

Statistical Learning of Biological Structure in the Human Brain

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”But above all, master technique and produce original data; all the rest will follow.”

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Bludau S*, **Bzdok D***, Gruber O, Kohn N, Riedl V, Mller V, Hoffstaedter F, Eickhoff SB. Medial prefrontal aberrations in major depressive disorder revealed by cytoarchitectonically informed voxel-based morphometry. *American Journal of Psychiatry*, in press. *equal contributions

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Review and opinion papers

Eickhoff SB, Thirion B, Varoquaux G, **Bzdok D**. Connectivity-based parcellation: critique & implications. *Human Brain Mapping*, in press.

Eickhoff, SB & **Bzdok D**. Neuroimaging and modeling. Where is the road to clinical application? *Der Psychiater*, 2014, in press.

Eickhoff SB & **Bzdok D**. [Statistical meta-analyses in imaging neuroscience.] *Klinische Neurophysiologie*, 2013, 44:199-203.

Book chapters

Bzdok D & Eickhoff SB. Statistical learning of the neurobiological of schizophrenia. In: *The neurobiology of schizophrenia*, Springer, Heidelberg.

1 Introduction

1.1 Analytical and heuristic accesses to nature

The world around us is complex and volatile. A large proportion of human research efforts are undertaken in an *analytical* fashion based on the "the unreasonable effectiveness of mathematics in the natural sciences." This was phrased by the Hungarian-American physicist, mathematician, and Nobel laureate Eugene P. Wigner (1960). The language of mathematics is a powerful tool to describe, formalize, and predict phenomena in nature. The author emphasizes that it is not imperative that natural regularities exist in the world. He goes on to say that it might be even more surprising that humans can actually find these regularities and use them to their advantage. Similarly, Albert Einstein said: "The most incomprehensible, is that the world is comprehensible." Starting from human-conceived axioms we have derived always more complicated properties of and relationships between mathematical objects by formal proofs (Connes A., "A view of mathematics"). A logical pyramid of theorems is built that lead to always more general assertions. We also have detailed knowledge of the limitations of these mathematical assertions. On the one hand, an identical regularity can often be equally well described in very distant branches of mathematics. On the other hand, identical mathematical conclusions have reemerged from derivation of a priori unrelated assertions. Indeed, the same formal language has proved very apt in the study of completely unrelated topics and diverging scientific disciplines. This includes movements of celestial objects in the universe studied in astronomy and the metabolism pathways governing the inner life of the cell studied in biochemistry. Many rules about the world can thus be perfectly grasped (Hardy, "Apology"). As another simple example, Fibonacci numbers (1, 1, 2, 3, 5, 8, 13, etc.) reappear in many natural phenomena. The number of petals of a flower and the spirals of a pineapple tend to be Fibonacci sequences. The family tree of honey bees is also governed by Fibonacci regularities. Even the proportions of human finger bones follow this formalism. Knowledge of such mathematical regularities allows to impose logical structure on the external world. It remains an unresolved philosophical debate whether we have *discovered* or *invented* mathematics. Yet, there is probably no doubt that mathematical conceptualization evolves as a feature of human cultural evolution (Tomasello, 2001). Even the most abstract mathematical concepts can be exchanged between individuals. Consequently, this knowledge resource can be easily passed on across generations and geographical distances. One may note that there is usually consensus among mathematicians about the architecture of their discipline. From an anthropological perspective, mathematical formalism appears to be one of the most powerful tools and most defining properties of the human species (S. Dehaene, "The Number Sense"). Indeed, Eugene Wigner concludes his praise of equations with the following words: "The miracle of the appropriateness of the language of mathematics for the formulation of the laws of physics is a wonderful gift which we neither understand nor deserve. We should be grateful for it and hope that it will remain valid in future research [...]." (1960, p. 14).

However, this dogma has repeatedly been challenged formally and empirically. In formal approaches, mathematics were shown incomplete and inherently contradictory because, in any axiomatic systems, some true assertions cannot be proven ("incompleteness theorems", Gödel, 1931). Additionally, it is possible to define a real number with equidistributed digits that can however not be computed ("Chaitin's constant Ω ", Chaitin, 2006). In empirical approaches, the omnipotence of mathematical equations has been challenged as the best possible way to describe and predict nature (Halevy et al., 2009; Hinton/LeCun/Bengio, 2015; Pietsch, 2017). This shift in the scientific discourse is made explicit by three recent empirical observations:

1. Sophisticated, more accurate models can be outperformed by simple models that are fit with massive training data.
2. Simple models trained with rich data can outperform models that have been designed according to extensive domain expertise.
3. There appears to be a minimal threshold of training data for deriving models to suddenly exhibit emergence properties.

One prominent example for modelling nature in such a *heuristic* fashion is automatic language translation of human text and speech. Translation systems based on human-derived systems of grammar rules have perhaps never achieved satisfactory success (P. Norvig, 2011, "On Chomsky"). That is, analytical approaches based on thousands of books pages storing domain expertise in form of deterministic rules appeared insufficient for building language models that can cope with real-world settings. Statistical machine translation was more successful by implementing probabilistic hidden Markov models (HMM) as a heuristic approach. The next word or N-gram is predicted only by the one (order 1) or few (order n) preceding ones with equal transition probabilities (Bengio, 1998 "Markovian Models"). This special case of a recurrent neural network computes the conditional probabilities of the next language element depending on the most recent history of these elements based on a dictionary of known elements. The transition matrix of human language can be easily *learned* from data by observing a preferably long stream of real-world language (i.e., a "corpus"). The class of HMMs thus became a dominating feature of computational linguistics. Today, virtually all professional translation software solutions for both written and spoken language are enabled by heuristic mathematical models.

As an example from human biology, we currently have only few means to predict the toxicity of environmental chemicals and potential effects of new drug compounds on health. The complex and unknown phenomenon in nature here pertains to the causal link from a protein's *known* primary structure (i.e., 1D string of aminoacids) to its *unknown* tertiary/quaternary structure (i.e., the combination of 3D foldings of the aminoacid string that subserves function). Among the millions of existing proteins we only know the tertiary/quaternary structure of approximately 30.000 ones. The structural configuration is however necessary to identify the position of bindings sites for protein-protein interaction. Knowledge of these sites

in 3D space is crucially important to infer that protein’s interplay with the human body. In this case, the learning problem is to derive a computational model from massive pairs of known primary protein structure and known protein properties, including toxicity, by intentionally treating the 3D structure as a black box. State-of-the-art neural network algorithms have very recently solved this heuristic learning problem better than any previous approach in academia or industry (Dahl et al., 2014; Unterthiner et al., 2015). These investigators thus showed that biological activity can be reliably predicted from single aminoacid strings even without recourse to biological domain expertise. There might currently not exist an analytical counterpart to such structure-function mapping of proteins. Similar probabilistic scenarios would include predicting political outcomes, optimizing advertisement strategies, algorithmic trading in stock markets, and controlling self-driving cars.

In sum, humans can create machines to derive algorithmic predictions from the data. Observing a phenomenon in nature a sufficient number of times might be sufficient to algorithmically extract the heuristics of its interaction behavior with the world. This has recently entailed a shift of attention from model complexity to data complexity and from purely mathematical treatment to giving up some control to self-emerging patterns. In the absence of an analytical alternative access, simple mathematical models can thus automatically formalize diverse classes of natural phenomena depending on the quality and quantity of the available data resources.

1.2 Two cultures of statistical modelling

Statistics is a branch of mathematics that has arguably been the overall most successful information science. Statistics aim at extracting information from data about the mechanisms in nature that generated these data. Given its eclectic character, it may come as no surprise that statistics has developed both analytical and heuristic strategies to model regularities of phenomena in nature. Yet, analytical and heuristic statistical cultures have developed independently (Breiman, 2011). They differ with regard to historical origin, mathematical foundation, and modelling goal.

The overwhelming majority of statisticians follow an analytical regime by adhering to *classical statistics* (CS) for *data modelling*. They hold that the phenomenon under study can be viewed as a black box whose inner workings can be described by a small set of underlying variables. It is up to the statistician in charge to choose the model that best reflects nature. Data are then used to estimate the parameters of that pre-specified model. Classical statistics have dominated research at the universities for almost 90 years now. Well known members of the CS family include for instance Student’s t-test, ANOVA, and Chi-squared test. *Statistical hypothesis testing* has been introduced in the beginning of the last century (Fisher, 1925; Neyman and Pearson, 1928). The same approach is still practiced today in its original form (Goodman, 1999). The ensuing *p-value* measures how likely it is to observe the data at hand assuming the non-preferred null hypothesis (H_0) to find indirect evidence for the preferred alternative hypothesis (H_1). Despite the prevailing

presence of p-values, it has not been conceived by Fisher as an acid test to judge existing versus non-existing effects in nature. Rather, the intention was a preliminary tool to filter which potential effects should be more explicitly tested (Nuzzo, 2014). Notably, the drawn conclusions may be wrong if the hand-selected model is a bad description of the natural phenomenon under study. Nevertheless, statistical hypothesis testing probably fit perfectly in its time of inception and adoption. Indeed, it was designed for use with mechanical calculators (Efron and Tibshirani, 1991). Gaussian distributional assumptions have been very useful in many instances for mathematical convenience and, hence, computational tractability. Additionally, it suited perfectly the Popperian view of critical empiricism in academic discourse (Popper, 1935/2005 "Logik der Forschung"): scientific progress is to be made by continuous replacement of current hypotheses by always more explanatory hypotheses by means of *verification* and *falsification*. The rationale behind hypothesis falsification is that even a lot of evidence cannot confirm a given theory in an *inductive* way, while a single counter example is able to proof a theory wrong in a *deductive* way. In sum, classical statistics was mostly fashioned for problems with few data points that can be modeled by plausible models with a small number of parameters chosen by the investigator.

In contrast, only a small minority of statisticians follow a heuristic regime by adhering to *statistical learning* (SL) for *algorithmic modelling*. This statistical framework is frequently adopted by computer scientists, physicists, ingenieurs, and others without formal statistical background that are typically working in industry rather than academia (cf. Daniel and Wood, 1971). They hold that natural phenomena can be studied by estimating regularities in the inputs and outputs to the black box without making assumptions about its internal "true" mechanisms. A statistical model is thus derived that expresses relationships between the input and output variables whose parameters are learned by training data (Abu-Mostafa, 2012). Put differently, a new function with potentially thousands of parameters is created that can predict the output from the input alone, without explicit programming model. The input data thus need to represent different variants of all relevant configurations of the examined phenomenon in nature. Well-known members of the SL family include for instance k-means clustering, Lasso/Ridge regression, and support vector machine classification. Please note that SL here summarizes the seemingly more specific terms "data-mining", "pattern recognition", "artificial intelligence", and "machine learning" that are often employed inconsistently. The independent historical origin of CS and SL families is even witnessed by the most basic terminology. In the CS literature inputs to statistical modeling are classically called *independent variables* or, more recently, *predictors*, while these are commonly referred to as *features* in the SL literature (Hastie et al., 2011). When evaluating whether a certain problem is a possible target for SL three requirements come into play (Abu-Mostafa, 2012):

1. A regularity exists (if there is no pattern, then it might still be worth trying SL).
2. The regularity cannot be formalized analytically (otherwise one can still apply SL, but it might not

create the best model).

3. We have data on the problem (the more, the better).

This statistical framework led to a surge of new computer-intensive statistical techniques since 1980 that can be difficult to compute on a normal calculator and that are less concerned with mathematical tractability (Efron, 1991). In the 95'ies support vector machines (SVMs) proofed to be better than the back then de-facto-standard neural networks in both classification and regression problems (Valpniek, 1996). This development has been flanked by changing properties of datasets that are always higher-dimensional (i.e., more features per observation) and based on larger samples (i.e., more observations). This is a trend that is not specific to neuroimaging research but also takes places in other scientific disciplines, including but not exclusive to weather forecasting and economic predictions (Manyika et al., 2011). In sum, statistical learning was mostly fashioned for problems with many data points with largely unknown data generating processes that are emulated by a mathematical function created en passant by a machine.

Importantly, some statistical methods cannot be easily categorized by the CS-SL distinction. Statistical methods do, in fact, span a continuum between the two poles of CS and SL (Jordan/Frontiers in Massive Data, p. 61). Nevertheless, the two families of statistical methods can be easily distinguished by a number of archetypal properties. Bayesian statistics are however orthogonal to the CS-SL distinction and can be adopted in both methodological families in various flavors. Neither can the terms univariate versus multivariate (i.e., relying on one versus more than one input variable) be clearly grouped into either CS or SL. More generally, neither CS nor SL can generally be considered superior. This is captured by the *no free lunch theorem* stating that no single statistical strategy can consistently do better in all circumstances (Domingos, 2012; Wolpert, 1996). The challenge relies in choosing the statistical approach that is best suited to the neurobiological phenomenon under study and the neuroscientific research object at hand.

Regarding modelling goals, CS and SL exhibit various differences. CS typically aims at modeling the black box by making a set of accurate assumptions about its content, e.g. the type of signal distribution. Contrarily, SL typically aims at finding any way to model the output of the black box from its input while making the least assumptions possible (Abu-Mostafa et al., 2012). In CS the phenomenon is therefore treated as partly known (i.e., the stochastic processes that generated the data), whereas in SL the phenomenon is treated as complex, completely unknown, and partly unknowable. It is in this way that CS tends to be analytical (i.e., imposing mathematical rigor on the phenomenon), whereas SL tends to be heuristic (i.e., finding useful approximations to the phenomenon). CS assumes a given statistical model at the beginning of the investigation, whereas in SL the model is generated in the process of the statistical investigation. In more formal terms, CS therefore closely relates to parametric statistics for *confirmatory* data analysis, whereas SL closely relates to non-parametric statistics for *exploratory* data analysis (Tukey, 1977 "Exploratory data analysis"). In more practical terms, CS is typically applied to experimental data that were generated

the investigator controlled the variables of interest (i.e., the system under studied is perturbed), while SL is typically applied to observational data without such structured influence by the investigator (i.e., the system is left unperturbed) (Domingos, 2012). The work unit for CS is the quantified significance associated with a statistical relationship between few variables given a pre-specified model. The work unit for SL is the quantified robustness of patterns between many variables or, more generally, the robustness of *special structure* in the data (Hastie et al., 2011). CS therefore tests for a particular structure in the data, whereas SL explores and discovers structure in the data. Formally, CS implements data modeling by imposing an a priori model in a top-down manner, whereas SL implements algorithmic modeling by fitting a model as a function of the data at hand in a bottom-up manner. Intuitively, the "truth" is believed to be in the model (cf. Wigner, 1960) in a CS-constrained world, while it is believed to be in the data (cf. Halevy et al., 2009) in a SL-constrained world.

As a drastically oversimplified, yet useful, conclusion, CS preassumes and tests *a model for the data*, whereas SL learns *a model from the data*. Indeed, both human and computer learning are theoretically more conceivable in a probabilistic rather than deterministic sense (Abu-Mostafa et al., 2012; Dayan et al., 1995; Friston, 2010; Gregory, 1980). Moreover, each probabilistic model can be viewed as a superclass of a deterministic model (P. Norvig, "On Chomsky"). Taken together, CS assumes that the data behave according to known mechanisms, whereas SL exploits computer algorithms to avoid the a-priori specifications of data mechanism.

1.3 The human brain as a complex phenomenon in nature

The human brain is a prime example of a black box that is complex, mysterious, and perhaps in part unknowable. It is frequently proposed that the human brain might be the most complex object in the known universe (Nature editorial, october 2014). With the language from above, the human brain might constitute a phenomenon in nature that can *not* be perfectly grasped by mathematical formalism alone. More concretely, the *most pertinent structure* that we should assume for the human brain, when measured by contemporary functional neuroimaging techniques (cf. next passages), is currently unknown. Hence, the neuroimaging access to neuroscience can readily be framed as a problem of *representation learning* (Bengio, 2014). It is conceivable that this task can be solved without exhaustive multi-level neurobiological knowledge (Bostrom, 2014). This is always more supported by empirical evidence (e.g., Helmstaedter, M. et al. "Connectomic reconstruction" 2013 Nature) and it is a contention that is embraced by the present dissertation.

From a global perspective, the genetic difference between our genetic equipment and that of our closest ancestors, the non-human primate, turns out to be strikingly small. This has encouraged the conviction that one or very few key genetic adaptations in the primate lineage have unchained an avalanche of cognitive and cultural inventions that led up to today's civilization (Tomasello, 2001). That is, the human species might be much more defined by the increasingly fast cultural evolution rather the ramifications of slow

biological evolution. Crucial cognitive improvements, such as the emergence of verbal language, might have fueled cultural improvements that, in turn, enabled further cognitive improvements et cetera pp. This form of *online learning* is a very plausible and decisive property of intact tissue of the central nervous system. As a first challenge in brain science, it might therefore be impossible to cleanly dissect the nature-nurture interplay into independent contributing factors that act during phylogeny (i.e., development of the species) and ontogeny (i.e., development of an individual organism). In this sense, investigating the limits between "nature" and "culture" in humans might equate with asking a paradoxical question (Dehaene & Cohen, 2007). Instead, a necessary factor for the high level of abstraction in human culture might have precisely been the inextricability, due to bidirectional influence, of neurobiological plasticity and relentless cultural exchange between human individuals in a non-stop, autopoietic optimization process (Vygotsky 1978, "Mind in Society"; Luhmann 1984, "Soziale Systeme"; Bengio 2013, "Evolving Culture").

Given this recent acceleration in cultural evolution (cf. Paul Virilio, "Open Skype"), it might be rather unlikely that the human brain has developed dedicated neuronal populations to subserve the panoply of novel behaviors. Rather, evolutionarily recent mental skills (e.g., reading and writing, explicit pedagogy, and symbolic mathematics) are realized by recombining low-level circuits that initially developed for other functional roles. This view has become known as "neural reuse" and "neural recycling" hypotheses (Anderson, 2010; Dehaene & Cohen, 2007). Non-human primates are lacking many of the sophisticated mental operations that are crucially important for maintaining human societies (Mesulam, 1998; Tomasello, 2003). In fact, the "social brain hypothesis" states that our computationally powerful brains are not an adaptation to solve problems posed by the physical environment, but for successfully coping with increasingly complex human social systems (Humphrey, 1984; Byrne et al., 1988; Dunbar and Shultz, 2007). Yet, it is becoming increasingly clear that socialaffective processing in the human brain is probably realized by domain-general brain regions and networks not specific to maintaining social interactions (Bzdok et al., 2015 "Neurobiology of Morality"; Behrens et al., 2009 Computation; Barret et al., 2013). These considerations entail a second challenge in brain science: It is probably impossible to know what purpose neural processing in a given part of the brain has originally evolved to serve. We can only observe external manifestations and correlative relationships of this latent biological purpose.

Importantly, no two human brains are alike. Quite the opposite, they differ with regard to the morphology of gyri and sulci, the topology of cytoarchitectonically and chemoarchitectonically distinguishable brain areas, the axonal connections linking these brain areas, as well as the history of their sensory inputs. The extent of a brain area and its inter-individual variability can be quantitatively examined with its relation to cognition and behavior, that is, performance in psychological tasks in the healthy or diseased brain. For instance, the volume of the amygdala is linked to interindividual differences in memory performance as well as many other (temporally transient) states and (temporally enduring) traits. As another challenge in brain science, it is currently unknown how brain-behavior correlations are mediated. The renowned neu-

roanatomist Santiago Ramón y Cajal wrote (1909): "The complexity of the nervous system is so great, its various association systems and cell masses so numerous and complex, and challenging, that understanding will forever lie beyond our most committed efforts." More specifically, it remains largely elusive whether distinct behavioral differences between individuals are associated with changes of cell bodies, dendrites, axonal connections, and/or glial cells (Kanai et al., 2011). That is, we do not have clear understanding of how this set of microstructures interact to solving neural computation problems, let alone their inter-individual differences. From a methodological perspective, the conventionally employed volumetric modelling techniques are naïve to many types of possible morphological differences. For instance, it is currently difficult to statistically grasp inversely proportional left and right hemisphere volumes or a condition that randomly affects either the left or the right brain per individual (Ashburner et al., 2011).

Worth to be proposed as an independent challenge of brain science, the secret of interhemispheric asymmetry is yet to be unveiled. The connectivity differences between the left and right brain are for instance currently underresearched. They are even hardly known in the monkey (Stephan, 2007) that usually serves a fallback system for human connectivity investigations (Mesulam, 2012 "The evolving"). In humans, the majority of homologous brain areas feature direct anatomical connections. Nevertheless, as two textbook examples, why the language and attention processes typically lateralize to the left and right hemisphere, respectively, is currently understood only in fragments (Corbetta 2000; Stephan et al., 2003; Price et al., 2010).

It is further unlikely that we will reach exhaustive understanding of the human brain by mere *observational*, as opposed to *interventional*, classes of research methods. This idea is reflected in Edward O. Wilson's words "disturb Nature and see if she reveals a secret" as well as in G. M. Shepherd's words "Nothing in neuroscience makes sense except in the light of behavior." Purposely induced focal lesions of brain tissue in rats have early been systemically related to resulting differences in behavioral performance indices (Franz and Lashley, 1917). In hamsters, cats, and monkeys, decortication entails only small sensory or motor effects, while such tissue impairments of the neocortex in humans result in much more pronounced and less reversible functional deficits than similar lesions in humans (Lashley, 1952; MacLean, 1982), which points to increasing corticalization of brain function. In humans, brain lesion studies and direct brain stimulation during neurosurgical interventions have been the most common approaches to localize brain functions until about 20 years ago. However, inferring neurobiological insight from lesion findings constitutes yet another challenge to brain science. It constitute an overly simplistic conclusion that changes in behavior after destroying brain tissue in a circumscribed brain area directly reveals functional roles of that brain area (Young, 2000). It is a limitation of these studies that they attempt to derive the *normal* function of an area from the effects of *damage* to that area. First, the destroyed brain area might primarily subserve inhibitory effects, such that abolition can increase neural processing subserved in remote areas mediated by network connections. Second, a large fraction of human lesion cases are stroke patients. The spectrum of lesion

patterns found in these populations is however seriously limited by the existing spectrum of brain vessel anatomy. Third, there is probably not a single psychiatric disorder that would be characterized by very *focal* (as opposed to distributed) differences in brain structure (cf. Goodkind, 2015 JAMA). More generally, it is still a matter of debate whether structure (i.e., locally specific micro- and chemoarchitecture), connectivity (i.e., short- and long-rang axonal targets), and function (i.e., lesion-induced behavioral changes) reflect three viewpoints on the same heterogeneity of a particular brain area (Passingham et al., 2002; Kelly et al., 2012 Neuroimage).

Each area in the brain exhibits activation patterns of neuronal populations with oscillatory regularities. These oscillatory circles and their associated behaviors are highly preserved in mammalian evolution (Buzsaki, 2013 "Scaling brain size"). Perhaps since Hubel and Wiesel's (1965) description of increasingly complex processing of neurons in the primary visual cortex neuroscientists tend to think information processing as serial sequences of incoming bottom-up sensory and modulating top-down information streams. Axonal feed-forward and feed-back connections are indeed a very good predictor of *what* the next processing step is. Yet, brain oscillations are capable of predicting *when* this next processing step will occur. Oscillation measured by EEG and MEG techniques might be the most attractive access to another challenge in brain science: *the binding problem* (Singer, 1999; Engel, 2001; Varela, 2001). We are far from understanding how environmental perturbation by multi-sensory stimulation is coherently integrated and linked with prior experience into a holistic higher-order percept via spatially distributed and temporally coherent electrophysiological activity. In animals, oscillatory but not spiking activity of neuronal populations appears to be closely associated with sensory input processing. The interpretation of oscillation findings is however demanding. This is because they simultaneously reflect a maintenance equilibrium, sensitivity to external stimuli, and formation of processing outputs. For instance, perception is an intrinsically probabilistic process with nonidentical results depending on the state of ongoing oscillatory circles. Additionally, different "rhythms" (i.e., frequency bands) flank each other in a same brain area in an interacting fashion. The same rythm can reflect different categories of computational processes in different brain areas and networks. Some brain structures are characterized by specific rythms that may not be found in the rest of the brain. Different frequency bands can subserve a same cognitive process, while different cognitive processes can be realized by the same frequency bands. Finally, high frequencies govern large-scale networks in the brain that, in turn, influence small local neuronal space with slow oscillatory patterns.

Also from a philosophical perspective the neuroscientist faces problems when articulating observations of phenomena in the brain. For instance, brain areas or experimental effects are frequently described according to "emotional" versus "cognitive" interpretational categories. However, this class of judgments implicitly preassumes the neurobiological validity of traditional psychological categories. That is, it assumes that those two concepts have a discrete representation in measurable neurobiology. Yet, as another major challenge to brain science, it remains elusive how and to what extent psychological terms, such as "emotion" and

"cognition" (Pessoa, 2008; Van Overwalle, 2011), map onto regional brain responses (Laird et al., 2009; Mesulam, 1998; Poldrack, 2006). Potentially unjustified a-priori hypotheses are imposed on the organization of human brain systems. It should hence be carefully called into question what terms are an adequate word choice to refer to discrete neurobiological processes. More globally, confusion introduced by human language itself is at the origin of many scientific problems (Wittgenstein, 1953/2001 "Philosophical Investigations"). The grammatical and lexical constraints of human language might be too tight to allow for unequivocal description of the diverse circumstances humans encounter in science and ever-day life. According to Wittgenstein the meaning of language is primarily defined by its practical use in concrete situations, rather than decontextualized abstractions necessarily pre-shared by the interlocutors. Words might not have an objective meaning equally accessible to and understood by everybody. This is all the more the case for language descriptions of phenomena that do not occur in every-day reality. Discussing subtleties of abstract neurobiological concepts, which can hardly be practically experienced, are frequent subject to ambiguity, thus leading to unnoticed misunderstanding and unresolvable paradoxes (cf. Bostrom, 2002; Watzlawick et al., 1967). Biological processes in the brain are an instance of such not directly experienceable phenomena underdetermined by human language that entail interpretative conundrum. More concretely, there is still no community-wide consensus on a comprehensive description system of human mental operations (Poldrack, 2006 and 2011). This has caused considerable heterogeneity in how neuroimaging experiments have been motivated and conducted. Moreover, it resulted in frequently inconsistent findings that are difficult to reconcile conceptually. Statistically, rather than falsely rejecting (i.e., type I error) or falsely accepting (i.e., type II error) the null hypothesis, previous experimental fMRI studies motivated by preassumed psychological categories might have committed "the error of the third kind" (Kimball et al., 1957): providing an accurate answer to an inadequate research question. It might be more useful to strive towards "an approximate answer to the right question" (John W. Tukey) given that "all models are wrong" (George Box) anyways. In sum, cognitive neuroscience has so far heavily relied on concepts borrowed more traditional, non-neurobiological scientific disciplines. These considerations are especially relevant to investigations whose conclusion heavily rely on CS. Statistical hypothesis testing makes the strong implicit assumption that the semantics concepts used to formulate the null and alternative hypotheses are "true".

The last challenges to the neuroscientist mentioned here are of epistemological origin. Biology as a whole has modest legacy in abstract theory. This probably includes the history of the biology of the brain. In particular, the spectrum of permissible conclusions that can be drawn from neuroscientific investigations is strongly conditioned by the following three questions (Carruthers, 2009; Dehaene, MBE 2007):

1. Does the human brain offer sufficient computational resources to grasp, formalize, and predict itself?
2. Is the human mind capable to reflect upon itself by directly contemplating itself (i.e., introspection) or by indirectly contemplating an internalized self-model acquired through interaction with others?

3. To what extent is the self-reflexive description of the phenomenology of the human mind by the human mind itself immanently limited and paradoxical?

Taken together, there are many intricacies about neurobiology and the mosaic knowledge that we currently have about it. Despite ≈ 200 years of neuroscience, we are probably not even close to something like a unified theory of brain function that neuroscientists from different fields would accept (cf. Friston, 2010 "Free energy principle"; Bar, 2009 "Predictions"). This caveat considerably complicates the formulation of precise, neurobiologically valid hypotheses that can be experimentally tested in targeted studies. Therefore, it might be helpful to use heuristics-establishing statistical approaches for pattern discovery instead of classical statistics alone. Discovering the mystery of the brain *exclusively* by successive falsification of entirely human-conceived, intimately language-dependent, and dichotomically framed hypotheses might be viewed as hubris by some (cf. Cajal, 1909; Cohen, 1994). Therefore, the present dissertation is built on the assumption that we might not reach an *exhaustive analytical understanding* of the brain any time soon and that a more pragmatic access may rely in the *heuristic approximation of brain mechanisms* by statistical learning models. Such an attempt to learn patterns from data would follow the same direction as recent research developments in language translation and drug discovery (cf. 1.1).

1.4 The curse of dimensionality

Not only conceptual and neurobiological challenges, but also the increasing quantities of analyzed data put neuroscientific research to the test (Gorgolewski & Poldrack, NNR). Today's neuroimaging methods offer very high resolution in space (especially fMRI and PET) and time (especially EEG and MEG) (Amunts et al., 2014 Science; Buzsaki & Draguhn, 2009 Science). The mere number of features poses serious statistical challenges to the investigator. It is the neuroscientific version of what Richard Bellman called the *curse of dimensionality* (1961). At the root of the problem, all data samples look virtually identical in high-dimensional data scenarios. Accustomed to regularities in 3D neighborhoods, human intuition is often led astray in how data behave in input spaces with an extreme number of variables.

The more dimensions an input space spans, the further the data points are away from each other (Hastie et al., 2011). Counter-intuitively, measuring the distance between a randomly selected data point and its closest uniformly distributed neighbors, reveals a shell-like occurrence probability of these neighbors, rather than a centered probability mass. Put differently, when approximating a hypersphere by a surrounding hypercube, the probability mass of the hypercube would almost entirely lie outside the hypersphere (Domingos, 2012). Put in yet another way, a space divided into isotropic units grows exponentially in the unit number with linearly increasing dimensionality. As the main practical conclusion, the amount of data necessary to populate these units also grows exponentially with linearly increasing inputs variables (Bishop, PRML).

Additionally, the target function is almost always unknown in statistical learning investigations. Hence, we frequently have no knowledge of whether or not special structure may exist in the input data that

can be exploited. Knowledge of special structure of the phenomenon under study can reduce both *bias* (i.e., difference between the target function and the average of the function space derivable from a model) and *variance* (i.e., difference between the best approximating function from the function space and the average of the function space). This is a rare opportunity in SL because increasing, for instance, the model complexity typically increases the variance and lowers the bias, and vice versa. In particular, the problem of overfitting in SL has an immediate relationship with the multiple-comparisons problem in CS (Domingos, 2012). The *bias-variance decomposition* captures the fundamental tradeoff in statistical modeling between approximating the behavior of the studied phenomenon and generalizing to newly generated data describing that behavior.

A peacefully coexisting conceptual framework exists in SL that is independent of the unknown target function. The *Vapnik-Chervonenkis (VC) dimensions* formalize the circumstances under which learning processes can be successful (Vapnik, 1989, 1996). This comprises any instance of learning from a number of observations to derive heuristic rules that capture properties of phenomena in nature, including learning in humans and machines. Formally, the VC dimensions measure the complexity capacity of a class of approximating functions (i.e., the function space). Practically, good models have finite VC dimensions and are therefore capable to generalize to new data. Bad models have infinite VC dimensions that are unable to make generalization conclusions on unseen data, regardless of data quantity.

More concretely, SL approaches that incorporate locally varying functions in small *isotropic* neighborhoods will fail to generalize in high-dimensional data scenarios. SL approaches that overcome the curse of dimensionality typically incorporate an explicit or implicit metric for *anisotropic* neighborhoods (Hastie et al., 2011). It is the *hyperparameters* that govern the smoothing behavior of the imposed local neighborhoods. In so doing, the *hypothesis set* (i.e., each function in the function space represent a hypothetical solution to the estimation problem) is hopefully reduced to a reasonable pre-selection (i.e., *regularization*). Guiding the statistical estimation process by complexity restrictions can alleviate the curse of dimensionality. First, we can deliberately exclude members of the hypothesis set. Viewed from the bias-variance trade-off, this calibrates the sweet spot between underfitting and overfitting. Viewed from Vapnik’s statistical learning theory, the VC dimensions can be reduced and thus the generalization performance increased. Second, there is an infinity of possibilities to restrict the hypothesis set. Yet, these choices are typically guided by external knowledge beyond the data at hand. Third, different complexity restrictions typically lead to different best approximating functions.

In sum, the choice of any statistical method constraints the spectrum of possible results and of permissible interpretations. Any scientific discovery in the brain is only valid in the context of the complexity restrictions that have been imposed on the neurobiological phenomenon of interest. No single statistical strategy, be it SL, CS, or other, can consistently do better in all neuroscientific investigations (Wolpert, 1996). The present dissertation is hence dedicated to the juggling with complexity restrictions to neurobiological reality

as observed by fMRI scanning.

1.5 Imaging neuroscience

Functional specialization in the Cortex cerebri of humans has been investigated in the nineteenth century predominantly by lesion reports (Harlow, 1848, 1868; Broca, 1865; Wernicke 1881 "Die acute, hmnorrhagische Poliencephalitis superior"). Brain lesion studies and brain stimulation during surgery were the mainstay of neuroscientific research for a long time, until they were complemented by axonal tracing studies for connectivity analysis in animals (cf. Mesulam, 1976). Today, functional magnetic resonance imaging (fMRI) is the most frequently chosen approach for non-invasive, in-vivo brain research in humans, counting more than 1,000 new neuroimaging publications per year. The impact of fMRI is explained by the availability of brain scanners in medical institutions, its non-invasiveness, and its significant spatial (1-2 mm, Engel et al., 1997) and temporal resolution (a few seconds, Jezzard 200X). fMRI enables the localization of neural activity changes at the synapse by means of measuring the accompanying changes in the oxy-to-deoxyhaemoglobin ratio in local draining veins (Roy et al., 1890; Ogawa et al. 1990/1993). For instance, onset of vibratory stimulation of a participants' hand entails regional accumulation of metabolic equivalents that cause regional blood flow increase ("neurovascular coupling") in the contralateral somatosensory cortex (Fox et al., 1986). In particular, the measured BOLD (blood oxygen-level dependent) signal exhibits an initial dip after the onset of neural activity increase that is attributed to the fast local increase in deoxyhemoglobin. The ensuing hyperperfusion and the thus generated (relative) hyperoxygenation then dictate the BOLD signal shape (i.e., "hemodynamic response function"). It is slightly different across the brain regions of an individual, across individuals, and probably across different tasks. Neural activation is finally followed by re-inhibition of blood flow observable as an undershoot at the end of the BOLD signal (Logothetis et al., 2001). Juxtaposing neural activity and corresponding BOLD signals, the BOLD signal is at least one order of magnitude noisier, scales roughly linearly with neural activity, and is better predicted by local field potentials than multi-unit spiking activity. The BOLD signal is possibly more associated with input to and processing in a local neuronal population rather than its output. There is thus no clear-cut quantitative relation between the spike rate of neuronal populations and the ensuing BOLD response. Rather, the BOLD signal reflects a mixture of transient spikes and continuous membrane potentials (Logothetis et al., 2004). As a central property, there is a tradeoff between coverage of sampled brain tissue, spatial and temporal resolution. For instance, augmenting the spatial resolution, while keeping brain coverage constant, deteriorates the temporal resolution. Finally, the regional responses in single individuals are transformed into a standard brain space (i.e., "spatial normalization" into the "Talairach-Tournoux" [cite] or "Montreal Neurological Institute" [cite] coordinate systems) for comparability and statistical analysis on the group-level.

Based on local changes in cerebral blood flow, experimental fMRI has provided insight into the cerebral localization of specific tasks related to sensory processing, motor actions, and affective functions (Brett et al.,

2002). This is achieved by performing fMRI on a person that lies inside the scanner magnet while attending and responding to psychological tasks, compared to the absence of that task. Usually, the neural correlates of a given task (i.e., a mental process of interest) are isolated by subtraction of the activation measured during a closely related task (i.e., control task) that is supposed not to evoke the psychological process of interest. This relies on the principle of "pure insertion" that cognitive subtraction between the psychological processes of both target and control tasks is possible due to large absence of interaction between them. Although this assumption may not be tenable in many practical cases, the principle of direct task comparison has been widely adopted since it has been proven neurobiologically useful, as well as statistically robust and reproducible (Friston, Zarahn, Josephs, Henson, Dale, 1999). In many instances, analysis and interpretation of the brain imaging data is often performed by integrating additional behavioral data (e.g., task reaction times in the simplest case). Dozens of scans of a same experimental condition that cover metabolic changes in the whole brain are acquired for enhanced sensitivity. The spectrum of neuroimaging-compatible tasks is practically only limited by the scanner surroundings and the interdiction of head movements. In this way, fMRI tasks have revealed the location patterns of various regionally specific effects in health and disease.

In contrast, in the absence of task (i.e., during mind wandering), the human brain is not at rest. While most fMRI studies focus on the minority of neural activity changes conditioned by external stimulation, increasing attention is devoted to the majority of neural activity patterns that underlie the biochemical maintenance of the neural "house-keeping" architecture. That is, the BOLD signal can also be measured in a task-unconstrained fashion by probing participants that lie in the scanner without following a defined psychological task. Participants are instructed to think of nothing in particular let their minds go, and leave their eyes open/closed or look at a fixation cross. During mind wandering humans typically mentally shift between various heterogeneous types of thoughts, memories, and predictions. This is why resting BOLD patterns are believed to reflect the repertoire of cognitive operations that the human brain can perform (Smith et al., 2009). From a neurophysiological perspective, intra- and inter-neuronal activity continues in the human brain's resting functionality. The resting-state BOLD signal reflects fluctuations in physiological signals recorded in the absence of task as reflected in a voxels' time courses. Importantly, the (small) amplitude of the resting-state signal is modulated by transient psychological states (e.g., arousal, attention, and alertness), but also cardiac and respiratory influences. Indeed, the decomposability of this signal measurement into independent components suggests a set of distinct influences rather than one coherent signal pattern (Fukunaga et al., 2006). More specifically, evidence exists in favor of a neuron-, metabolism-, vasculature-, and oxygen-driven genesis of the resting-state BOLD signal. More specifically, correlation analysis can detect temporal coincidence in the spontaneous, slow fluctuations (0.01 - 0.1 Hz) of rest BOLD. This is taken as a measure of functional coordination between topographically distant parts of the brain. Measuring these coherent spatiotemporal couplings in resting-state BOLD fluctuations yields a set of robust neural networks. It led to the discovery of a set of so-called *resting-state networks*. In sum, the biggest

fraction of the various brain signals does not correlate with a particular behavior, stimulus, or experimental task. These partially uncouple in a task setting, but the relative change is very small. It is commonly agreed that the variability in the RS signal is related to the individual's (unconstrained) mental operations. It likely represents a physiological instantiation of a human beings' default mental repertoire.

A property of the brain that we might not have discovered without the advent of neuroimaging methods is the so-called *default mode network* (DMN). The present dissertation is closely related to this particular resting-state network that is a pure result of serendipity (Shulman et al., 1997; Gusnard et al., 2001). 15 years ago, the soon to be called DMN was initially proposed to be exclusive in decreasing neural activity consistently during experimental paradigms requiring stimulus-guided behavior. That is, the DMN was believed to increase neural activity in the idling, unconstrained mind and decrease activity during stimulus-driven, goal-directed tasks (Gusnard et al., 2001). On a macro-scale, the metabolic baseline turnover is not equally distributed across the brain. Interestingly, the brain areas of the DMN include the hot spots of highest metabolic consumption that locate, first, to the posterior cingulate cortex extending into the adjacent retrosplenial cortex and precuneus and, second, to the medial prefrontal cortex extending into the anterior cingulate cortex (Raichle et al., 2001; Reivich et al., 1979). It was later even argued that this network is systematically anti-correlated with brain regions more active during task performance (Fox, et al., 2005). Indeed, goal-directed task performance improves with increased activity in saliency-related areas and decreased activity in default-mode areas (Weissman et al., 2006). Conversely, increased activity in DMN areas were linked to increased occurrence of task-independent thoughts (i.e., mind-wandering) during task execution (Mason et al., 2007). Two fMRI studies employing Granger causality analysis further corroborated the anti-correlation by indicating negative influence of the default-mode on the saliency network (Pisapia et al., 2012) and vice versa (Sridharan et al., 2008). This anti-correlation was recently challenged by repeated reports of brain regions exhibiting both task-constrained and task-unconstrained increases in neural activity (Buckner, et al., 2008). More specifically, the DMN is now known to consistently increase neural activity during a small set of complex cognitive tasks, including the contemplation of others and ones own mind states, spatial navigation, as well as scene construction processes when envisioning past, fictitious, and future events (Spreng, et al., 2009); more generally, envisioning situations detached from reality. It was speculated that the human brain might have evolved to, by default, predict environmental events using mental imagery. Constructing detached probabilistic scenes could thus influence perception and behavior by estimating saliency and action outcomes. This would invigorate a possible relationship between the physiological baseline of the human brain and an introspective psychological baseline (Schilbach et al., 2008). In sum, the DMN routinely defies neuroscientific intuitions and challenges established methods. Neuroimaging research on the DMN corroborated that this particular network consistently decreases activity during externally focused mental tasks and typically increases activity during a small set of internally focused mental tasks. It may reflect unfocused every-day mind wandering in form of continuous environmental

tracking in a generative, integrative process. But we are not even close to certain knowledge of what this might mean in detail.

1.6 Statistical learning approaches in brain imaging

HCP / TERA

Their popularity of SL in neuroimaging increased dramatically in the attempt of "mind-reading" or "decoding" cognitive processes from neural activity patterns (Haynes and Rees, 2005; Kamitani and Tong, 2005)

haynes This therefore represents the first direct evidence that human V1 is sensitive to stimulus orientations outside conscious awareness. We also investigated orientation prediction based on signals from visual areas V2 and V3.

We were able to make such predictions even when the stimuli were completely invisible to the participants. Thus, human V1 can represent information about the orientation of visual stimuli that cannot be used by participants to make a simple behavioral discrimination. orientation selective processing

Since the Cox and Savoy (2003) study, classification studies have become ubiquitous in fMRI, and we review several of these studies below.

when used as a tool to establish significance, there is in principle very little difference between the effectiveness of encoding and decoding models (Friston, 2009). Thus, an important advantage of decoding models is that they can be used to assess if the activity in an ROI is related to behavioral performance. Thus, encoding models are better than decoding models for determining which set of features is preferentially represented within a specific ROI.

As our comparison of encoding and decoding shows, the major advantage of encoding models is that they can be easily compared to one another. By comparing multiple encoding models, it is possible to discover what features are preferentially represented by an ROI and it is even possible to discover the features that provide a complete functional description of an ROI.

MULTIVARIATE Multivariate approaches can utilize hidden quantities 1) Rather than looking at the overall increase/decrease of gray matter volume

2) Multivariate analyses can utilize information jointly encoded in multiple voxels. -¿ illustrated as picture shows covariance structure of the content of two voxels.

3) Friston 2008: Although it is difficult to generalise, multivariate inference is usually more powerful than mass-univariate topological inference because the latter depends on focal responses that survive some threshold (and induce a topological feature). Multivariate models relax the naive (independence) assumption and enable inference about distributed processes

4) The domain of multivariate Pattern recognition the target of machine learning...

CHALLENGES

The practicality of current classifiers, however, is restricted by two major challenges. First, due to the high data dimensionality and low sample size, algorithms struggle to separate informative from uninformative features, resulting in poor generalization performance. - curse of dimensionality

crucial challenges: mechanistic interpretability/understanding (Brodersen et al., 2011) - linked to first point

lack of generative models; most are discriminative

multivariate approaches explicitly account for dependencies among voxels. Second, they reverse

Advances in computing power might suggest that the importance of computational efficiency should become less critical over time; but neuroimaging has repeatedly experienced how new ideas radically increase demands on computation time and thus the importance of fast algorithms. One example is provided by large-scale analyses such as searchlight approaches (Kriegeskorte et al., 2006; Nandy and Cordes, 2003), in which we must potentially evaluate as many classification results as there are voxels in a whole-brain scan. The speed of

Kriegeskorte2006

"information-based" vs. fMRI is purely localizing Here we propose to ask a more general question of the data: Where in the brain does the activity pattern contain information about the experimental condition? To address

Spatial smoothing accentuates extended activations by removing the salt-and-pepper fine structure of the activity patterns, which is treated as noise. Our approach is information-based, in that it localizes regions containing information about the experimental condition. This information can lie in a change of the spatial-average activity level or in a change of the activity pattern.

encoding model $f: Y_t \rightarrow X_t$ (forward inference) decoding model $g: X_t \rightarrow Y_t$ (reverse inference)

with $X_t \in \mathbb{R}^v(\text{voxel})$ *BOLD/brain space with $Y_t \in \mathbb{R}^c$ context/cause/consequence*

- both can be called prediction: The goal of prediction is to find a highly accurate encoding or decoding function.

GLM: mass univariate encoding model

To establish that a link exists between some context Y and activity X , the direction of the mapping is not important.

Inference about how the brain represents things reduces to model comparison.

decoding/Naselaris: GLM estimated for each voxel; can be viewed as encoding models the GLMs estimated for individual voxels could theoretically be used to predict the activity in the voxels, so GLMs can be viewed as encoding models.

A linear classifier can be viewed as one specific and restricted form of a decoding model, a model that uses voxel activity to predict sensory, cognitive, or motor information. Decoding models may also be used to perform identification (Kay et al., 2008) and reconstruction (Miyawaki et al., 2008; Naselaris et al., 2009;

Thirion et al., 2006). In identification, patterns of activity are used to identify a specific stimulus or task parameter from a known set. In reconstruction, patterns of activity are used to produce a replica of the stimulus or task. These more general forms of decoding are themselves special cases of multi-voxel pattern analysis, which encompasses many unsupervised methods for analyzing distributed patterns of activity

Encoding and decoding models are complementary

In these terms, the key difference between encoding and decoding models is the direction of the linear mapping between feature space and activity space.

On the decoding side, the most commonly used computational technique is the linear classifier

- Classification approaches were early used in structural neuroimaging (Herndon et al., 1996) and contributed to improved image preprocessing performance (Ashburner and Friston, 2005).

Brodersen/2009: Whether, where, when, and how First, the question of pattern discrimination: does the recorded neural activity carry information about a variable of interest? Second, the question of spatial pattern localization: where in the brain is class information encoded? Third, the question of temporal pattern localization: when does information take shape in, or become available to, a certain brain area? Fourth, the question of pattern characterization: how is information encoded in the brain? I

Much of the success of cognitive neuroscience over the past decades has been a result of implementing a mass-univariate analysis of neuroimaging data obtained from human subjects as part of a general linear model (GLM). GLM treats each volumetric pixel, i.e. voxel, as independently to perform serial univariate statistics (Friston et al., 1995). Univariate approaches are recognized to be an excellent approximation for topographically localizing activations, i.e. a differential increase of neural activity, in individual voxels. Multivariate (ML) approaches on the other hand can be used to examine responses that are jointly encoded in multiple voxels. In other words, a univariate statistical model considers a single voxel at a time, while a multivariate model considers many voxels simultaneously and can make inferences on distributed responses without requiring strong independence assumptions.

Statistical methods with non-parametric properties, often summarized as "multivariate pattern analysis" (MVPA), have recently gained popularity in neuroimaging. In particular, ML approaches are well suited for discovering complex structure between high-dimensional neuroimaging data (mostly functional magnetic resonance imaging) and variables of interest (e.g. external stimuli or experimentally imposed cognitive sets).

For decades histopathology, lesion studies, and invasive research in non-human primates have been the main neuroscientific workhorses. The advent of neuroimaging methods then leveraged unprecedented insight into brain biology. Task-based neuroimaging studies typically attempt to solicit target mental operations in participants by means of sensory, cognitive, or affective paradigms. This research greatly increased our understanding of the healthy and diseased human brain. Yet, such work rests on a set of strict assumptions, including that a) historically inherited psychological categories are useful description systems for neurobiological phenomena, b) target and non-target mental operations can be statistically distinguished by so-called

cognitive subtraction, and c) a few dozen participants are sufficient to reliably establish fundamental (patho-)physiological mechanisms in the brain. All these assumptions have repeatedly been questioned. Apart from that, structural neuroimaging approaches, such as voxel-based morphometry, may be used to identify locations in which two groups of subjects, such as patients versus controls, differ from each other in local gray matter (GM) volume. While not being affected by the choice of a particular task, these approaches are also frequently criticized for insufficient sample sizes. In addition, they only allow characterizing presence, absence, or a group-mean effect at a particular location. Finally, methods for individual structural analyses are manifold and have repeatedly been in disagreement.

As a complementary methodological family, machine learning (ML) approaches are characterized by a) making the least assumptions possible, b) being more motivated by mathematical models rather than cognitive theory, and c) automatically mining structured knowledge from massive data resources. Given the widely acknowledged intricacies of and slow progress in schizophrenia research, ML methods lend themselves particularly well. They have the potential to decipher and subsequently render explicit biological indices that might assist diagnosis, treatment, and clinical outcome prediction.

It has been argued that classical functional neuroimaging applications are insufficient to infer structure-function relationships without formal modelling (Stephan, 2004). (e.g. Flechsig 1905; Meynert 1890) -> towards formalized descriptions of SFRs

Typical big-data problems concern classification or regression of an output variable y with respect to a large number of input parameters x , also called predictor variables or covariates, on the basis of large training sets.

Note that this curse of dimensionality does not automatically apply to all big-data algorithms. To the contrary, it occasionally turns out helpful to artificially increase the dimensionality of the parameter space in methods like decision trees or support vector machines

- Their popularity of SL in neuroimaging increased dramatically in the attempt of "mind-reading" or "decoding" cognitive processes from neural activity patterns (Haynes and Rees, 2005; Kamitani and Tong, 2005)

Third, regarding data analysis techniques, it has been proposed to leverage ML as a particularly powerful tool to investigate the neural correlates of two interacting brains (Konvalinka & Roepstorff 2012). ML promises to extend the representational agenda of fMRI investigations (i.e., activation-based analysis) and to an informational agenda (i.e., pattern-information-based analysis) (Kriegeskorte et al., 2006; Mur et al., 2009). In particular, multivariate ML approaches are able to address the four questions whether, where, when and how (Brodersen, 2009). ML can provide new evidence whether a given type of information is encoded by neural activity, where a given type of information is neurally encoded, when it is processed/generated/bound and how information is neurally processed in the human brain. Moreover, single-individual fMRI analyses already pose a high-dimensional statistical problem. Performing two-individual fMRI analyses thus imposes

an even more challenging "curse of dimensionality" (Hastie et al., 2011). Automated statistical learning of robust structure (i.e., informational patterns) in large quantities of (neuroimaging) data is a core feature of ML approaches. In this way, the flexibility and capability of ML algorithms for pattern mining in extensive data resources make it particularly attractive for the statistical mastery of online two-brain interaction.

. This prompted the current drift towards more data-driven (i.e., fewer assumptions), higher-dimensional (i.e., more features per observation) neuroimaging analyses on larger samples of neuroimaging data (i.e., more observations).

Pietsch: The notion of a qualitative change from hierarchical to horizontal modeling is further corroborated by a concurrent paradigm shift in statistics, which has been described as a transition from parametric to non-parametric modeling (e.g. Russell & Norvig 2010, Ch. 18.8), from data to algorithmic models (Breiman 2001), or from model-based to model-free approaches.

As argued in the following chapters, we need to discover the low-dimensional manifolds that are embedded within the high-dimensional neuroimaging data.

Helmstaedter 2011 / deep learning

2 Unsupervised modelling of brain regions

2.1 Motivation

2.2 Methodological approach

2.3 Experimental results

2.4 Discussion

3 Supervised modelling of brain networks

3.1 Motivation

3.2 Methodological approach

3.3 Experimental results

3.4 Discussion

4 Semi-supervised modelling for structure discovery and structure inference

4.1 Motivation

4.2 Methodological approach

4.3 Experimental results

4.4 Discussion

5 Conclusion

6 References