Seeing below the resolution of MRI
The Brooklyn Research Cluster provides flexible computing, including for NYU Tandon's Visualization, Imaging, and Data Analytics research center.

- An app that translates sign language into spoken English using Brooklyn Research Cluster Platform
- An Event-Driven Model for Estimation of Phase-Amplitude Coupling at Time Scales of Cognitive Phenomena
- Drug design for treatment of heart attack and stroke
  - How the hSCAN-1 enzyme is activated
- How carcinogenic chemicals slip past DNA repair mechanisms
- Seeing below the resolution of MRI
- The link between Atlantic Ocean warming and Antarctic climate change

Biological tissue, porous rock and composite material samples appear uniform at the macro-scale and well-organized at the micro-scale, but their structural disorder at the meso-scale - such as the cellular level - is an important indicator for categorizing samples and identifying diseases.

One non-invasive technique is to measure molecular diffusion of, for example, water, through the sample. Mesoscopic structural parameters such as pore or cell sizes and shapes can then be inferred from the time-dependent diffusion behavior.

Making this inference is, however, a difficult and ill-posed problem, requiring a structural model which predicts the bulk diffusion coefficient, against which the measured one could be compared.

Drs. Dmitry Novikov and Els Fieremans of NYU School of Medicine, working with Drs. Jens Jensen and Joseph Helpern of the Medical University of South Carolina, have proposed that the structural disorder in a sample can be adequately and parsimoniously represented with just a small set of "structural universality classes", as illustrated below.
These are characterized by a structural exponent $\rho$ in the relation $= \frac{(\rho + \delta)}{2}$, where $\delta$ is the number of spatial dimensions and $\delta$ is the dynamical exponent characterizing diffusion in the long-time limit. Dr. Novikov and colleagues used the NYU HPC clusters to run simulations, based on Monte-Carlo methods, showing the time dependent diffusion behavior of each structural universality class. In this example the steady-state diffusion of each simulated sample is the same, but the structural disorder is clearly visible in the time-dependent behavior, each sample showing a distinctly different curve determined by its structural exponent $\rho$. 
The novel disorder classification paradigm allowed the authors to make important conclusions on what slows down water diffusion in muscle and in brain, and to elucidate the cellular-level changes responsible for the decrease of diffusion coefficient in acute stroke, which is used as a clinical MRI contrast.

Drs. Novikov and Fieremans's work is published in PNAS at [http://www.pnas.org/content/111/14/5088](http://www.pnas.org/content/111/14/5088).