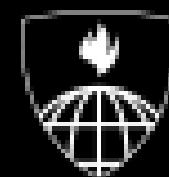


Highlights In Big Data From the Bloomberg School of Public Health

Roger D. Peng, PhD

Department of Biostatistics

Johns Hopkins Bloomberg School of Public Health

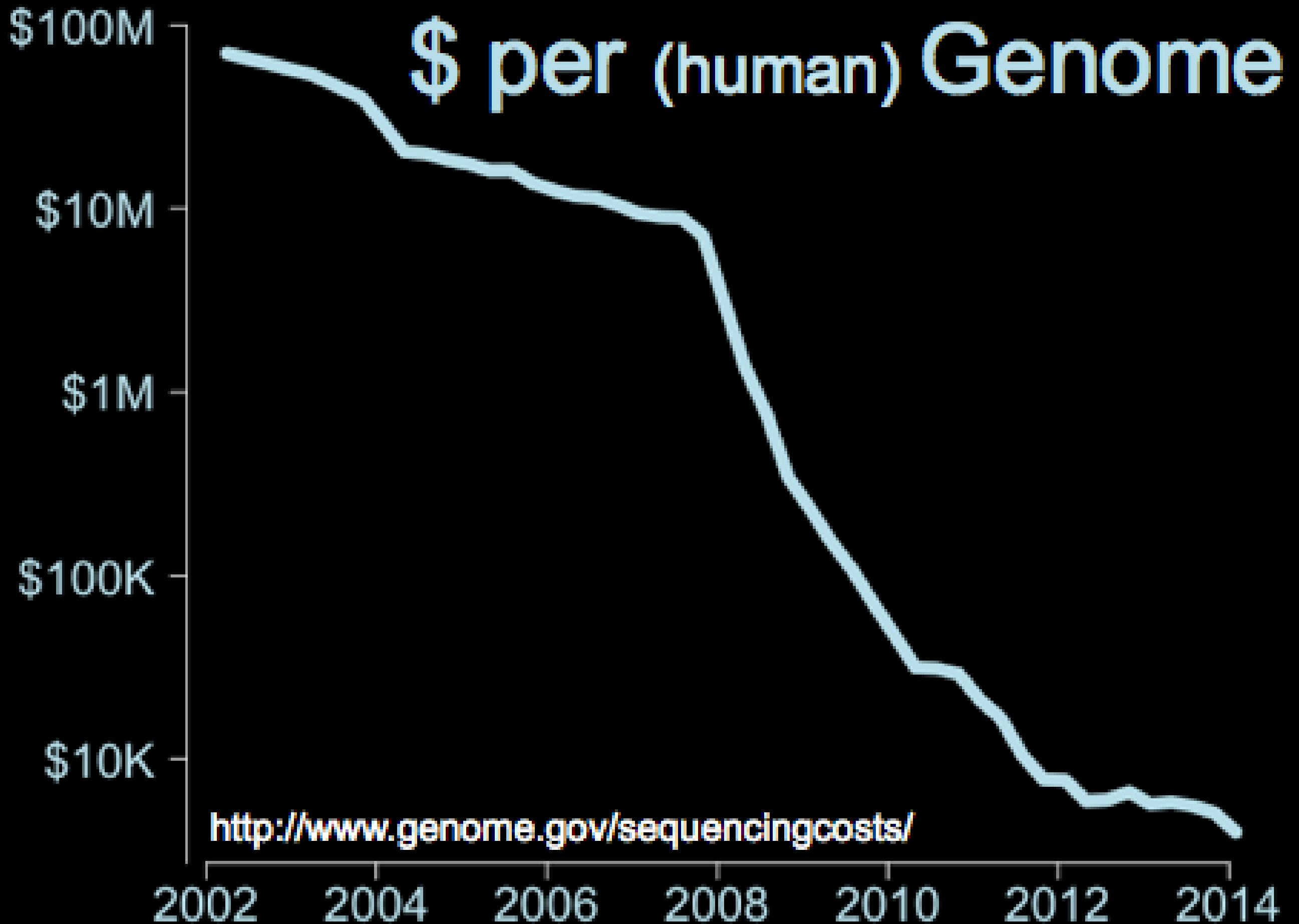


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of PUBLIC HEALTH

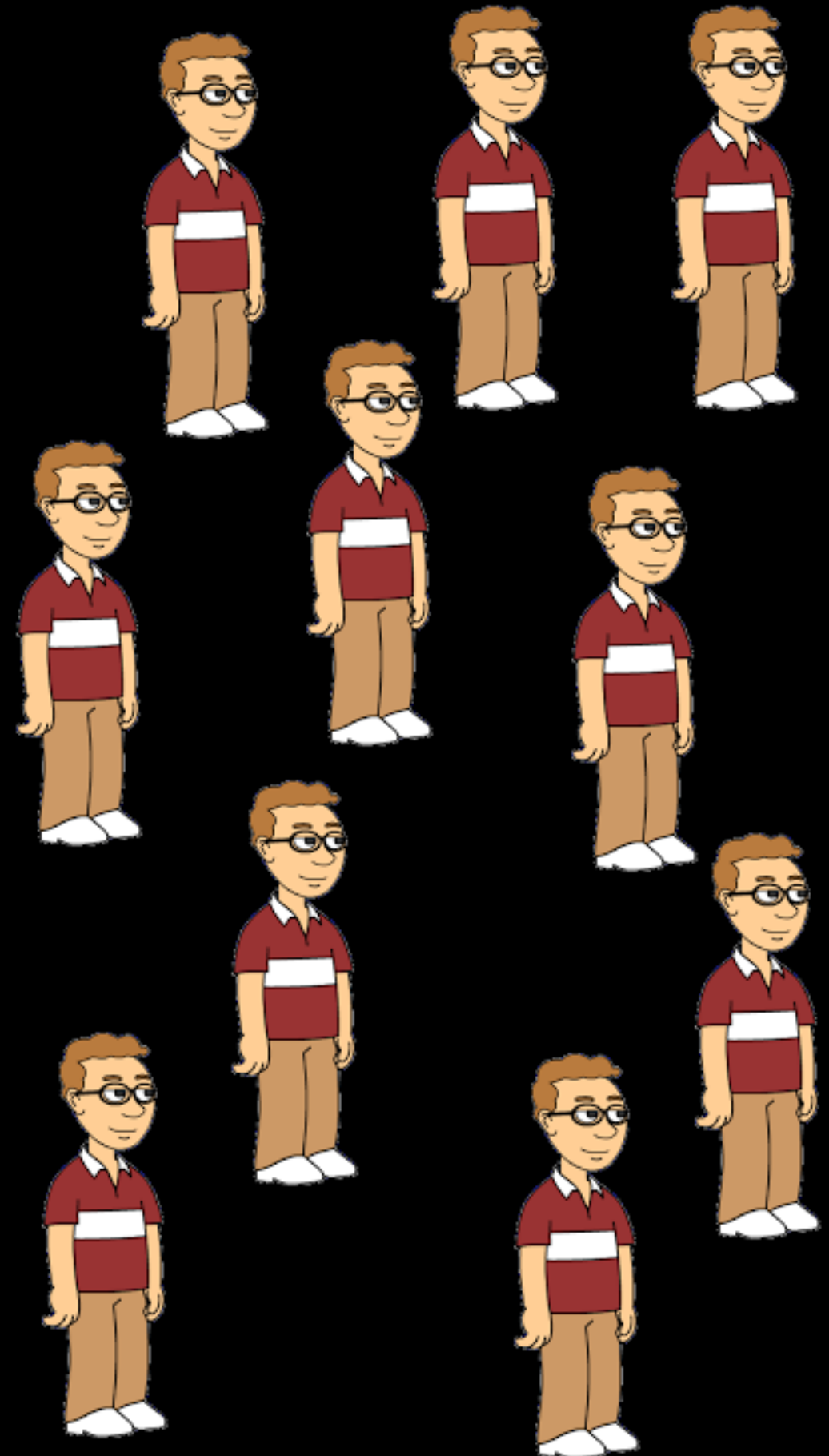
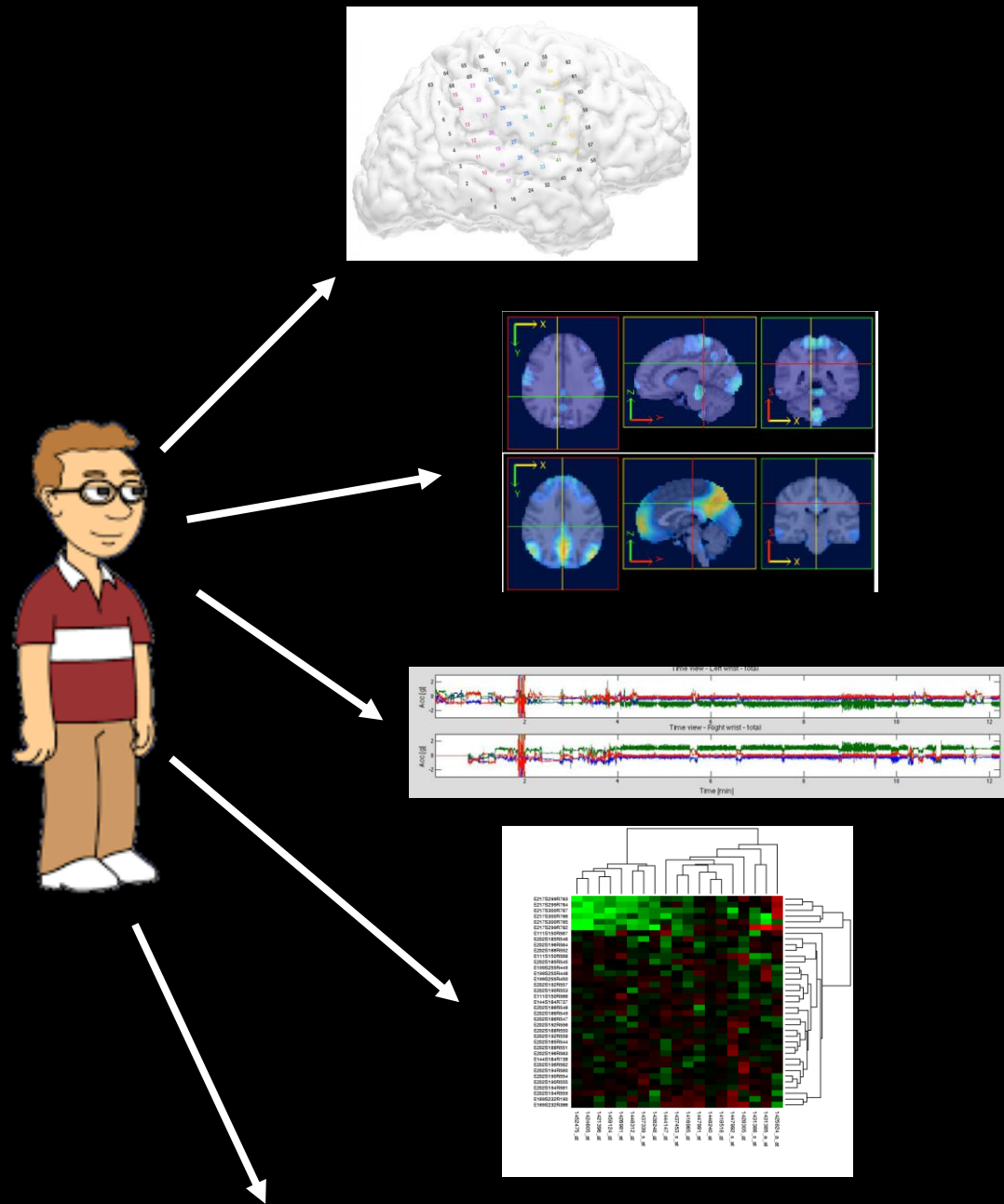


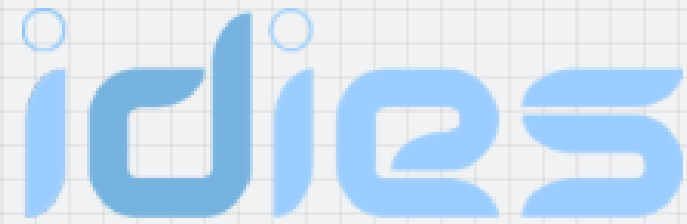
Protecting Health, Saving Lives —
Millions at a Time
↑
(of data points)

The Measurement Revolution...

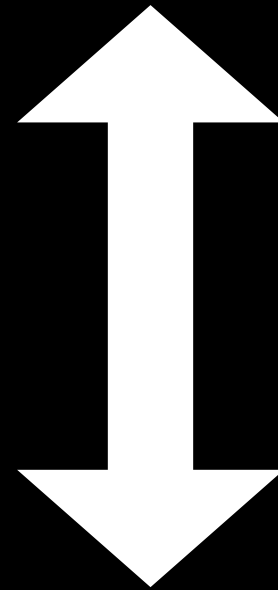


The Measurement Revolution... Multiplied!





The Institute for Data Intensive Engineering and Science



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The Center for Computational Biology

A joint research center in the McKusick-Nathans Institute of Genetic Medicine, the Department of Computer Science, and the Department of Biostatistics

The Center for Computational Biology (CCB) is a multidisciplinary center dedicated to research on genomics, genetics, DNA sequencing technology, and computational methods for DNA and RNA sequence analysis. CCB brings together scientists and engineers from many fields, including computer science, biostatistics, genomics, genetics, molecular biology, physics, and mathematics, all of whom share a common interest in gaining a better understanding of how genes and genomes affect biological functions. We develop and apply technology that uses sequence data to study a wide range of questions, including how genes cause disease, how genes change in response to different conditions within the cell, and how genomes evolve.

In addition to its research program, CCB provides bioinformatics expertise to departments and centers throughout the Schools of Medicine and Public Health, through a consulting group trained in the latest computational methods. CCB provides the computing hardware for the analyses run through its consulting group.

[More about CCB ...»](#)

News

- **June 24, 2014.** Three CCB faculty - Mihaela Perteau, Art Delcher, and Steven Salzberg - are named 'Highly Cited' by Thomson Reuters. By analyzing the number of ...[\(read more\)](#)
- **March 20, 2014.** An international team led by David Neale at UC Davis published the genome of the loblolly pine tree, the largest genome sequenced and assembled ...[\(read more\)](#)
- **March 2014.** Kraken, a new tool developed by Derrick Wood and his advisor Steven Salzberg, is published in *Genome Biology*. Kraken is very fast program for classifying ...[\(read more\)](#)
- **February 2014.** Ben Langmead is awarded a Sloan Research Fellowship. Since 1955, these fellowships have been given out annually to early-career scientists "whose achievements and potential ...[\(read more\)](#)
- **February 2014.** Steven Salzberg and Mihaela Perteau published a new method for fast, accurate detection of mutations in exome studies and in comparisons of normal versus diseased ...[\(read more\)](#)

Kasper Hansen

Margaret Taub

Jeff Leek

Hongkai Ji

Ingo Ruczinski

Alexis Battle

Cristian Tomasetti

Elana Fertig

Rob Scharpf

Ben Langmead

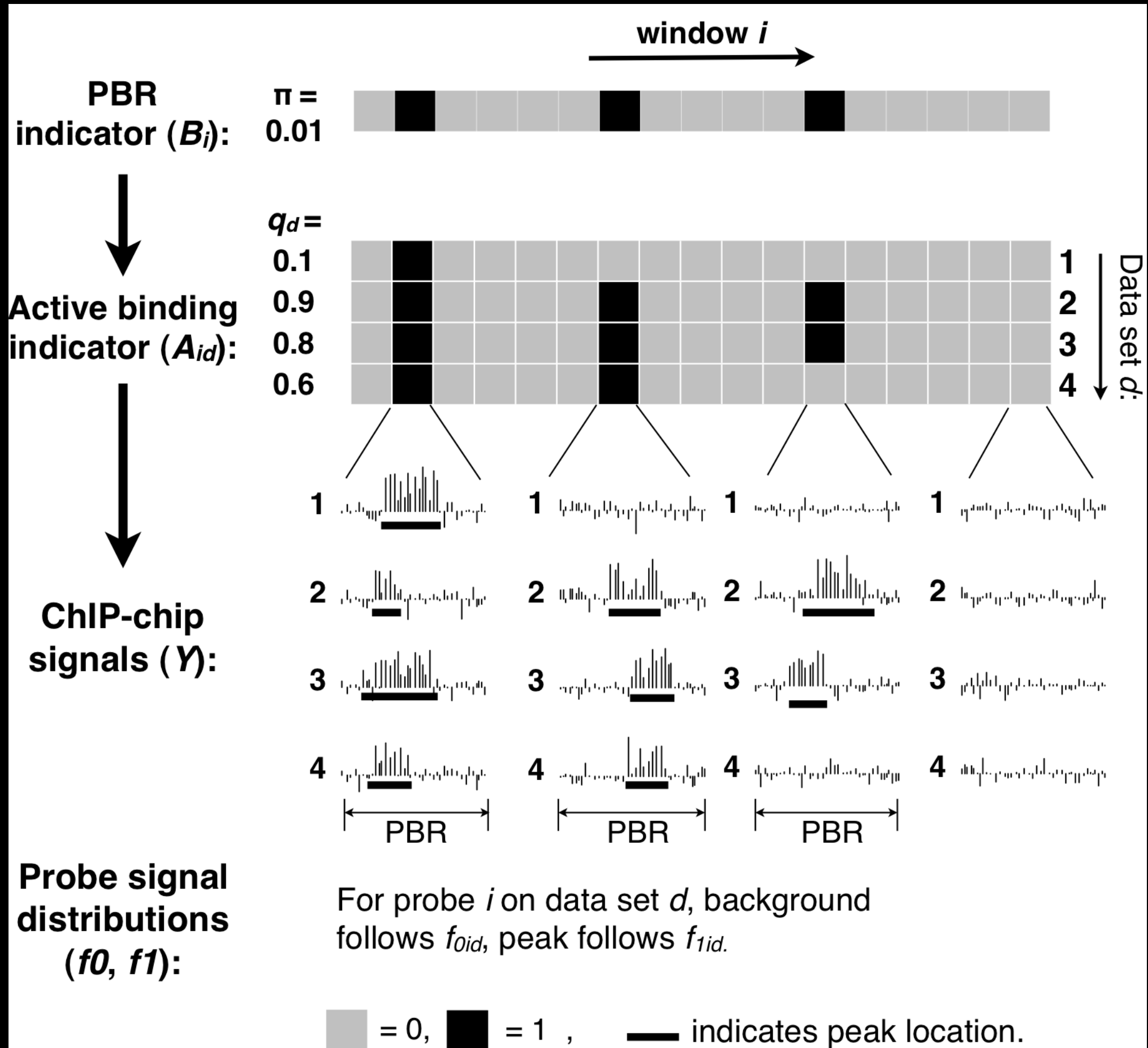
James Taylor

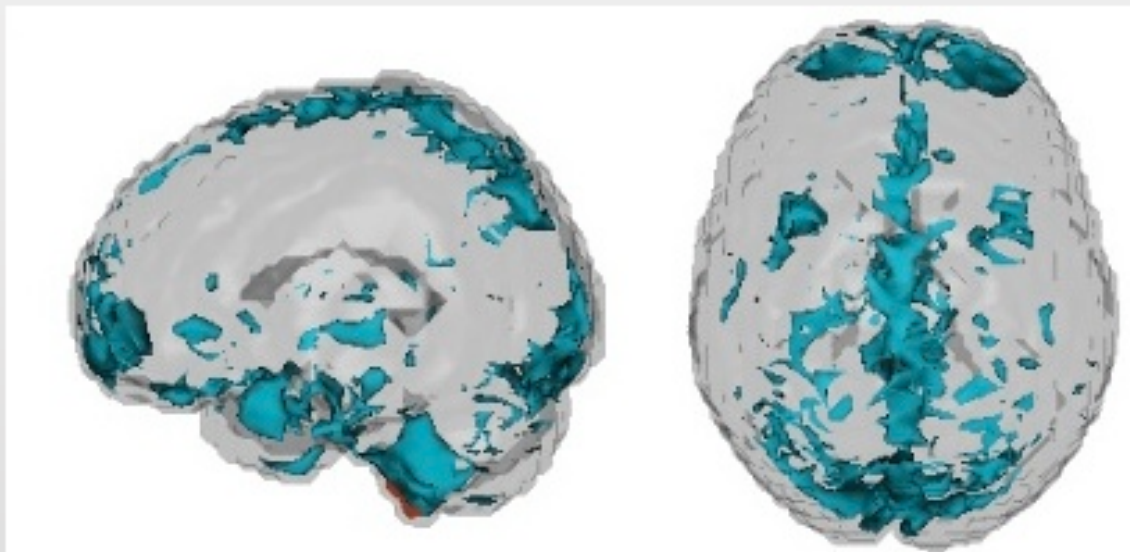
Mihaela Pertea

Lilliana Florea

Steven Salzberg

Multiple ChIP-chip Experiments





Brain imaging Prediction

An important application of imaging is to try to predict health outcomes using various brain imaging modalities. The SMART group has many parallel efforts in using brain imaging for prediction. This includes efforts to produce better, more biologically motivated predictors as well as efforts in parsimonious prediction based models ... [read more](#)

[Previous](#) [Pause](#) [Next](#)

Home

This is the webpage for the Statistical Methods and Applications for Research in Technology (SMART) working group of the [Department of Biostatistics](#) in the [Bloomberg School of Public Health](#) at [Johns Hopkins University](#). The group was started by [Ciprian Crainiceanu](#) and [Brian Caffo](#) though it now boasts a core group from around the world

Navigation

[Statistical methods](#)

[Scientific areas of interest](#)

[Software & Tutorials](#)

<http://smart-stats.org>

Brian Caffo

**Ciprian
Crainiceanu**

Ani Eloyan

Martin Lindquist

**Vadim
Zipunnikov**

Jeff Goldsmith

Sonja Greven

Jaroslav Harezlak

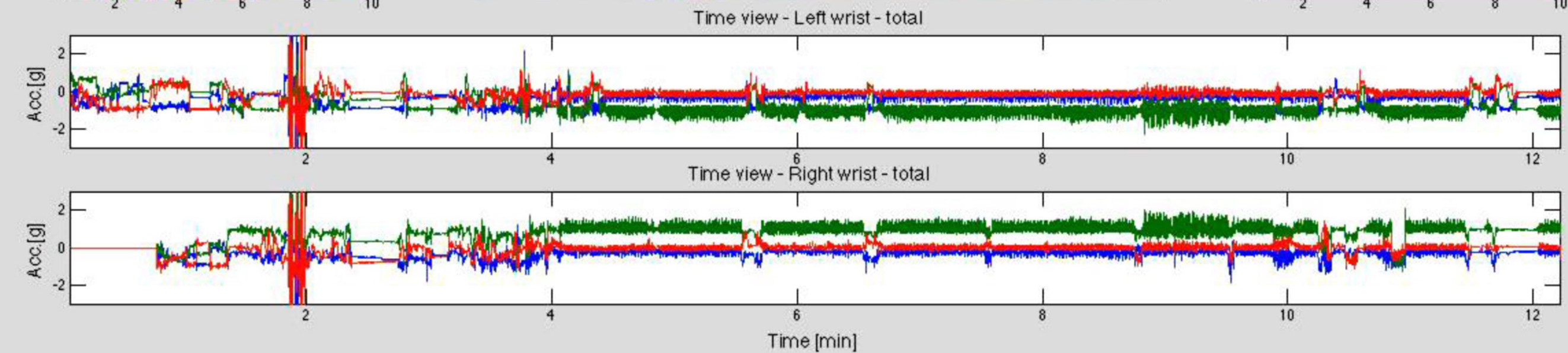
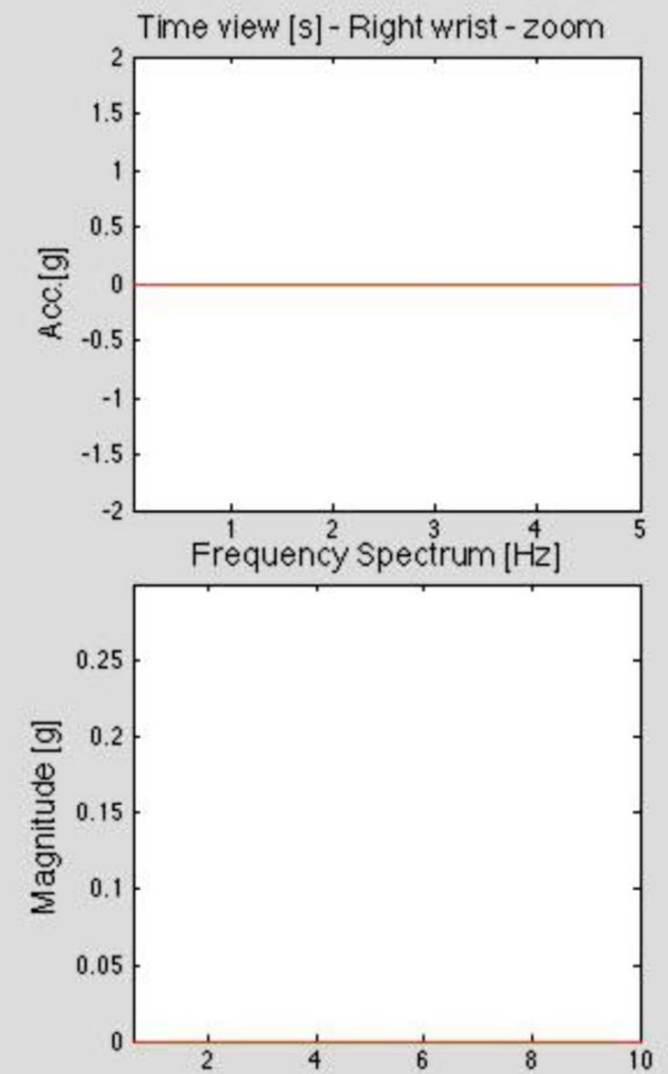
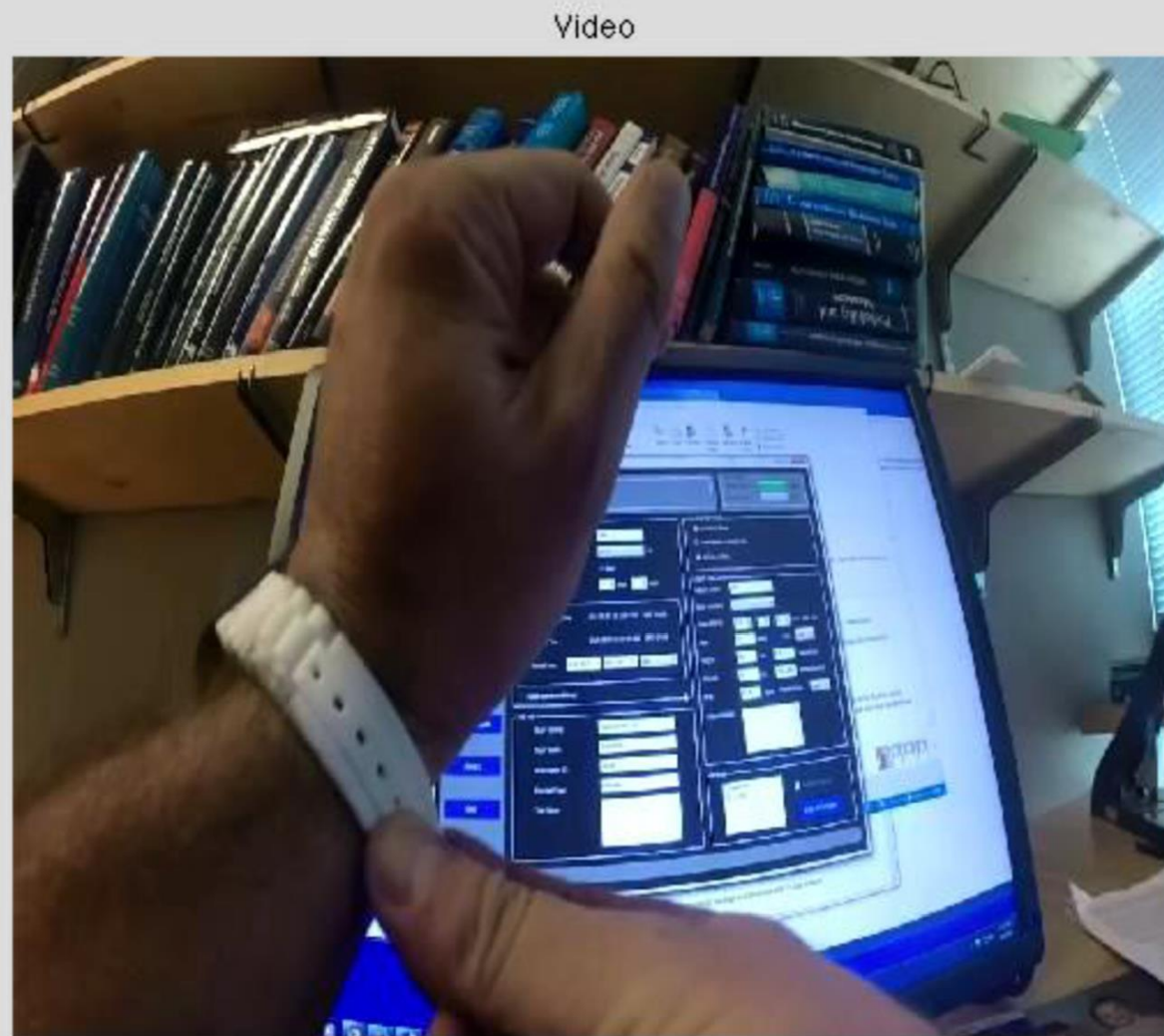
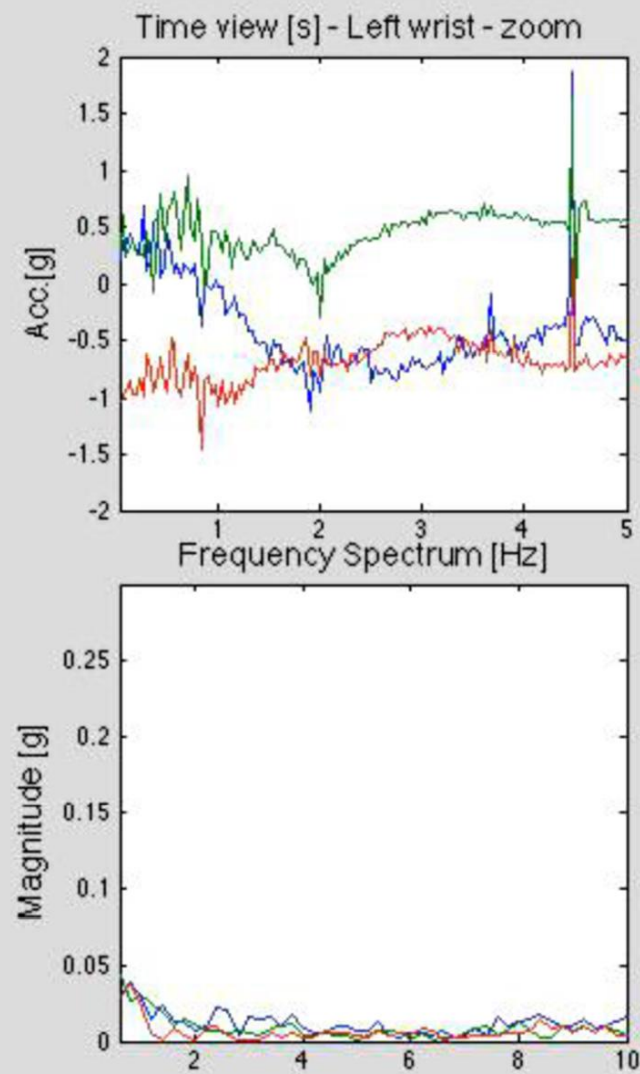
Ana-Maria Staicu

Philip Reiss

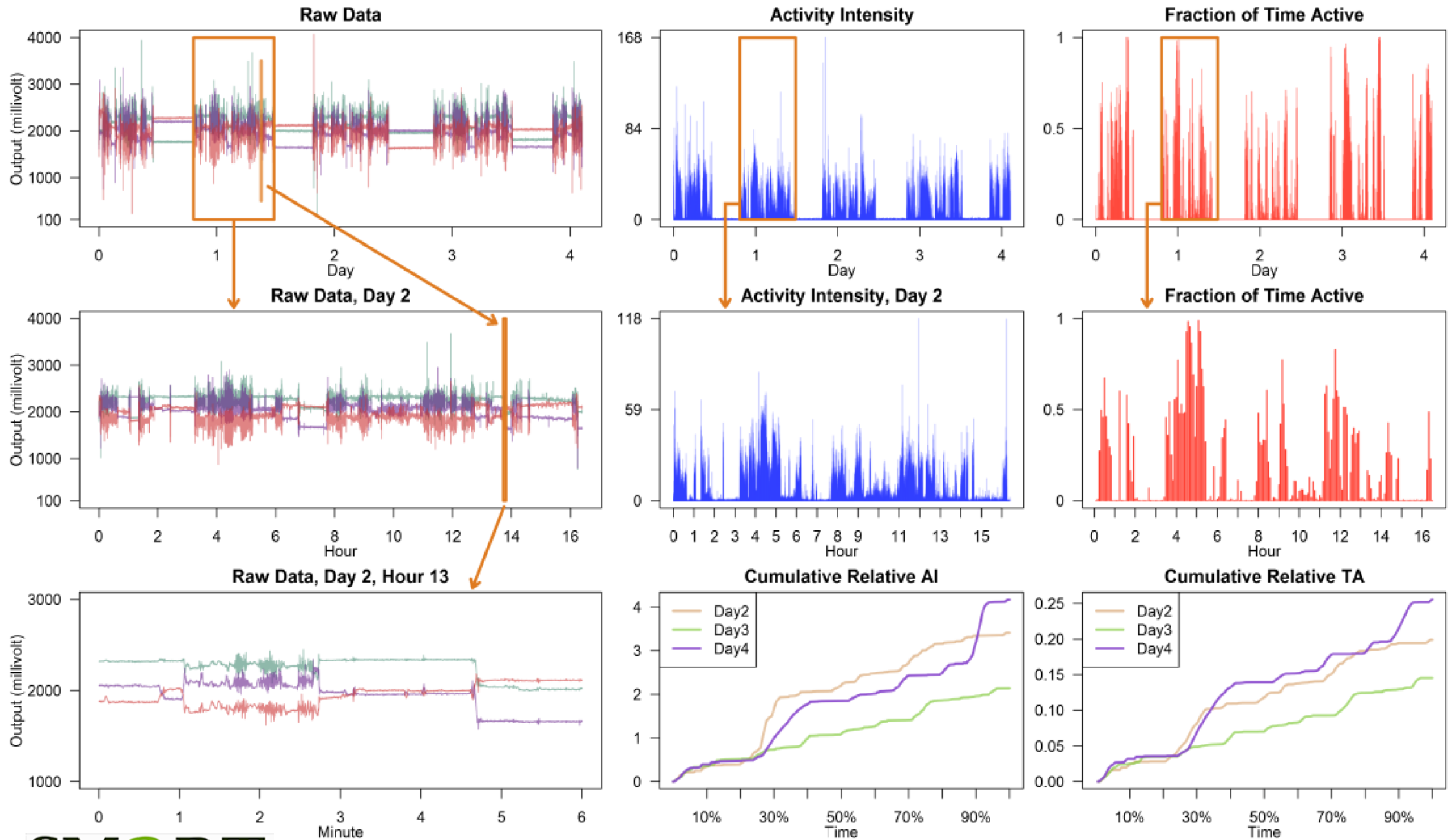
Taki Shinohara

What kind of sensors?

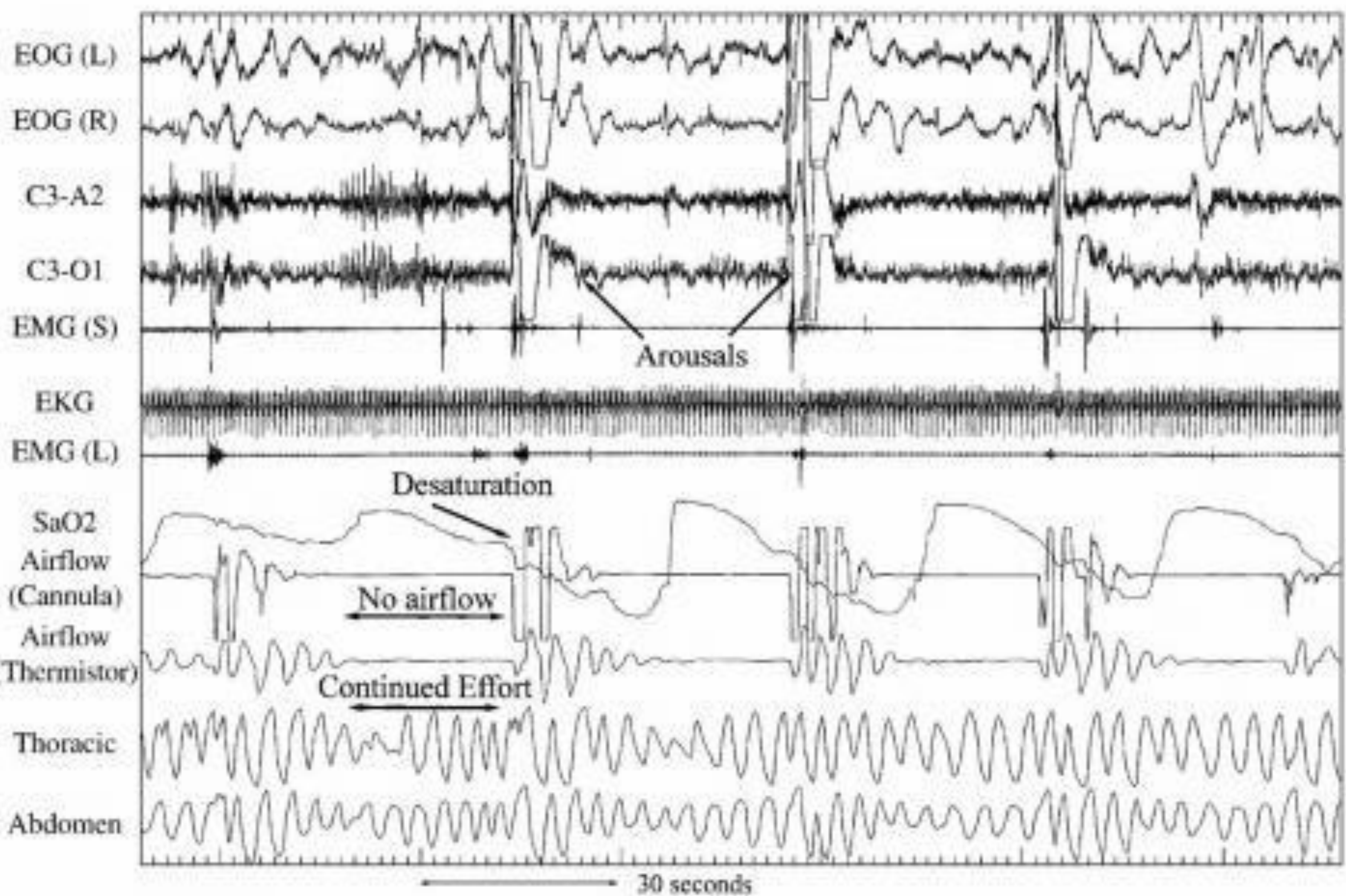




The many levels of activity data

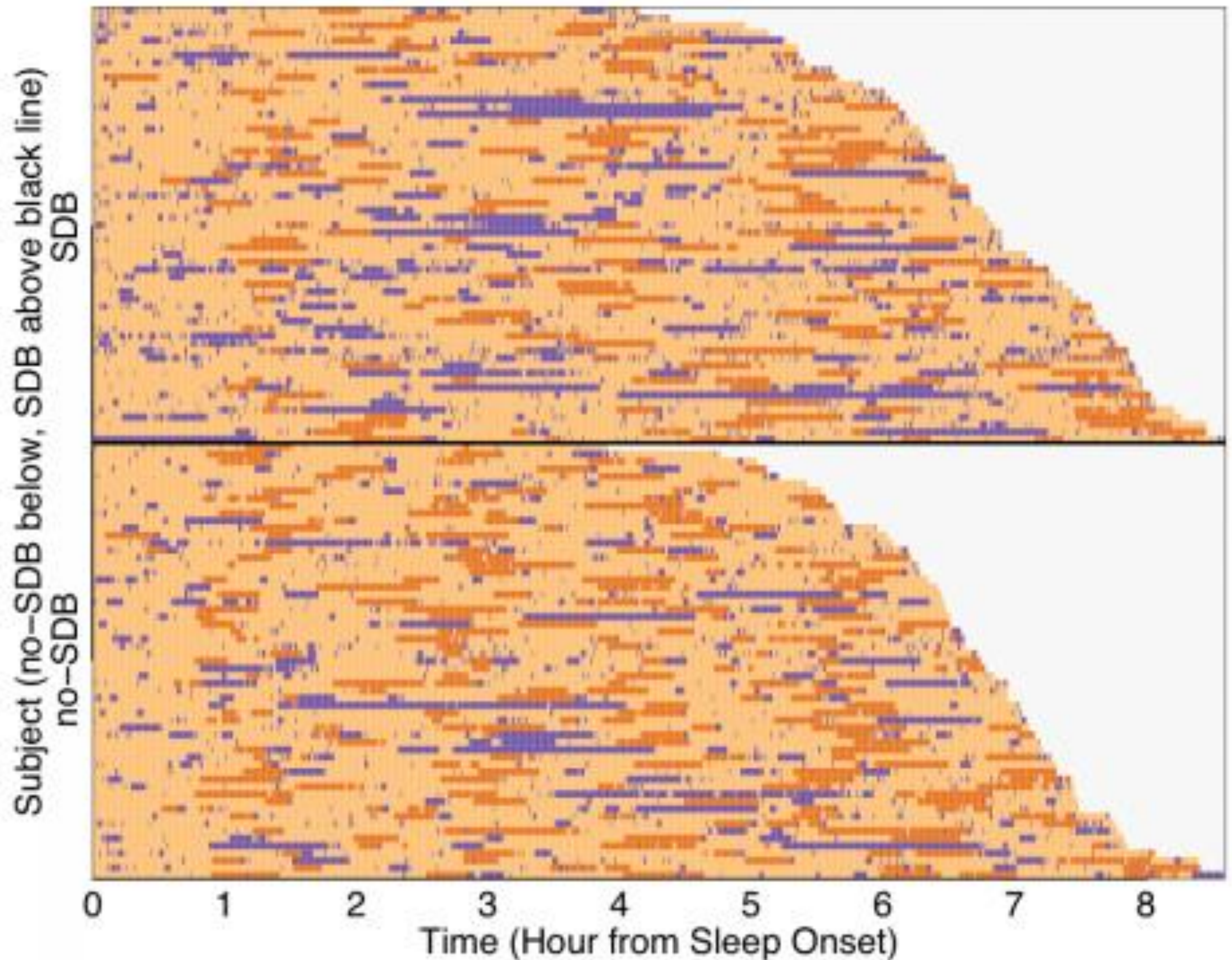


Sleep



Sleep

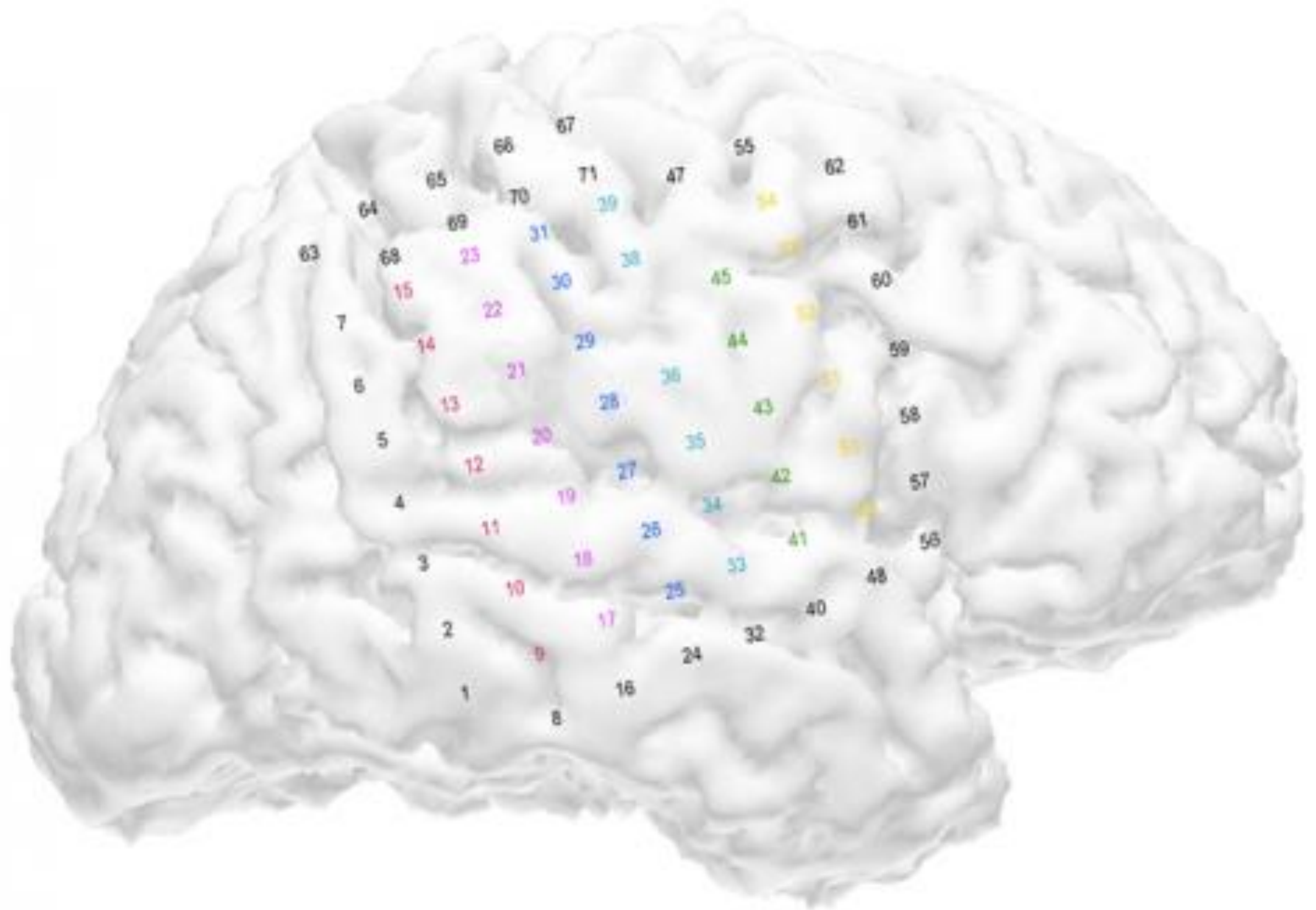
Lasagna Plot of Sleep States: Entire-row Sorted



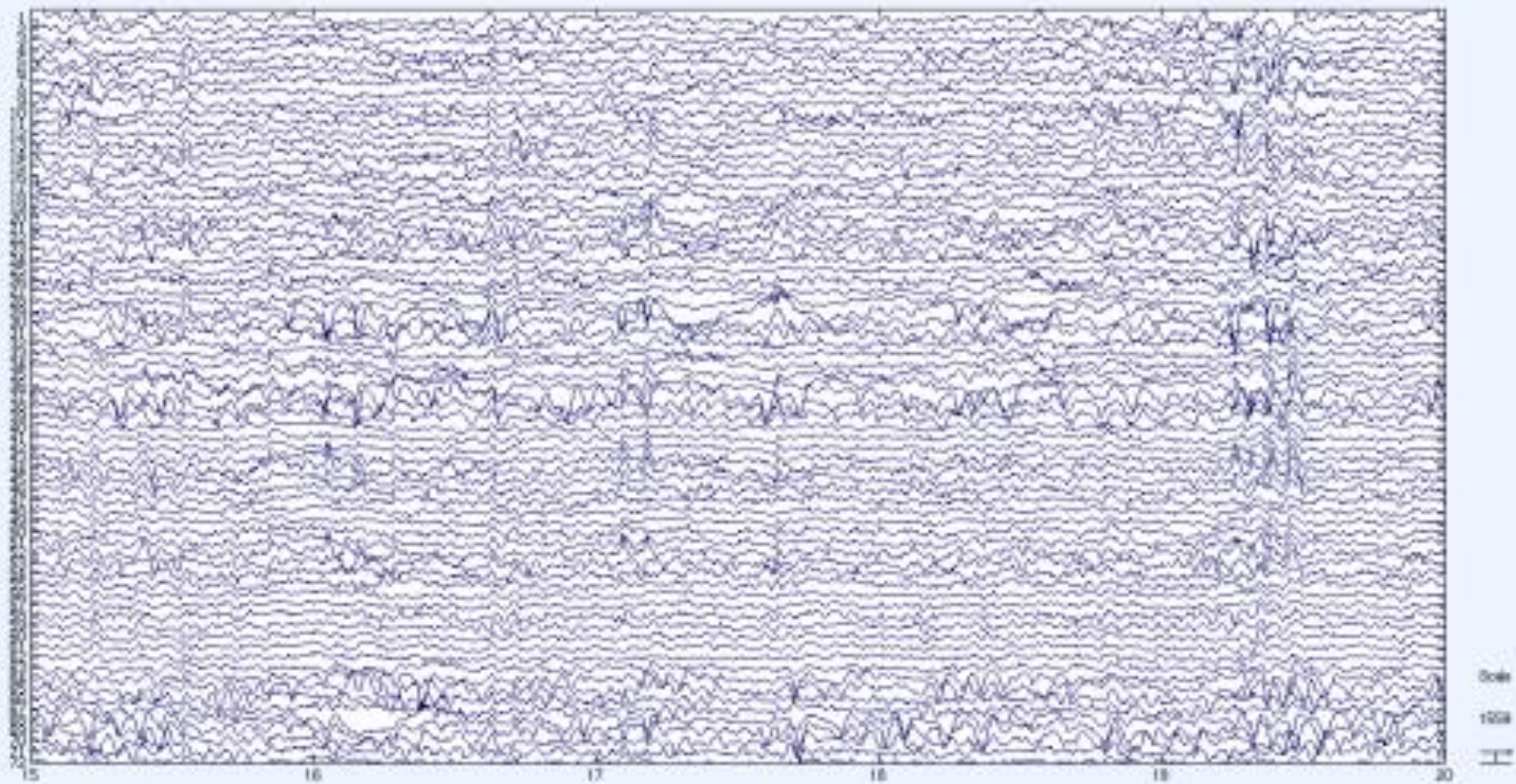
Stroke and Motion Integrity



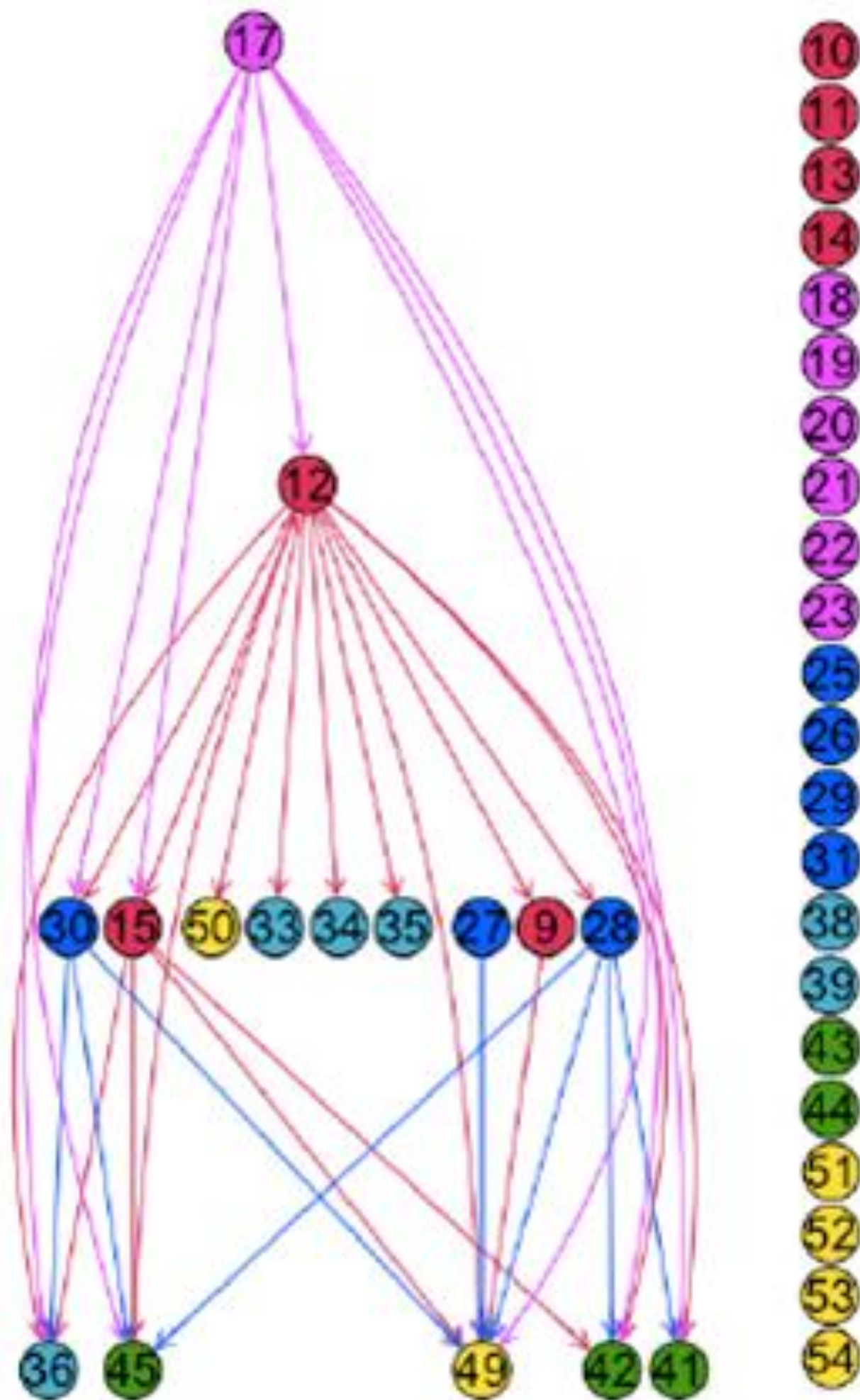
ECoG



ECoG

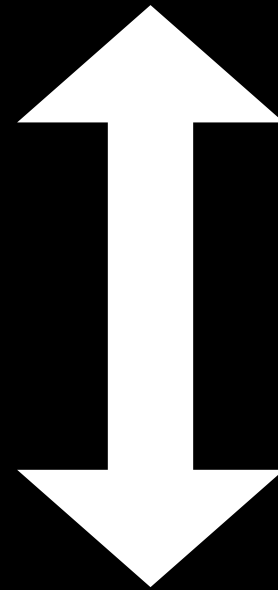


ECoG





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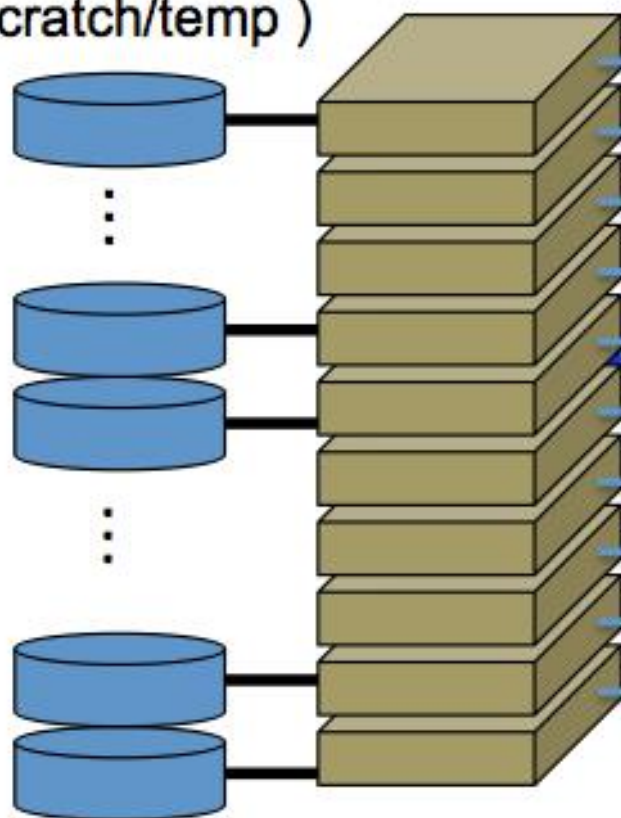
Current Public Health High Performance Computing

**“compute farm”
of compute nodes (hosts)**

direct attached
local disks (internal)
(/tmp, /scratch/temp)

2316

compute cores



1000 Mbps switches

1000 Mbps

Login server
jhpce01/02

100 Mbps

**workstations,
desktops &
laptops**



storage farm
(NFS exported file systems)

/home (and archives)
(70.5TB raw)

/thumper
(24TB raw)

/thumper2
(24TB raw)

/nexsan
(10.5TB raw)

/nexsan2
(14TB raw)



Sun 7210 (plus expansion tray)



Sunfire X4500 servers



Nexsan Sataboys

Future Public Health High Performance Computing



Thank You!