

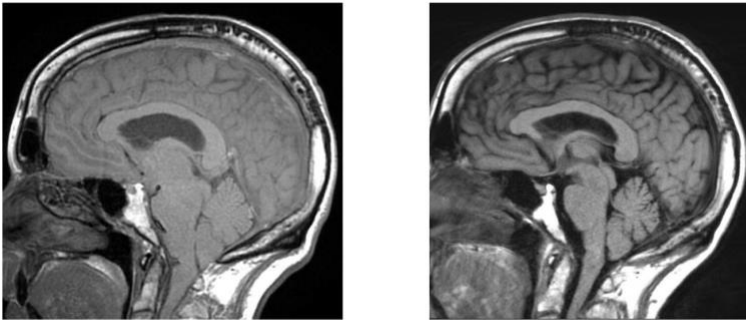
More validation about why we must end the current reliance on animal experiments
From [CAARE Citizens for Alternatives to Animal Research](#)
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Dementia is a complex disorder that can be caused by a range of brain pathologies. There are myriad forms of dementia, many of which have not been fully understood or identified.

In the first piece, we discuss a breakthrough in understanding one rare form of dementia that was found by studying human patients. Such a discovery could only come from relevant human research.

This is yet another example of why we must end the current reliance on animal experiments if we are to see cures and breakthroughs for the hundreds of human diseases that presently have no cure.

Potential hidden cause of dementia detected



Credit: Cedars-Sinai

Researchers at Cedars-Sinai have found a [potential cause of behavioral-variant frontotemporal dementia](#) (bvFTD), previously considered untreatable, through a human-based study.

By performing specialized CT scans on 21 patients with symptoms of bvFTD, they identified cerebrospinal fluid leaks in nine patients. Once they surgically closed the leaks, the bvFTD symptoms were completely reversed. Scientists hope that the scans will become more widely available to identify and treat patients with the cerebrospinal fluid leaks.

This previously unidentified cause and treatment of bvFTD was discovered through the use of advanced imaging on human patients, rather than damaging animals' brains to try to induce dementia that ultimately does not accurately replicate the human condition.

DNA sequencing method lifts 'veil' from genome black box



Despite decades of use, scientists haven't understood how genome-targeting drugs treat cancer. Now, researchers from the University of Cambridge have created a new method, called [Chem-map](#), that shows exactly how drugs interact with the human genome.

Chem-map allows in situ mapping of small molecule-genome interactions by detecting with great precision where the small molecule binds to genomic DNA. Researchers tested the technique with the anticancer drug doxorubicin on human leukemia cells.

A more precise understanding of how drugs interact with the human genome can result in more effective cancer treatments, something that would not have been possible by studying animals.

Study offers first glimpse of how many suffer from previously unknown illness



New human genetic studies have allowed researchers to identify a rare immune-related rheumatoid syndrome, something that would not have been possible through animal research.

Previously considered a mystery illness, VEXAS syndrome afflicts people already diagnosed with other conditions that cause fevers and low blood oxygen levels and carries a high mortality rate.

A [new study](#) led by researchers from NYU Grossman School of Medicine builds upon a previous genetic study that identified a mutation in UBA1 as linked to the condition. In the current study, researchers analyzed 163,096 health records to screen for UBA1 mutation. Of the twelve patients with the gene, all had been experiencing VEXAS symptoms.

Because some therapeutics can improve symptoms, identifying this genetic condition could help improve treatments and save lives.

Using machine learning to predict brain tumor progression

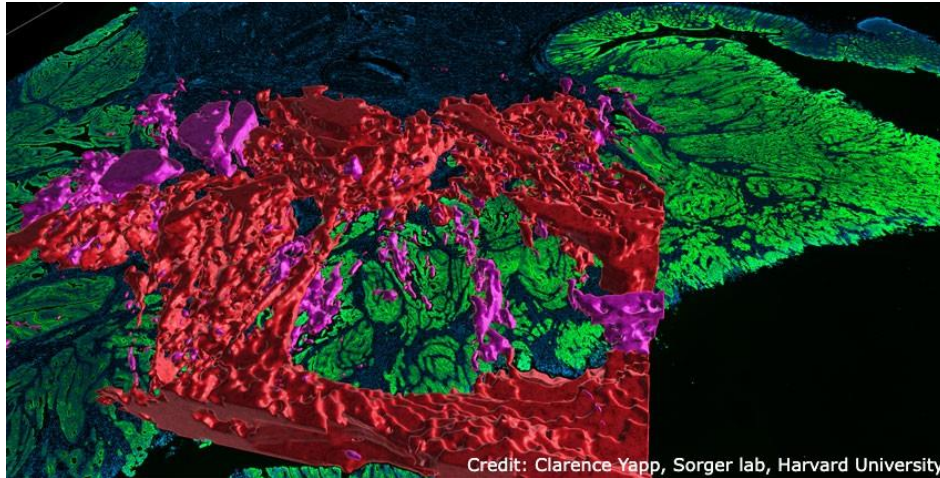


Glioblastoma multiforme (GBM) is an invasive brain cancer that is difficult to treat. A team led by researchers at the University of Waterloo in Canada have [created a computational model](#) that can allow doctors to better estimate the tumors' diffusivity and proliferation rate which may improve treatment.

They analyzed two sets of MRIs from five patients with GBM, taken months apart. Because these patients had declined treatment, the MRIs showed GBM's progression when left untreated. With this data, they used a deep learning model to develop a predictive model for GBM growth. This model was validated through testing on patients and on synthetic tumors.

Mice are used by the tens of thousands to study GBM but have failed to provide effective outcomes. By studying GBM with innovative and human-relevant methods such as MRIs and machine learning, scientists are hoping to find better treatments for this deadly cancer.

An unprecedented look at colorectal cancer



New [animal-free research](#) from Harvard University advances upon traditional diagnostic techniques for colorectal cancer and provides a map that will be a part of the National Cancer Institute's Human Tumor Atlas Network, a freely available database for the scientific community.

Colorectal cancer is traditionally diagnosed through histology analysis, or by examining tumor samples under a microscope. In the current study, researchers use single-cell molecular imaging data through a technique called cyclic immunofluorescence, which, when combined with histology, can provide large-scale 2D and 3D spatial maps of colorectal cancer.

Then, computational scientists utilized machine learning to identify more about the tumors, including how they form, progress and their relationship with the immune system.

This novel, human-relevant technology will help scientists to learn more about colorectal cancer and improve treatment and diagnosis in ways that are impossible through animal experiments.