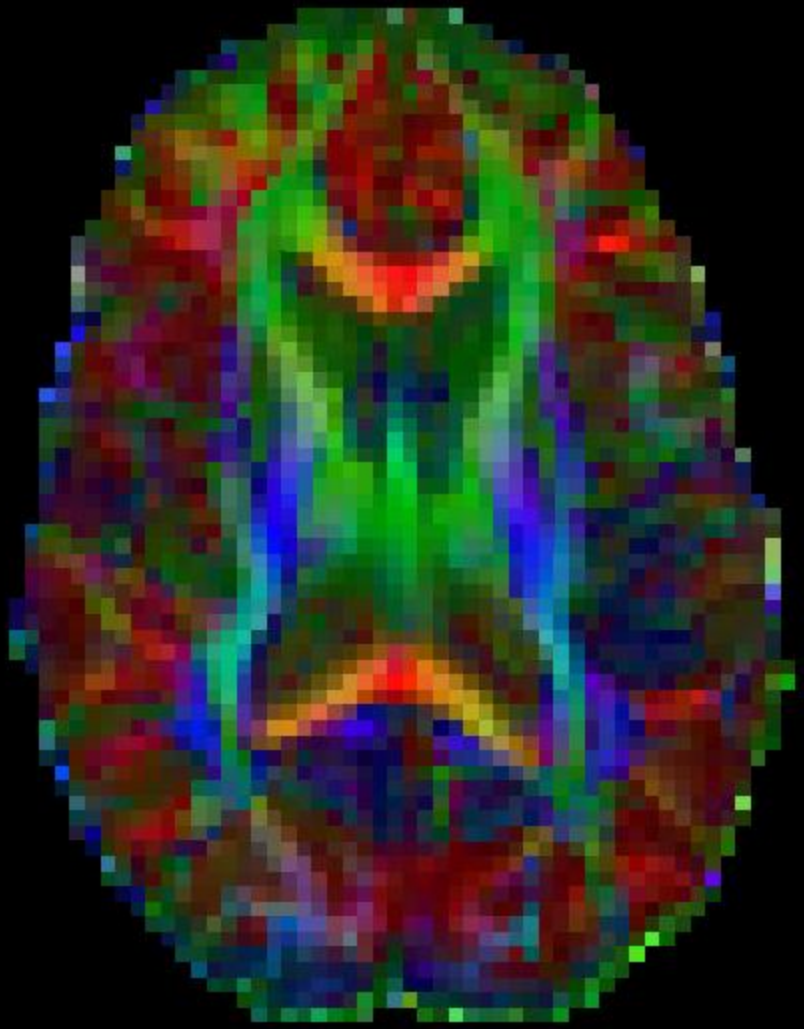
Tractography

..reconstructing tracts from FA and eigenvectors

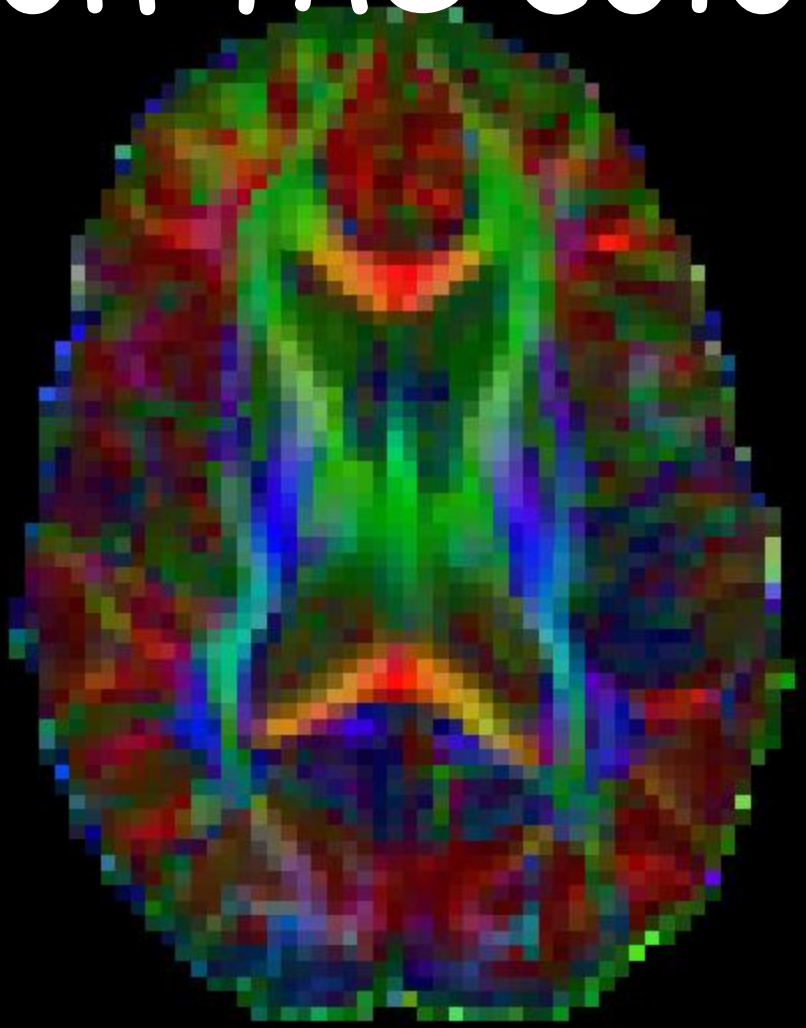


The goals are both display and discovery.

It's hard to examine a tract

that weaves in and out of the plane of section.

And, on the color map,



a tortuous tract changes colors as it meanders through the brain.

So, we want to reconstruct the tracts, and view the results in 3D.

There are lots of algorithms,

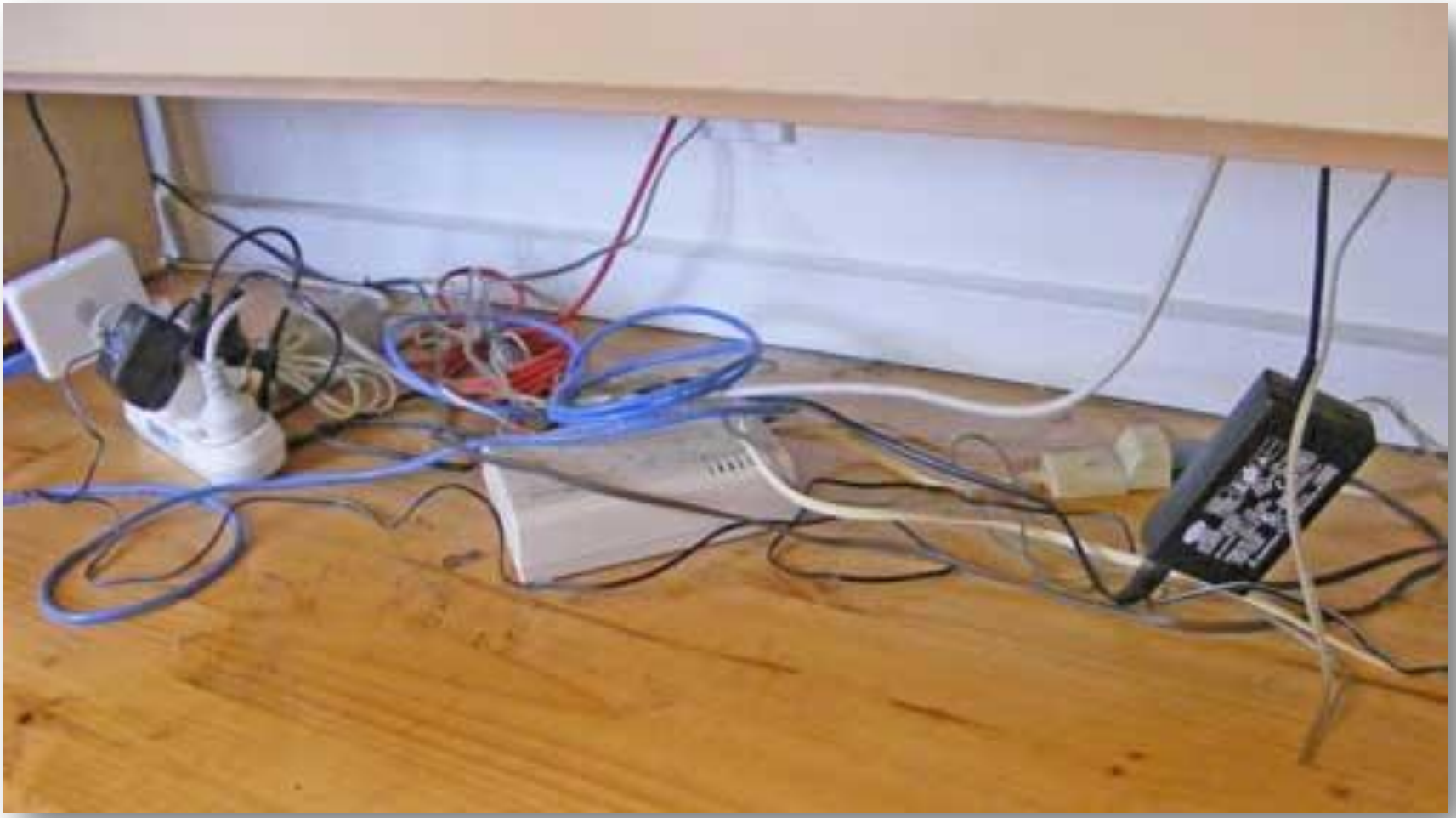
But 2 broad approaches:

1) Deterministic tractography

2) Probabalistic tractography

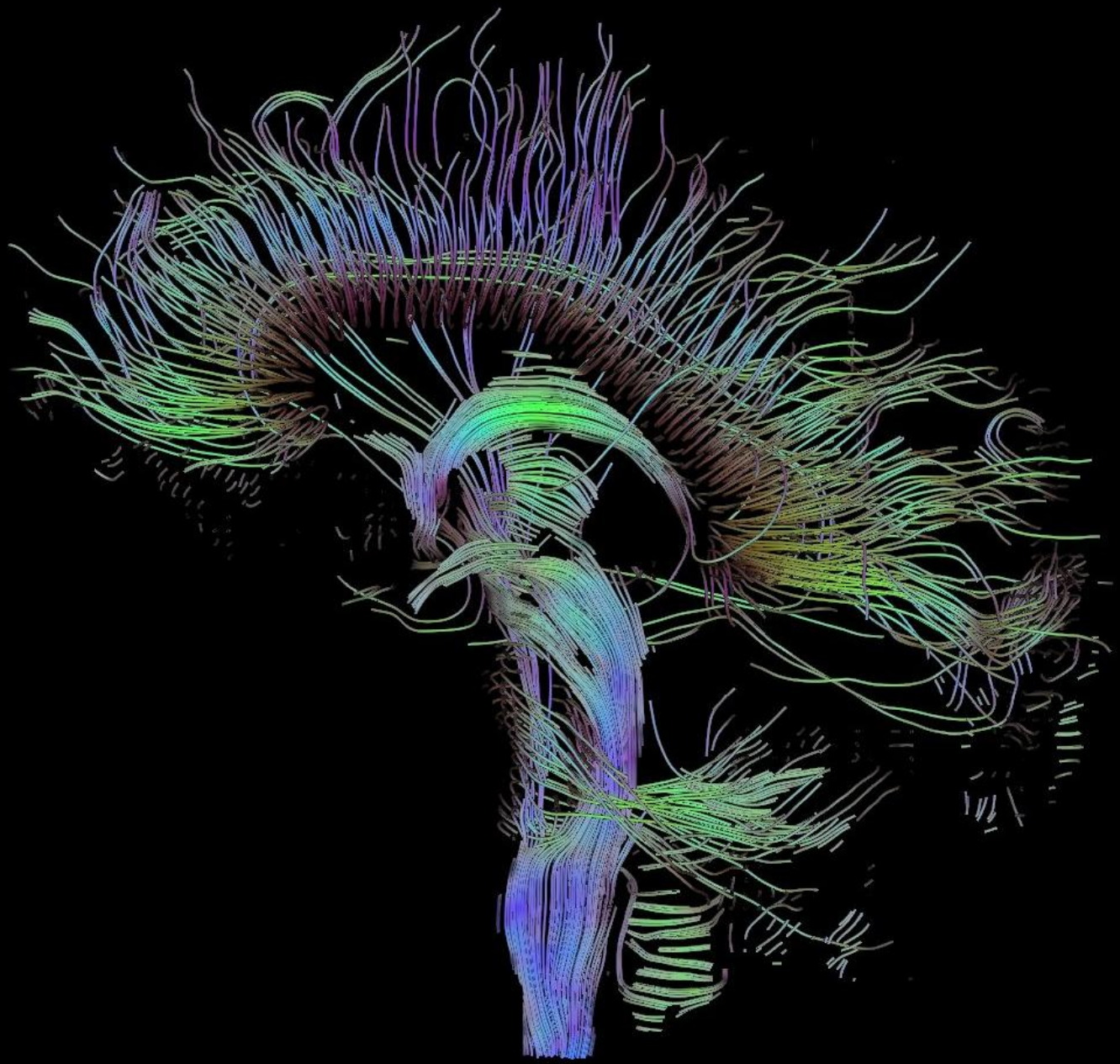
In good tracts with high anisotropy, lots of algorithms work.

But, tracts are often untidy.



So let's compare approaches.

Deterministic tractography results look beautiful,

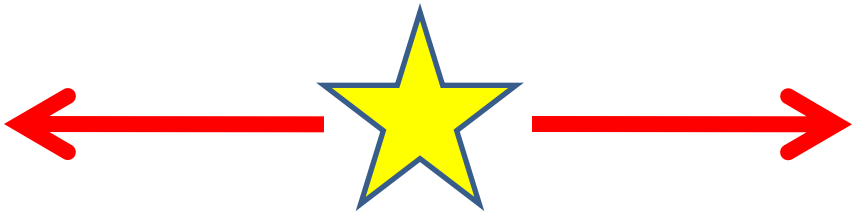


but they have sometimes been called black magic.

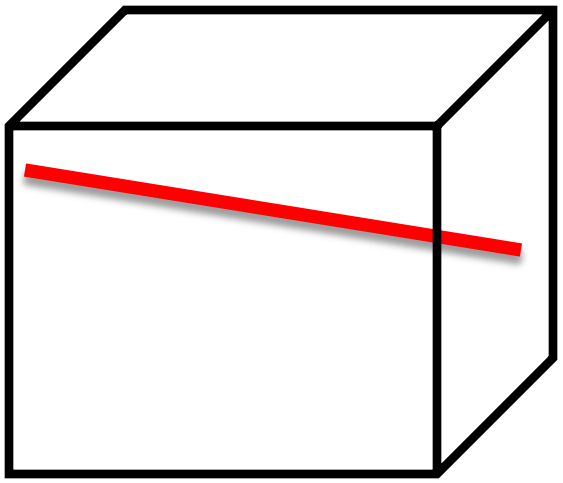
Black Magic?
Why?

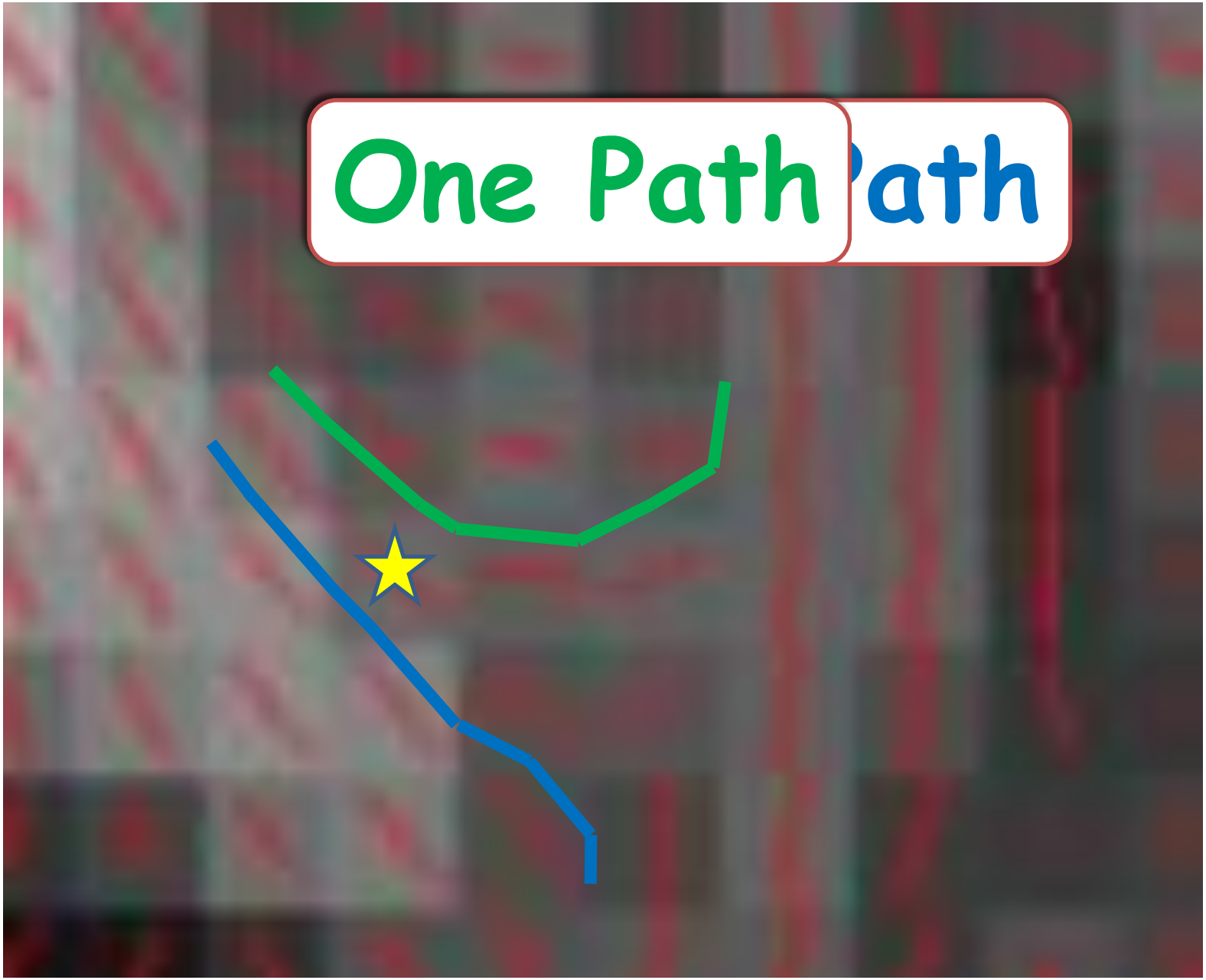
Well, in their simplest form, they work like this:

A path is propagated bidirectionally from a "seed point"



by moving parallel to V1 (the principal eigenvector)




One Path
ath

As you can see,

these deterministic paths

are altered by where you begin in the seed voxel...

And being deterministic,

the algorithm chooses ONLY ONE possibility at each decision point,

so it can't account for branching fibers.

In addition,

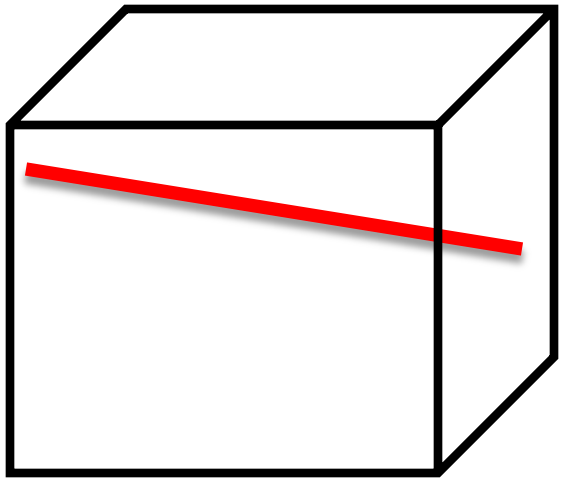
deterministic approaches

don't account for uncertainty in reconstruction

What uncertainty?

There's uncertainty in the estimate of

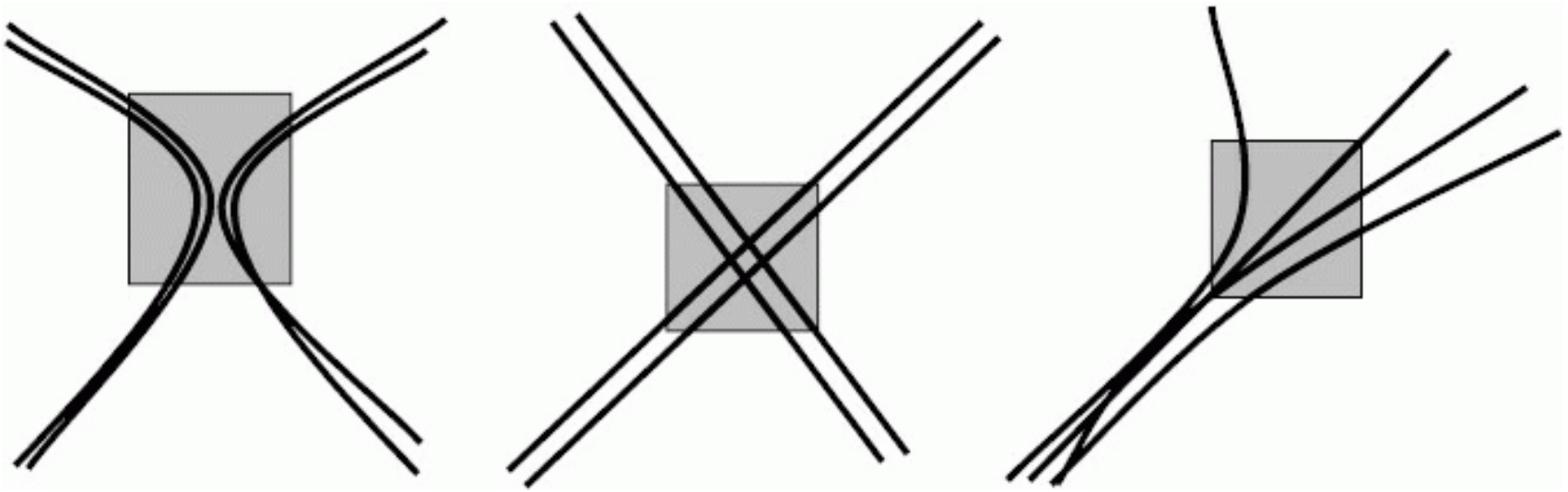
V1



While V1 estimation is fine in good tracts with high anisotropy,

we can't assume that there's only one thing in each voxel.

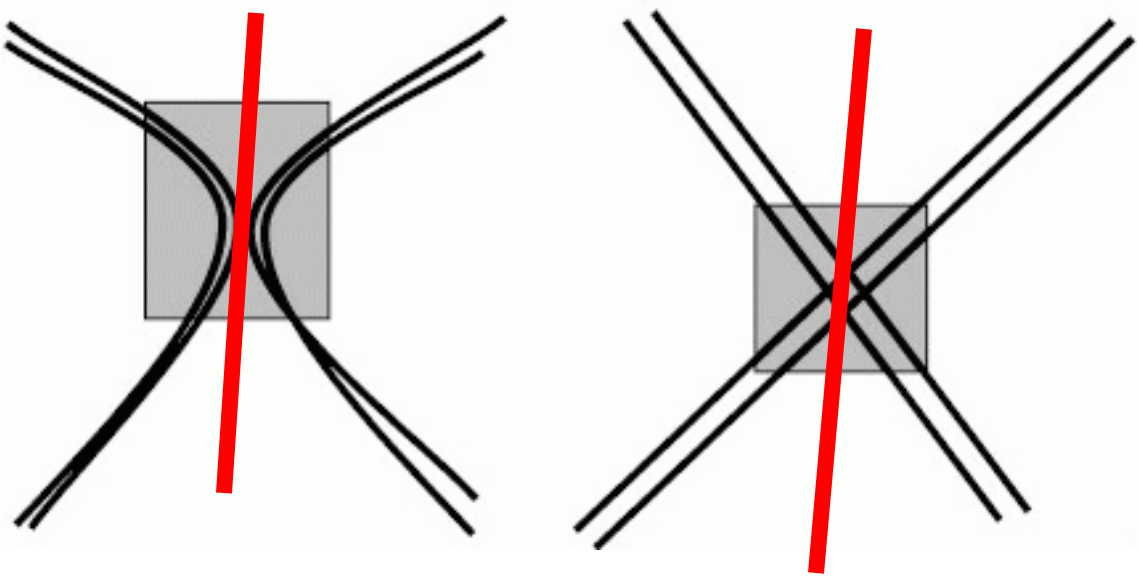
There could be other tracts, like this…



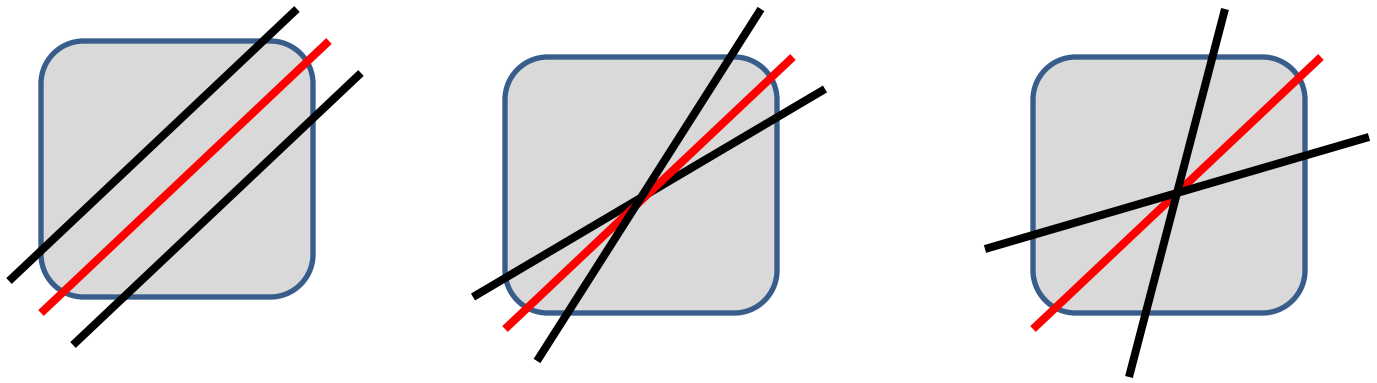
Kissing Crossing Fanning

And, since V1 is a "best fit" estimate

Crossing fibers can result in gross inaccuracies,



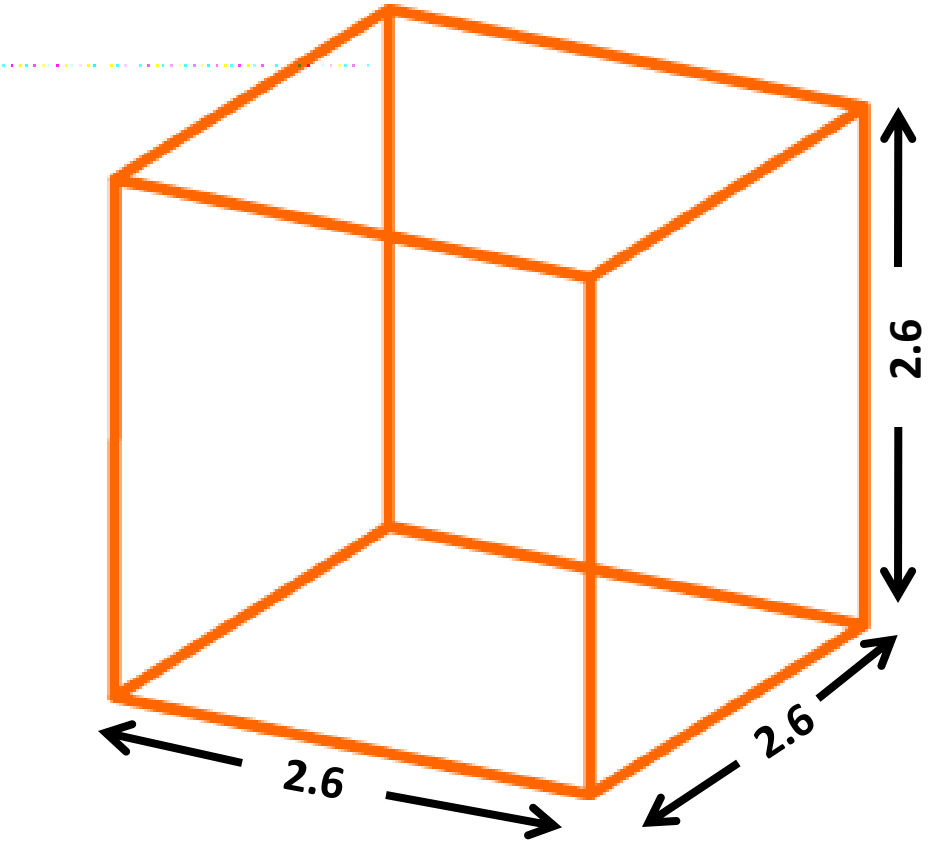
and oversimplification,



demonstrating that V1 can be quite uncertain.

Finally, resolution issues reduce V1 certainty again.

Our voxel size is 2.6 mm isotropic



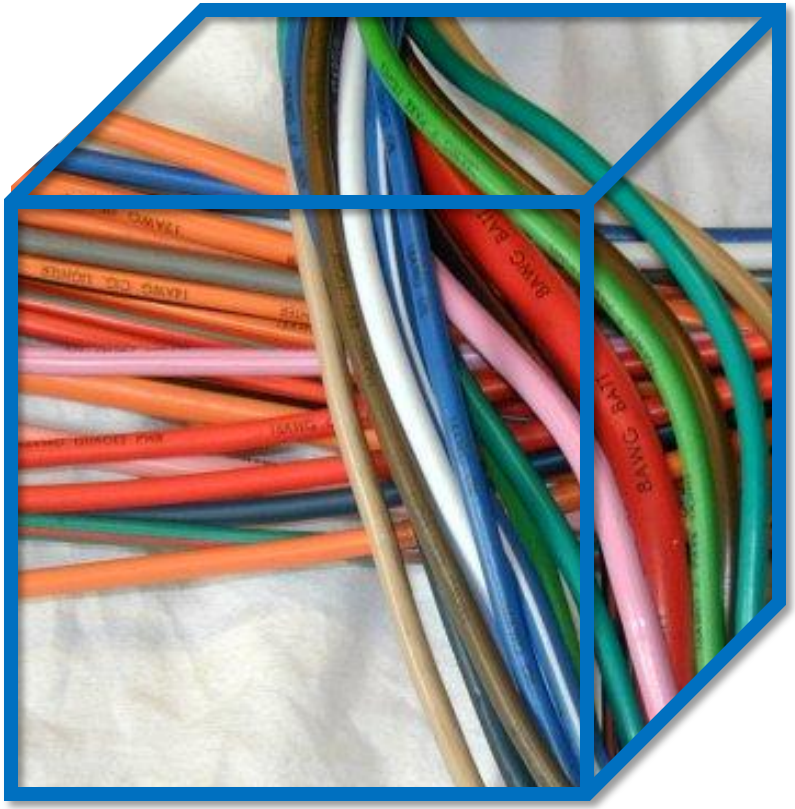
Low spatial resolution

->

partial voluming of small diameter tracts.

And when the tract is only part of the volume,

then other stuff in the voxel…



Like little blood vessels, csf, and other tracts…

affects V1
and FA.

To calculate V1,

we need to collect data in 6 or more directions.

The more directions we collect data, the higher the angular resolution.

The GE scanner allows a maximum angular resolution of 25 directions,

but people sometimes collect 60+ directions

With fewer angular samples, the estimate of V1 is less precise.

Finally, dti images are gathered over 10+ minutes, so subjects may move.

Even if they hold still, the brain pulses with every hearbeat.

And any movement makes things blurry.

Summary

Tractography shows us tracts in 3D space

But there are problems

Deterministic approaches don't account for branching,

and fail to indicate the probability that they are right.

And there are plenty of ways to get the path wrong:

Crossing fibers,

Poor Spatial Resolution,

Small blood vessels,

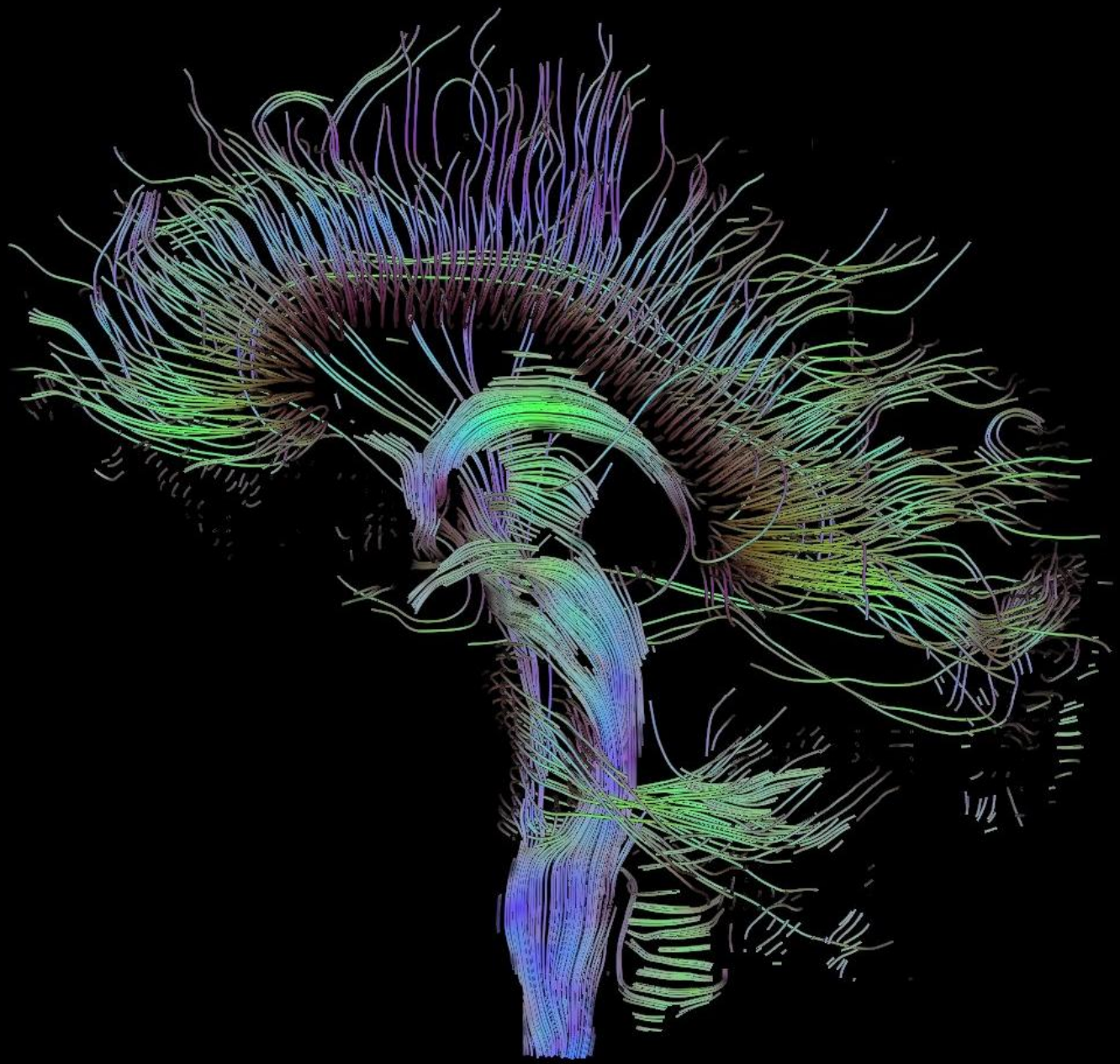
Poor Angular Resolution,

Brain pulsation,

Movement….

Finally,

because the deterministic reconstructions are so beautiful,



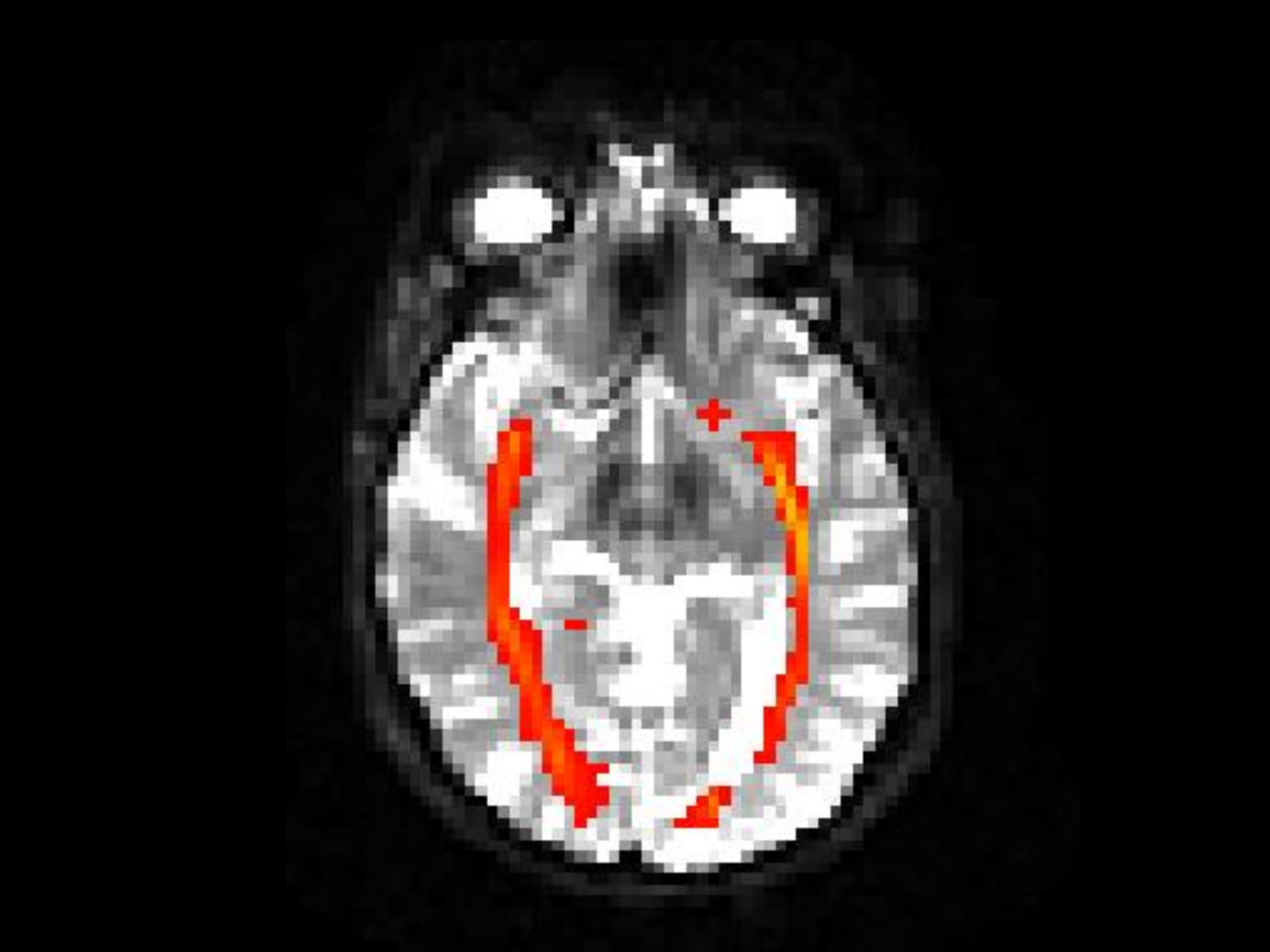
they give the impression of tracking individual fibers.

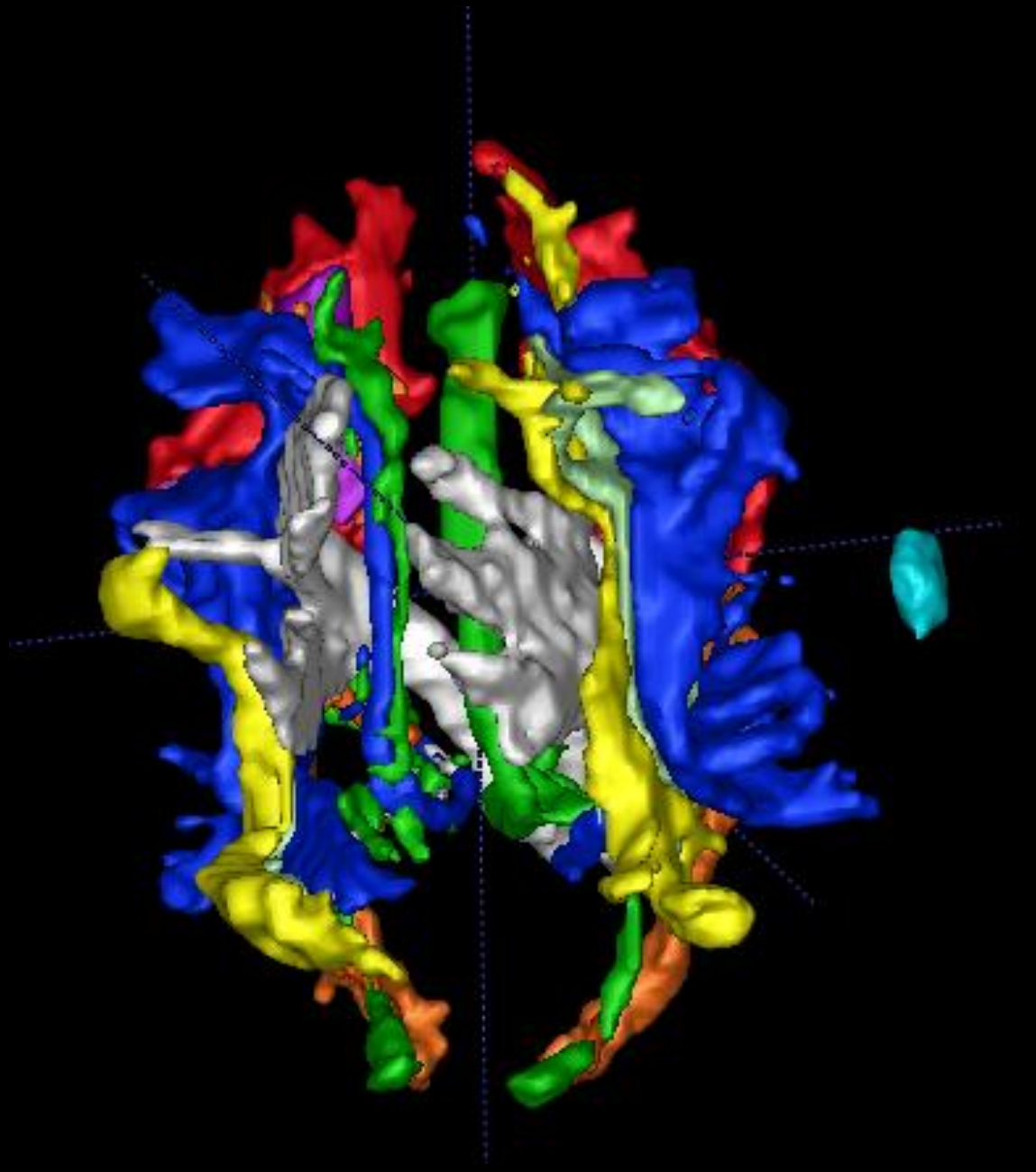
But, there is room for ~26,000 or more axons in one of our voxels,

so streamlines do NOT correspond to axon fibers.

Let's look at probabalistic tractography in FSL 4.0

It is not as pretty

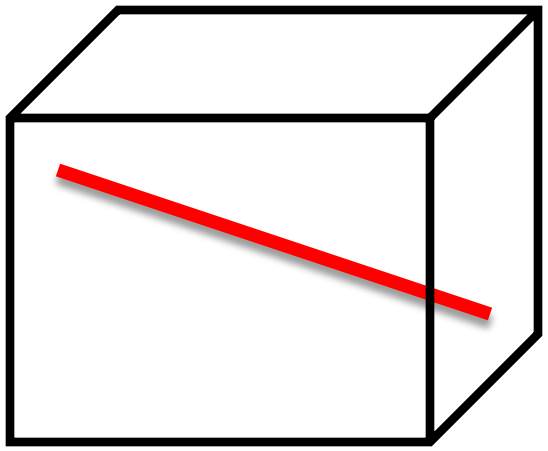




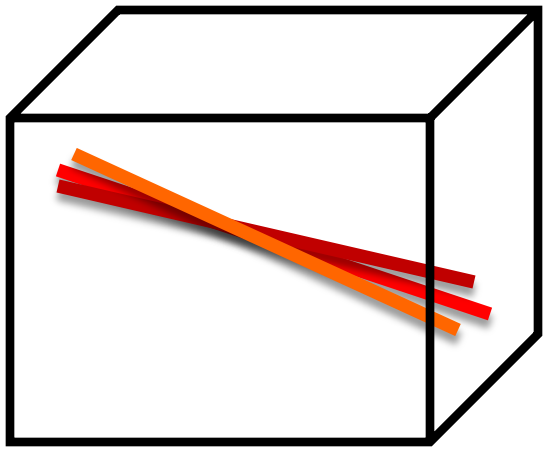
But, it is a bit more realistic

Here's why:

For each voxel, we calculate V1 with some wiggle room



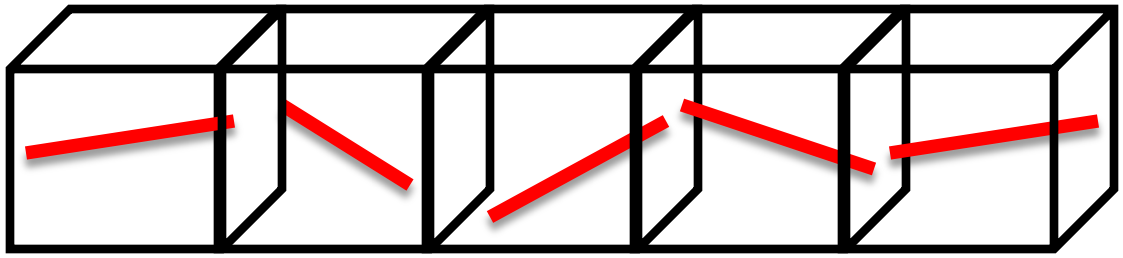
Now, take the probability distribution of V1 at each voxel



and run the deterministic approach 5000 times for each seed voxel,

using a slightly different estimate of V1 each time.

Because every voxel in the path has a probability distribution,

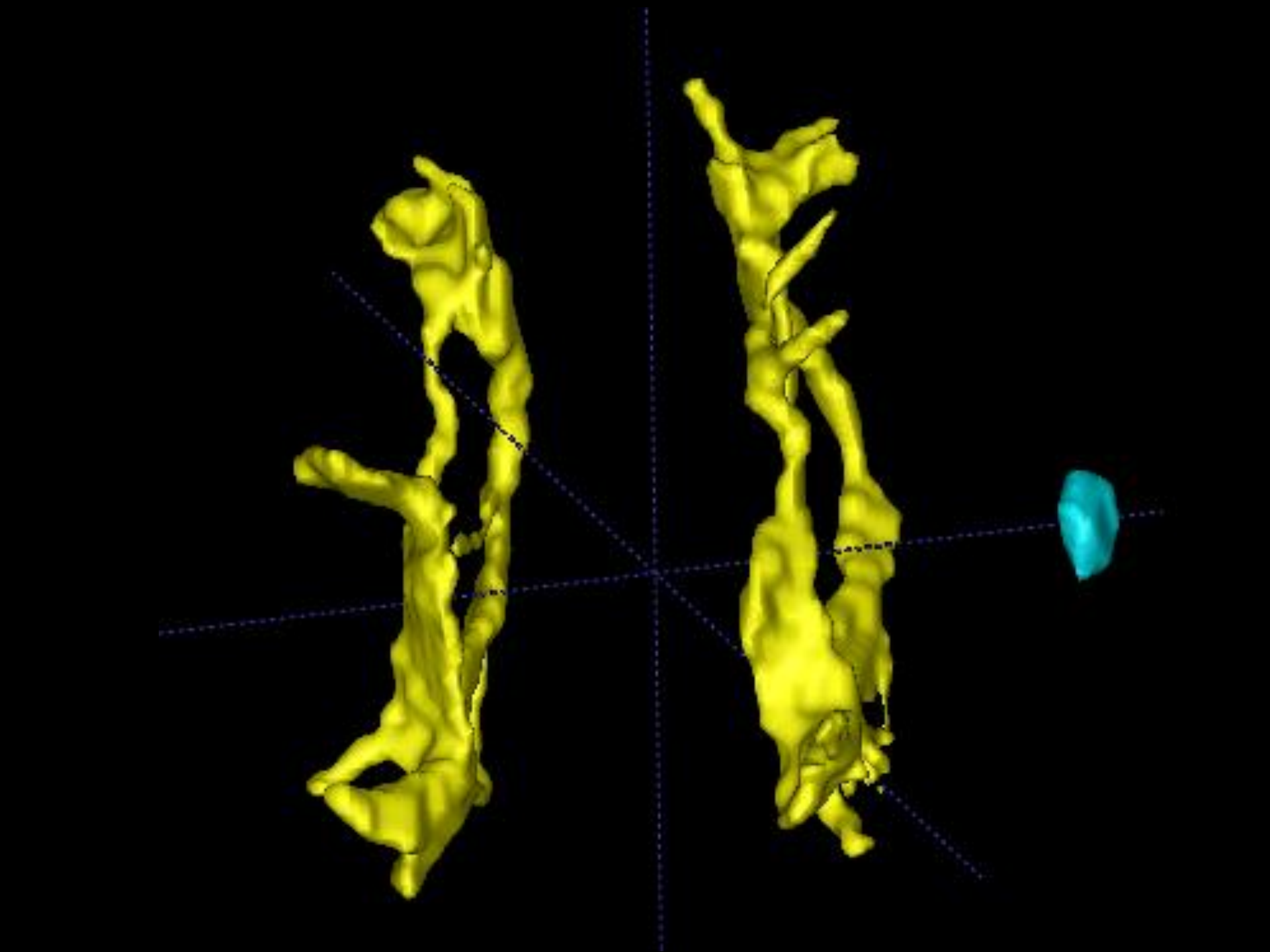


knowledge about uncertainty is incorporated into our path estimate.

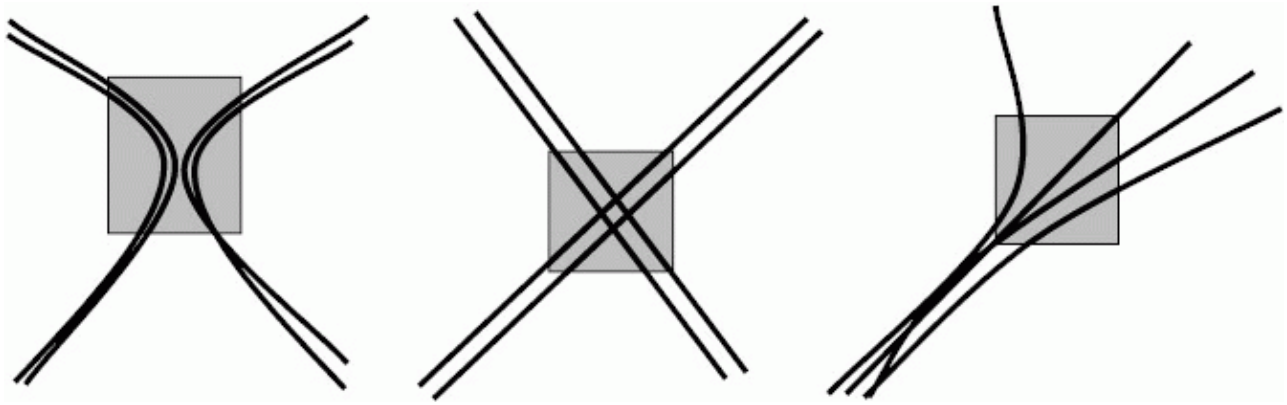
We get a more accurate view of where the path is **most likely** to lie

Number of times we pass through each voxel

and we get to see branches.



FSL 4 also has better modeling of multiple fibers.

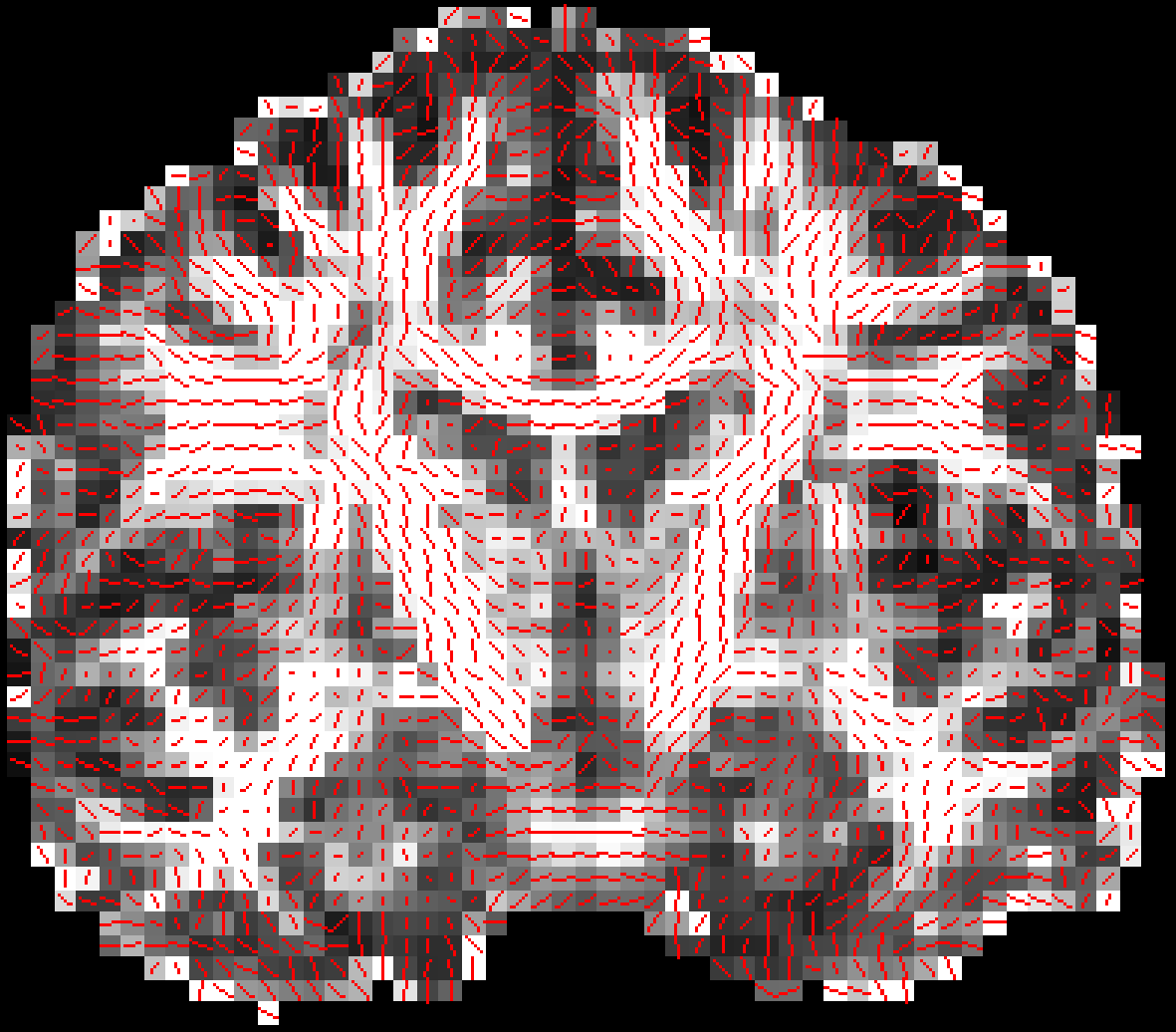


Given good signal (low noise) and lots of angular resolution,

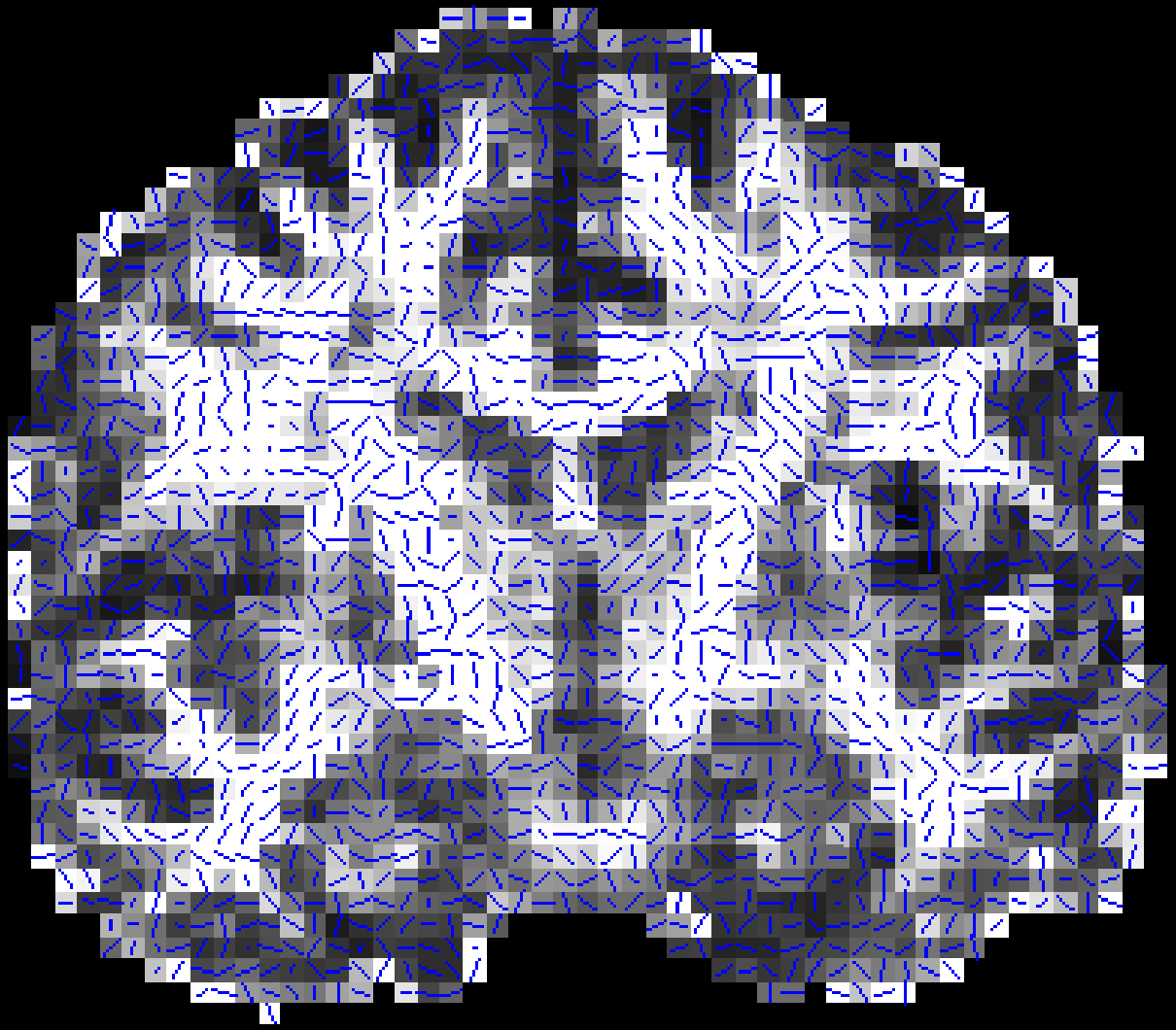
we can calculate the number of crossing fibers at each voxel.

And their principle directions

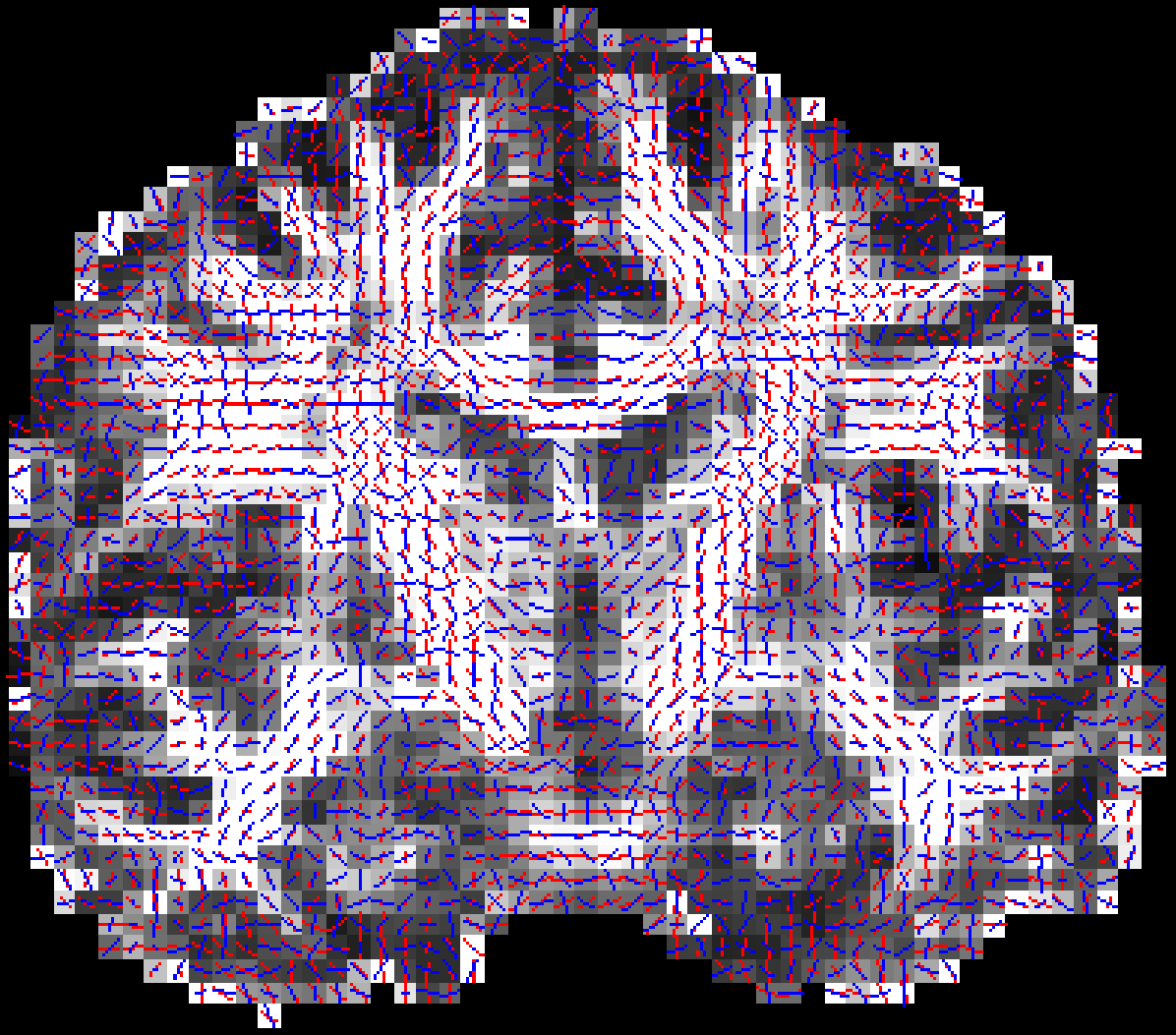
Primary Set



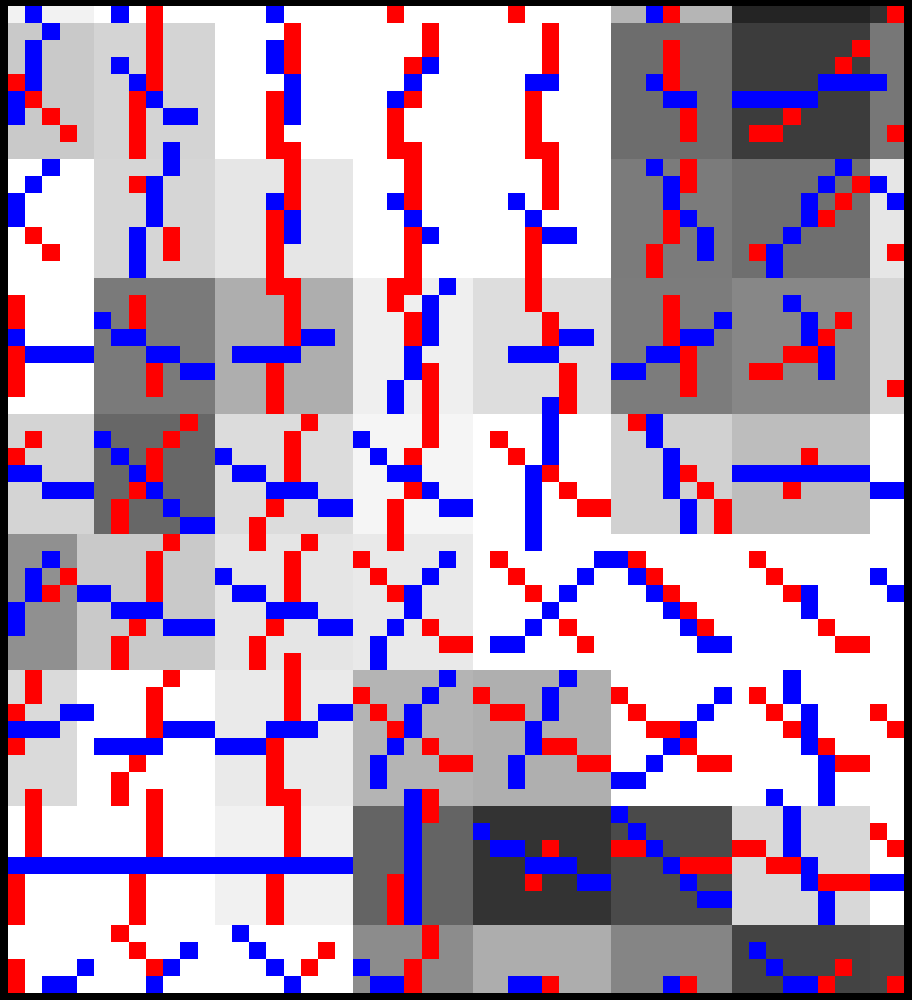
Secondary Set



Both Sets

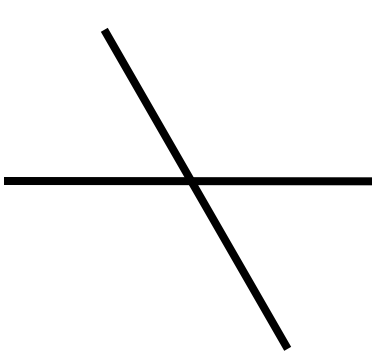


Both Sets

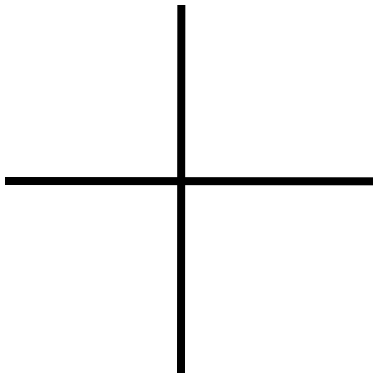


Our GE scanner allows us to distinguish crossing tracts

at somewhere between 60 & 90 degrees.



to

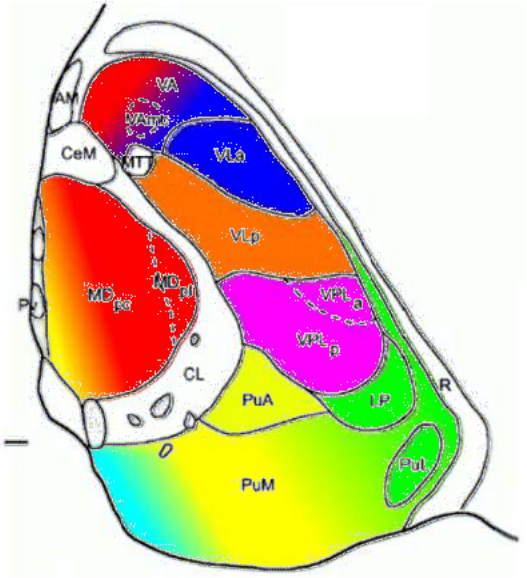


Another technique

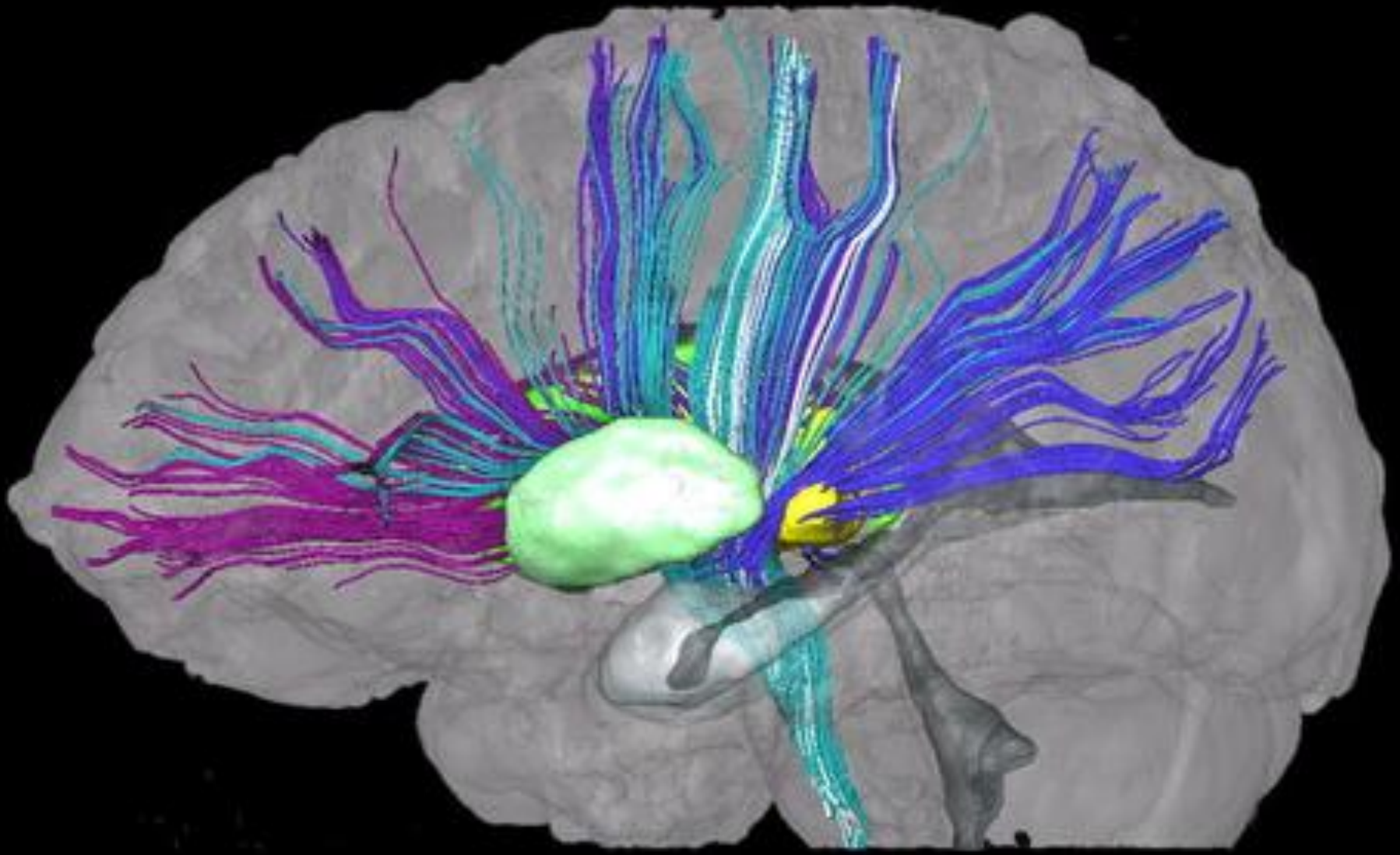
that results directly from tractography

is parcellation

Parcellation divides a structure (e.g., the thalamus)



based on its cortical connections



to different regions of the brain.

prefrontal cortex

premotor cortex

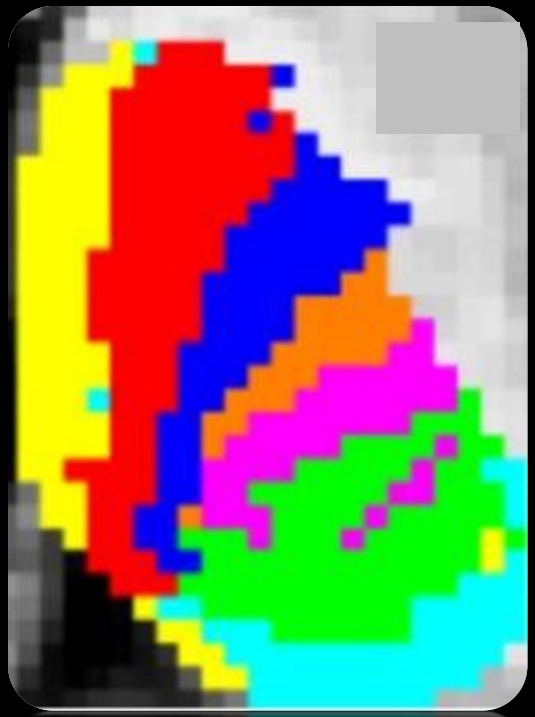
primary motor cortex

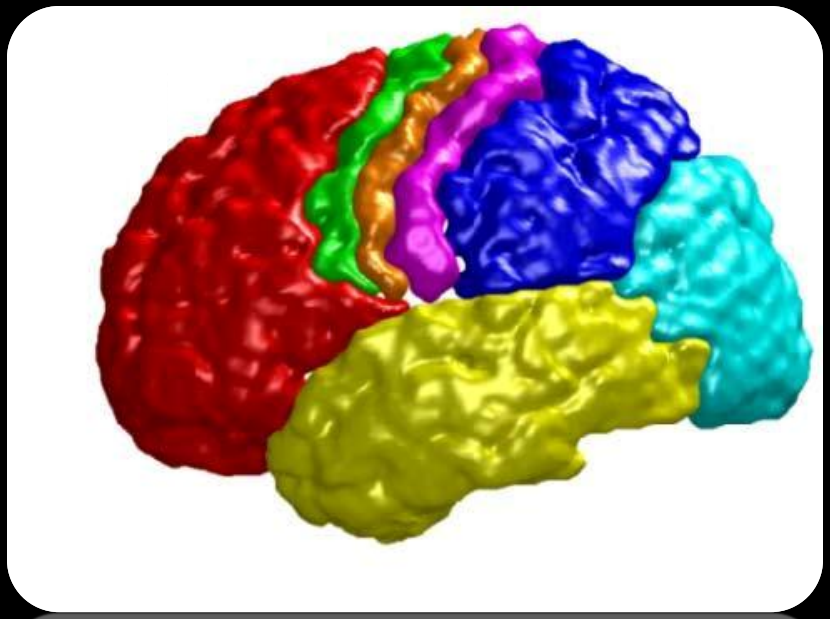
primary sensory cortex

posterior parietal cortex

occipital cortex

temporal cortex





Summary

Tractography has been implemented in lots of ways

Newer implementations,

such as those
in FSL 4,

are more sophisticated in several respects:

They include information about the uncertainty of their results.

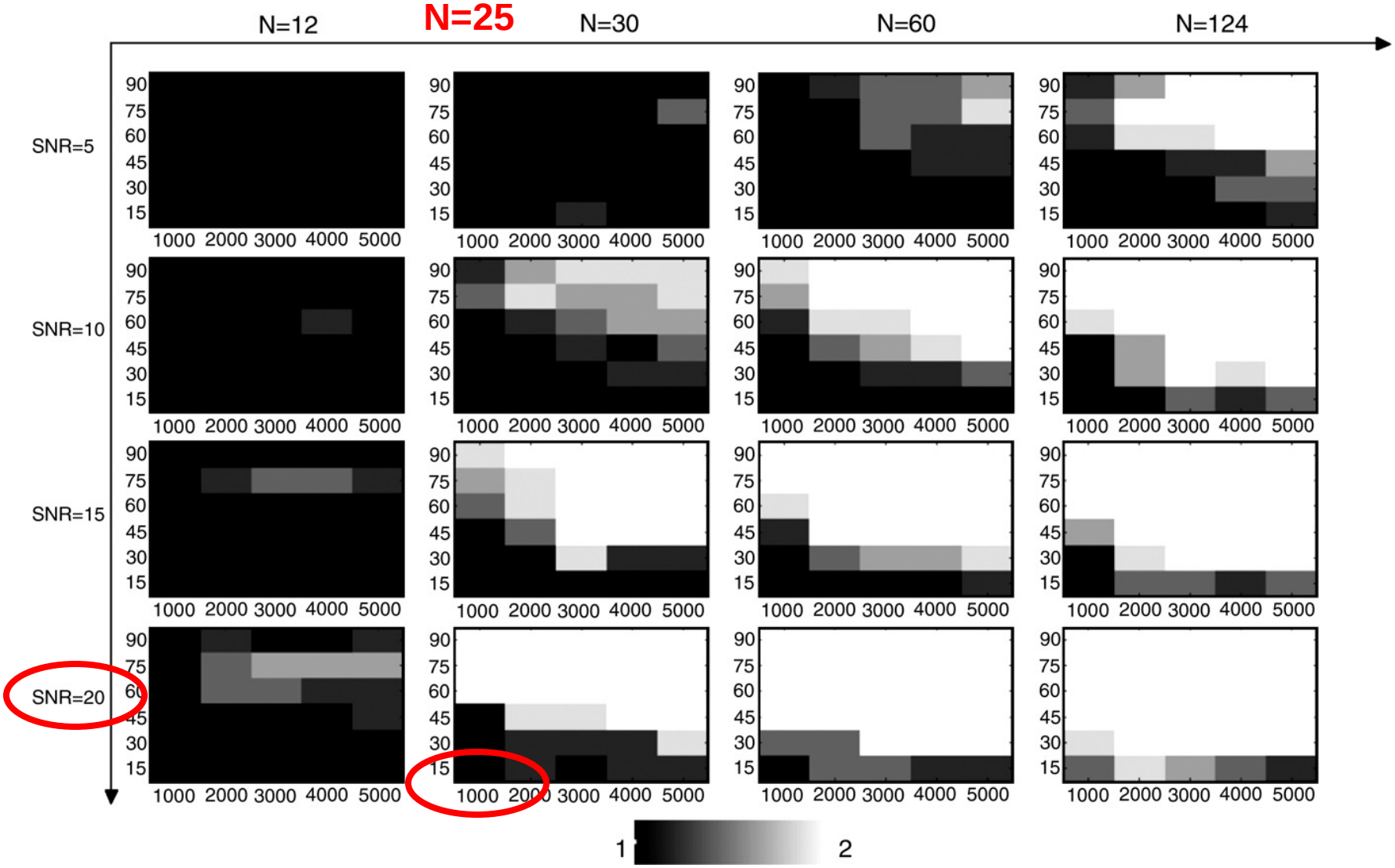
They are capable of finding branching tracts.

They can identify crossing tracts, and thus reveal small pathways,

that would otherwise be swamped by the crossing fibers.

However, DTI is young and has important limitations

However, DTI is a young technology and still has important resolution limitations.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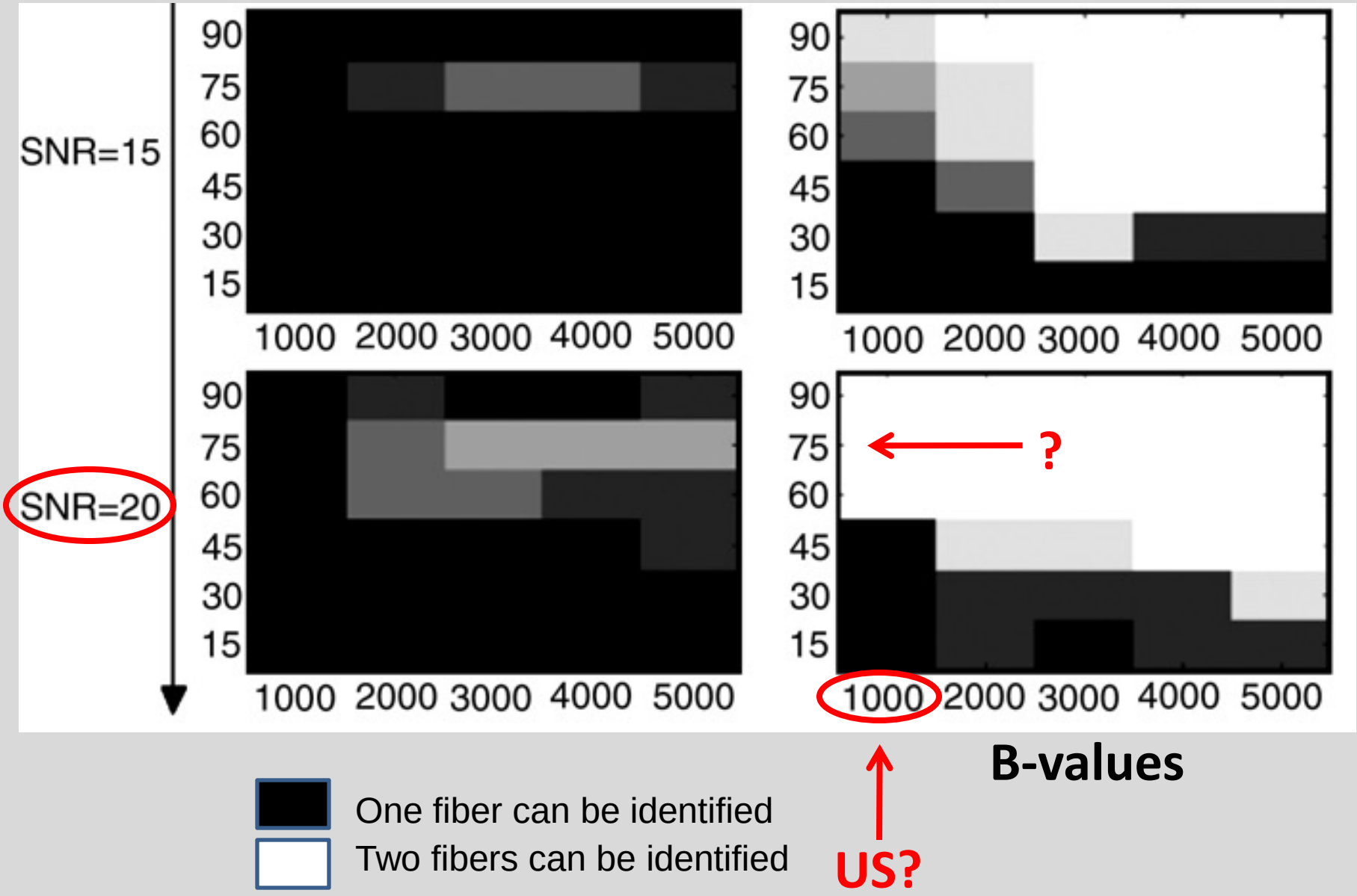
N=30
N=60
N=124
SNR=5
SNR=10
SNR=15
SNR=20
90
75
60
45
30
15
1000 2000 3000 4000 5000
1
2
One fiber can be identified
Two fibers can be identified


N=12
N=25
N=30
SNR=15
SNR=20
90
75
60
45
30
15
1000 2000 3000 4000 5000
?
B-values
One fiber can be identified
Two fibers can be identified
US?