is a problem there are problems.
Yes thank you.
And the whole reason why I was asking that question is because the EGA power that you
presented is coming from nearly 10,000 samples of our data hospital and still that is not
adequate enough we need more.
So an appeal to all the clinicians when I come to you asking for 10,000 samples or 20,000
samples don't look at me like I am crazy.
Now there are some other clinical experts who are also agreeing that you know this sample
size is required.
This foundation medicine models they were developed on the 40, 40 million whole slide
ges sample.
So data is like a huge gold mine for all of you.
We need more data.
Yes.
Thank you.