Midwest Workshop on Big Neuroscience Data, Tools, Protocols & Services

Provide and a service of the service



Computational Neuroscience Network (ACNN)

http://www.NeuroscienceNetwork.org/ACNN Workshop 2016.html

Predictive Big Data Analytics

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Characteristics of Big Biomed Data

IBM Big Data 4V's: Volume, Variety, Velocity & Veracity

BD Dimensions	Tools
Size	Harvesting and management of vast amounts of data
Complexity	Wranglers for dealing with heterogeneous data
Incongruency	Tools for data harmonization and aggregation
Multi-source	Transfer and joint modeling of disparate elements
Multi-scale	Macro to meso to micro scale observations
Incomplete	Reliable management of missing data
	Dipov at al (2014)

Example: analyzing observational data of 1,000's Parkinson's disease patients based on 10,000's signature biomarkers derived from multi-source imaging, genetics, clinical, physiologic, phenomics and demographic data elements.

Software developments, student training, service platforms and methodological advances associated with the Big Data Discovery Science all present existing opportunities for learners, educators, researchers, practitioners and policy makers

DINOV, EL UI. (2014)



Big Data

Raw Observations
Data Aggregation
Data Scrubbing
Semantic-Mapping

Information
Processed Data
Data Fusion
Summary Stats

Derived Biomarkers

Knowledge Maps, Models

Causal Inference

Networks, Analytics

Linkages, Associations

Action

Actionable Decisions Treatment Regimens Forecasts, Predictions Healthcare Outcomes 000 000

Dinov, GigaScience, 2016

End-to-end Pipeline Workflow Solutions



Dinov, et al., 2014, Front. Neuroinform.;

Dinov, et al., Brain Imaging & Behavior, 2013

Predictive Big Data Analytics in Parkinson's Disease

A unique archive of Big Data: Parkinson's Progression Markers Initiative (PPMI). Defining data characteristics – large size, incongruency, incompleteness, complexity, multiplicity of scales, and heterogeneity of information-generating sources (imaging, genetics, clinical, demographic)

- introduce methods for rebalancing imbalanced cohorts,
- utilize a wide spectrum of classification methods to generate phenotypic predictions,
- reproducible machine-learning based classification
- Results of machine-learning based classification show significant power to predict Parkinson's disease in the PPMI subjects (consistent accuracy, sensitivity, and specificity exceeding 96%, confirmed using internal statistical 5-fold cross-validation). Clinical (e.g., Unified Parkinson's Disease Rating Scale (UPDRS) scores), demographic (e.g., age), genetics (e.g., rs34637584, chr12), and derived neuroimaging biomarker (e.g., cerebellum shape index) data all contributed to the predictive analytics and diagnostic forecasting.
 Model-free Big Data machine learning-based classification methods (e.g., adaptive boosting, support vector machines) outperform model-based techniques (GEE, GLM, MEM) in terms of predictive precision and reliability (e.g., forecasting patient diagnosis). UPDRS scores play a critical role in predicting diagnosis, which is expected based on the clinical definition of Parkinson's disease. Even without longitudinal UPDRS data, however, the accuracy of model-free machine learning based classification is over 80%. The methods, software and protocols developed here are openly shared and can be employed to study other neurodegenerative disorders (e.g., Alzheimer's, Huntington's). Dinov, et al., PLOS, 2016



Predictive Big Data Analytics: Applications to Parkinson's Disease

Best Machine Learning Based Classification Results (according to average measures of 5-fold cross-validation)													
Data Strata	Classi fier	FP	ТР	TN	FN	Accu- racy	Sensi- tivity	Speci- ficity	positive predictiv e value	negative predictive value	log odds ratio (LOR)		
balanced control/PD	ada	0.2	102	115	0.6	0.99632	0.99414	0.99826	0.998039	0.9948097	11.4882		
balanced control/PD	svm	2.6	102	113	0.6	0.98529	0.99414	0.97743	0.975096	0.9946996	8.902166		
balanced control/PD&SWEDD	svm	3.4	101	112	1	0.97978	0.99023	0.97049	0.967557	0.9911348	8.1120092		
balanced control/PD&SWEDD	ada	1.4	101	114	1.8	0.98529	0.98242	0.98785	0.986275	0.9844291	8.4214		
unbalanced control/PD	ada	0.2	25	54	0.8	0.98753	0.96875	0.99634	0.992	0.9855072	9.039789		
unbalanced control/PD&SWEDD	ada	1.2	24	61	1.8	0.96599	0.92969	0.98083	0.952	0.971519	6.516987		
					Dir	ovetal PLOS	2016						



SOCR Big Data Dashboard http://socr.umich.edu/HTML5/Dashboard

□ Web-service combining and integrating multisource socioeconomic and medical datasets

□ Big data analytic processing

Interface for exploratory navigation, manipulation and visualization

Adding/removing of visual queries and interactive exploration of multivariate associations

Powerful HTML5 technology enabling mobile on-demand computing

Husain, et al., 2015, J Big Data



SOCR Dashboard (Exploratory Big Data Analytics): Associations





- The foundation for Compressive Big Data Analytics (CBDA) involves
 - Iteratively generating random (sub)samples from the Big Data collection.
 - Then, using classical techniques to obtain model-based or nonparametric inference based on the sample.
 - Next, compute likelihood estimates (e.g., probability values quantifying effects, relations, sizes)
 - Repeat the process continues iteratively.
- Repeating the (re)sampling and inference steps many times (with or without using the results of previous iterations as priors for subsequent steps).

Dinov, J Med Stat & Info, 2016

Define the nested sets

$$S_k = \{x: \|x\|_o \stackrel{\text{def}}{=} |supp(x)| \le k\},\$$

where the data x, as a vector or tensor, has at most k non-trivial elements. Note that if $x, z \in S_k$, then $x + z \in S_{2k} \supseteq S_k$

• If $\Phi_{n \times n} = (\varphi_1, \varphi_2, \varphi_3, ..., \varphi_n)$ represents an orthonormal basis, the data may be expressed as $x = \Phi c$, where $c_i = \langle x, \varphi_i \rangle$, i.e., $c = \Phi^T x$, and $||c||_o \le k$. Even if x is not strictly sparse, its representation c may be sparse. For each dataset, we can assess and quantify the error of approximating x by an optimal estimate $\hat{x} \in S_k$ by computing

 $\sigma_k(x)_p = \min_{\hat{x} \in S_k} \|x - \hat{x}\|_p$

• In compressive sensing, if $x \in \mathbb{R}^n$, and we have a data stream generating mlinear measurements, we can represent y = Ax, where $A_{m \times n}$ is a dimensionality reducing matrix $(m \ll n)$, i.e.,

$$A_{m \times n}: \mathbb{R}^n \to \mathbb{R}^m$$

• The null space of A,

$$N(A) = \{z \in \mathbb{R}^n : Az = 0 \in \mathbb{R}^m\}.$$

uniquely represents all $x \in S_k \Leftrightarrow N(A)$ contains no vectors in S_{2k} .

• The spark of a matrix A represents the smallest number of columns of A that are linearly dependent. If $A_{m \times n}$ is a random matrix whose entries are independent and identically distributed, then spark(A) = m + 1, with probability 1.

A



○ If the entries of A are chosen according to a sub-Gaussian distribution, then with high probability, for each k, there exists $\delta_{2k} \in (0,1)$ such that

 $(1 - \delta_{2k}) \|x\|_2^2 \le \|Ax\|_2^2 \le (1 + \delta_{2k}) \|x\|_2^2$ (1) for all $x \in S_{2k}$ (RIP=Restricted isometry property)

 O When we know that the original signal is sparse, to reconstruct x given the observed measurements y, we can solve the optimization problem:

 $\hat{x} = \arg\min_{z:Az=y} \|z\|_0$

- Linear programming may be used to solve the optimization problem if we replace the zero-norm by its more tractable convex approximation, the l_1 -norm, $\hat{x} = \arg\min_{z:Az=y} ||z||_1$
- Given that $A_{m \times n}$ has the above property and $\delta_{2k} < \sqrt{2} 1$, if we observe y = Ax, then the solution \hat{x} satisfies

$$\|\hat{x} - x\|_2 \le C_0 \frac{\sigma_k(x)_1}{\sqrt{k}}$$

- Thus, in compressive sensing applications, if $x \in S_k$ and A satisfies the RIP, condition (1), we can recover any k-sparse signal x exactly (as $\sigma_k(x)_1 = 0$) using only $O(k \log(n/k))$ observations, since $m = O\left(\frac{k \log(n/k)}{\delta_{2k}^2}\right)$
- Finally, if $A_{m \times n}$ is random (e.g., chosen according to a Gaussian distribution) and $\Phi_{n \times n}$ is an orthonormal basis, then $A_{m \times n} \times \Phi_{n \times n}$ will also have a Gaussian distribution, and if *m* is large, $A' = A \times \Phi$ will also satisfy the RIP condition (1) with high probability.



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 Repeating the (re)sampling and inference steps many times (with or without using the results of previous iterations as priors for subsequent steps).

Bootstrapping techniques may be employed to quantify joint probabilities, estimate likelihoods, predict associations, identify trends, forecast future outcomes, or assess accuracy of findings.
 The goals of compressive sensing and compressive big data analytics are different.

- CS aims to obtain a stochastic estimate of a complete dataset using sparsely sampled incomplete observations.
- CBDA attempts to obtain a quantitative joint inference characterizing likelihoods, tendencies, prognoses, or relationships.
- However, a common objective of both problem formulations is the optimality (e.g., reliability, consistency) of their corresponding estimates.

- O Suppose we represent (observed) Big Data as a large matrix Y ∈ R^{n×t}, where n= sample size (instances) and t = elements (e.g., time, space, measurements, etc.)
- To formulate the problem in an <u>analytical framework</u>, let's assume $L \in \mathbb{R}^{n \times t}$ is a low rank matrix representing the mean or background data features, $D \in \mathbb{R}^{n \times m}$ is a (known or unknown) design or dictionary matrix, $S \in \mathbb{R}^{m \times t}$ is a sparce parameter matrix with small support $(supp(S) \ll m \times t)$, $E \in \mathbb{R}^{n \times t}$ denote the model error term, and $\Lambda_{\Omega}(.)$ be a sampling operator generating incomplete data over the indexing pairs of instances and data elements $\Omega \subseteq \{1, 2, ..., n\} \times \{1, 2, ..., t\}$

• In this generalized model setting, the problem formulation involves estimation of *L*, *S* (and *D*, if it is unknown), according to this model representation: $\Lambda_{\Omega}(Y) = \Lambda_{\Omega}(L + DS + E)$ (2)

 Having quick, reliable and efficient estimates of L, S and D would allow us to make inference, compute likelihoods (e.g., p-values), predict trends, forecast outcomes, and adapt the model to obtain revised inference using new data

 When D is known, the model in equation (2) is jointly convex for L and S, and there exist iterative solvers based on sub-gradient recursion (e.g., alternating direction method of multipliers)

 However, in practice, the size of Big Datasets presents significant computational problems, related to slow algorithm convergence, for estimating these components that are critical for the final study inference

- One strategy for tackling this optimization problem is to use a random Gaussian sub-sampling matrix $A_{m \times n}$ (much like in the compressive sensing protocol) to reduce the rank of the observed data $(Y_{m \times l}, where$ $(m, l) \in \Omega$) and then solve the minimization using least squares
- This *partitioning* of the difficult general problem into smaller chunks has several advantages. It reduces the hardware and computational burden, enables algorithmic parallelization of the global solution, and ensures feasibility of the analytical results
- Because of the stochastic nature of the index sampling, this approach may have desirable analytical properties like predictable asymptotic behavior, limited error bounds, estimates' optimality and consistency characteristics



Data Structure (Representation)

Sample Data (Instance)

• One can design an algorithm that searches and keeps only the most informative data elements by requiring that the derived estimates represent optimal approximations to y within a specific sampling index subspace $\{(m, l)\} \subseteq \Omega$

 We want to investigate if CBDA inference estimates can be shown to obey error bounds similar to the upper bound results of point imbedding's in high-dimensions (e.g., Johnson-Lindenstrauss lemma) or the restricted isometry property

• The Johnson-Lindenstrauss lemma guarantees that for any $0 < \varepsilon < 1$, a set of points $\{P_k\}_1^K \in \mathbb{R}^n$ can be linearly embedded $(\Psi: \mathbb{R}^n \to \mathbb{R}^{n'})$ into $\{\Psi(P_k) = P_k'\}_1^K \in \mathbb{R}^{n'}$, for $\forall n' \ge 4\left(\frac{\ln(K)}{\frac{\epsilon^2}{2} - \frac{\epsilon^3}{3}}\right)$, almost preserving their pairwise distances, i.e., $(1 - \epsilon) \|P_i - P_j\|_2^2 \le \|P_i' - P_j'\|_2^2 \le (1 + \epsilon) \|P_i - P_j\|_2^2$ • The restricted isometry property ensures that if $\delta_{2k} < \sqrt{2} - 1$ and the estimate $\hat{x} = \arg \min_{z:Az=y} ||z||_1$, where $A_{m \times n}$ satisfies property (1), then the data reconstruction is reasonable, i.e., $\|\hat{x} - x\|_2 \leq C_0 \frac{\sigma_k(x)_1}{\sqrt{k}}$ Can we develop iterative space-partitioning CBDA algorithms that either converge to a fix point or generate estimates that are *close* to their

corresponding inferential parameters?

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http://SOCR.umich.edu

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