# Next-generation Personal Genomic Studies: Extending Social Intelligence Genomics to Cognitive Performance Genomics in Quantified Creativity and Thinking Fast and Slow

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**Abstract**

A significant shift is underway as the fields of health and biology are re-organizing into the larger ecosystems of information sciences and complexity sciences. The era of big data is transforming all economic sectors including health and biology. Three big health data streams are being integrated into a standardized investigative method in the realization of personalized medicine – creating individualized risk profiles and interventions such that medical conditions may be combatted during the 80% of their life-cycle while they are still pre-clinical. These three big health data streams are traditional medical data, 'omics' data (genomics, microbiomics, proteomics, etc.), and biometric quantified-self daily analytic data. Sequencing costs have continued to decrease such that consumer 'omics' data is increasingly available. Simultaneously, the potentially fast-arriving wearable electronics platform (smartwatches, disposable patches, augmented eyewear, etc.) means that it could become possible to unobtrusively collect vast amounts of previously-unavailable objective metric data for each individual and parlay this into personalized physical and mental health optimization platforms. Two experimental protocols are presented here putting this model of integrated health data streams into action and extending recent social intelligence genomics research into the realm of cognitive performance genomics. The DIYgenomics Quantified Creativity study investigates potential linkage between personal genomics and the creative process of the individual. The DIYgenomics Thinking Fast and Slow study examines cognitive bias in thinking (loss aversion and optimism bias) versus personal genomic profiles. The studies integrate big health data streams including traditional health data, personal genomics, quantified self-reported data, standardized questionnaires, and personalized intervention.

## Introduction

### Manipulating Biology as an Information Science

Biology was recognized as an information science as early as the 1940s by John Von Neumann (Von Neumann 1966) and more recently by other scientists, philosophers, and thinkers such as Craig Venter (Venter 2008), Juan Enriquez (Enriquez 2005), and Drew Endy (Endy 2008). Now for the first time, tools for the large-scale understanding and manipulation of biology as an information science are starting to be available.

### Era of Big Health Data

One of the most profound advances in artificial intelligence in the last few decades has been the technique of amassing large data corpora and running simple machine learning algorithms over them. This has proved fruitful in a number of efforts from Google in spelling correction, translation, and news aggregation (Halvey 2009), and recently in image recognition, where computers recognize pictures of cats (Le 2012). These methods could be useful too in health and biology, particularly in the realization of preventive medicine - keeping people healthy and preventing the clinical onset of conditions. The present status of the industry is building and gathering large health information data streams which could become data corpora over which machine learning algorithms could be run.

At least three Big Health Data Streams may be identified: traditional medical data, newly-available 'omics' data, and Quantified Self data streams (Swan 2012a). The first category is traditional medical data streams, which are slowly starting to be available in a

unified accessible digital format. This includes personal and family health history, prescription history, lab test data, demographic information, and possibly, standardized instrument responses (e.g.; user-reported questionnaires).

The second kind of Big Health Data Streams is the new 'omics' health data that low-cost sequencing and profiling is starting to make widely available. These data comprise the genome, microbiome, transcriptome, metabolome, proteome, diseasome, and environmentome. As of January 2013, consumer genomic profiling is available for $99 (23andMe provides sequencing for one million of the most researched genomic SNPs (single nucleotide polymorphisms)), and consumer microbiomic profiling is similarly available for the low cost of $99 (http://www.indiegogo.com/americangut). However, a broad consumer application of integrated 'omics' data streams is currently unavailable as institutional projects (Chen 2012) have only just begun, and readily-applicable findings are neither forthcoming nor easily fitted into a template. One nice next step for the consumer would be the low-cost availability of wide-scale proteomic profiling, particularly as related to pre-clinical disease status.

The third category of Big Health Data Streams is the new Quantified Self (QS) data streams collected as individuals track and monitor themselves with smartphone applications, biomonitoring gadgets, and other tools in an attempt to understand and possibly change health and behavior. QS data streams may be a mix of self-reported data, self-tracked data, and objectively-collected data. Self-tracked and self-reported data may come from exercise, nutritional intake, and mood journals, automated time-tracking applications, quantified-self tracking devices (e.g.; Fitbit, Global Corporate Challenge pedometer, MyZeo, WiThings, etc.), and now biosensor data. Biosensor data is Internet-connected sensors and wearable electronics platforms including smartwatches, smartrings, wearable disposable electronic patches and tattoos, electronic t-shirts, consumer EEG rigs wearable 24/7, and augmented reality glasses such as Google Glass (Swan 2012b).

**Big Data Objective Metrics**

For the first time, many of the 'omics' and QS personal health data streams are allowing objective metrics to be collected for elucidating and quantifying human health and behavior in ways that were previously impossible. Some examples are in diverse areas such as mood and mental health, happiness, relaxation, creativity, cognition, and productivity (Swan 2012b).

Integrating QS data, 'omics' data, and traditional health data streams allows the creation of a new era of Big Health Data. Billions of data points may be obtained for every individual and eventually organized into a sophisticated real-time algorithmic analysis of health risk and preventive intervention to address medical conditions during the 80% of their life-cycle when they are pre-clinical. Putting this model of integrated health data into action, two experimental study protocols are now discussed within the growing context for personal genomics (the leading 'omics' data stream).

## Expanded Context for Personal Genomics

The context for personal genomics continues to grow. Activity can be loosely organized into three waves: ancestry genomics, disease risk genomics, and social intelligence genomics. In the first of the three phases, personal genomics was used by institutions to determine ancestry, pregnancy screening characteristics, and identity (paternity and forensics). In the second phase, personal genomics was offered by consumer genomics companies and physicians to assess disease risk, drug response, and athletic performance capability. Unfortunately, the ongoing lack of scientific agreement over a standardized list of core SNPs that should be reviewed in each case of specific conditions such as cancers and heart disease has prohibited the wider-spread validity and utility of personal genomic testing for disease risk (Swan 2010). In the third and contemporary wave of personal genomics - social intelligence genomics – genomic testing is used by researchers to investigate different aspects of personality attributes and social intelligence.

In social intelligence genomics, there are several interesting personality attribute findings. In studies, it has been identified that there is a genetic predisposition (though not phenotypic determinism) for qualities such as optimism, empathy, extraversion, altruism, and openness to experience. There are specific genes and SNPs related to optimism and empathy: OXTR rs53576 (Saphire-Bernstein 2011, Kogan 2011, Rodrigues 2009), extraversion: DRD2/ANKK1 rs1800497 (Smillie 2011), altruism: COMT Val158Met rs4680 (Reuter 2011), and openness to experience: DRD2 rs4274224, rs4581480, rs12364283, rs2283265, and rs1076560 (Peciña 2012).

Studies such as the DIYgenomics Social Intelligence Genomics and Empathy-Building Study have confirmed the finding that individuals with a 'GG' genotype for the oxytocin receptor SNP OXTR rs53576 score higher on standardized test instruments (e.g.; the Empathy Quotient, and the Interpersonal Reactivity Index) than those with other genotypes (http://genomera.com/studies/social-intelligence-genomics-empathy-building).

The research in personality attribute and social intelligence genomics is used as a conceptual and practical base from which to extend personal genomics into a genomic analysis of cognitive performance. Here creativity, loss aversion, and optimism bias are examined in the following study protocols. The DIYgenomics

Quantified Creativity Study investigates the creative process and genomic linkage. The DIYgenomics Thinking Fast and Slow Study (inspired by the book "Thinking, Fast and Slow" (Kahneman 2011)) examines cognitive bias in thinking (loss aversion and optimism bias) against personal genomic profiles. The studies integrate big health data streams including traditional health data, personal genomics, quantified self-reported data, standardized instrument performance, and personalized intervention.

## Quantified Creativity Study

Creativity is a complex human ability that may have several contributing factors including genomics, brain structure, personality, attitude, culture, and socialization (Taylor 2012). The complexity and subjective assessment of creativity have defied objective definition in many ways; however several new means of assessing creativity are now available. The DIYgenomics Quantified Creativity Study seeks to examine potential linkage between genomic profiles, responses to standardized creativity assessment instruments, creativity process interviews, creativity journals, and guided problem-solving with EEG gamma spike assessment.

### Enumerating the Creative Process

Scientists have made creativity more accessible and tangible by enumerating the steps that occur in the creative process. One example is the five-step schema proposed by flow state and creativity scientist Mihaly Csikszentmihalyi (Csikszentmihalyi 1996). The five steps are: preparation (becoming immersed in the area), incubation (allowing the ideas to turn around unconsciously), insight (the "Aha!" moment when things start to make sense), evaluation (deciding whether to pursue the insight), and elaboration (translating the insight into its final form). This schema is helpful as a framework in the Quantified Creativity study within which individuals may consider their own creative process and study operators may organize results.

### Personal Genomics and Creativity

Genes associated with related characteristics of mental performance may also be implicated in the propensity for creativity. These could include genes associated with neuroplasticity, dopamine and serotonin transportation, neuregulin (neuronal development), neurotrophic factor (related to growth of new neurons and synapses), risk-taking, and openness to experience. These genes and SNPs are for neuroplasticity BDNF Val(66)Met rs6265 (Soeiro-de-Souza 2012), dopamine and seratonin transportation 5-HTT rs25531 (Volf 2009) and COMT Val(158)Met rs4680 (He 2012), neuregulin and neurotrophic factor NRG rs6994992 (Keri 2009), risk-taking DRD2/ANKK1 rs1800497 (Smillie 2011), and openness to experience DRD2 rs4274224, rs4581480, rs12364283, rs2283265, and rs1076560 (Peciña 2012).

In the Quantified Creativity study, the favorable genotypes for creativity in these genes and SNPs are reviewed against participant surveys with established instruments: the Kirton Adaptation Innovation Inventory and Buffalo Creative Process Inventory. Further, participants are asked to introspect about and describe their creative process and keep a creativity journal. This may be carried out with the aid of a mobile-application based environment for lightweight scientific study operation such as PACO (the personal analytics companion, https://quantifiedself.appspot.com/Main.html), or studycure (http://studycure.com/). A lab-based or consumer EEG product such as the Emotiv or Neuorsky headset is used to measure neural activity and potential gamma spikes as participants creatively solve problems in a lab environment. Research has indicated an EEG-recorded spike of high-frequency (gamma band) activity about 0.3 seconds before the critical "Aha!" moment (Sheth 2009, Kounios 2009). In the future, it is possible that real-time feedback from wearable consumer EEGs could help to catalyze creativity and flow states.

DIYgenomics studies generally have a personalized intervention component. In the Quantified Creativity study, participants are randomly segmented into cohorts that journal their creativity while trying either programmed or self-identified interventions. Participants are asked to detail their own creative process in different contexts and examples, identify contributing factors and motivations, remember particularly creative times or moments, and experiment with these findings in a one-month study to investigate the impact of interventions. Personalized recommendations for creativity enhancement may be available from study results.

## Thinking Fast and Slow Study

Any topic concerning cognitive performance and possibly improving the workings of the brain is of perennial interest to humans. Recent work in behavioral economics and neuroeconomics has been helping to explain cognitive processes as discussed in books like "Thinking, Fast and Slow." This book takes up two pervasive phenomena that shape human thinking: loss aversion and optimism bias. A study is outlined here to examine a potential link between genetic predisposition for loss aversion and optimism bias and the phenotypic display of such behaviors.

### Loss Aversion

Loss aversion is the human condition of a strong preference for avoiding loss as opposed to experiencing gain, generally to the degree of preferring loss-avoidance twice as much or more than experiencing gain. To examine

the genetic propensity for loss aversion, a suite of related genes and SNPs can be examined from studies in areas where genetic polymorphisms have been associated with areas such as reward processing, reward anticipation, action-taking, risk-taking and risk-avoidance, and addiction or propensity for gambling. Neurotransmitter operations are critical in decision-making, reward processing, and loss aversion, particularly those regulated by serotonin SNP 5-HTTLPR rs25531 (He 2012) and dopamine SNP COMT Val(158)Met rs4680 (He 2012, Farrell 2012, Schmack 2008). Serotonin receptor polymorphism T102C rs6313 is also implicated, in the area of impulse control (Wilson 2012). The usual 'propensity for risk-taking SNPs' may be evaluated in the loss aversion context: DRD2/ANKK1 rs1800497 (Smillie 2011) and DRD2 rs4274224, rs4581480, rs12364283, rs2283265, and rs1076560 (Peciña 2012). Regarding gambling, the dopamine SNP COMT Val(158)Met rs4680 may be evaluated (He 2012), and for addiction, PDYN rs1022563, rs910080, and rs1997794 (Clarke 2012).

The Thinking Fast and Slow study pairs genomic SNP analysis with standardized instruments to test phenotypic manifestation. To measure loss aversion, the Loss Aversion Task (Tom 2007) is used which evaluates loss aversion in prospect theory (where the impact of losses is greater than that of gains) as discussed in the book "Thinking, Fast and Slow." In addition, the Iowa Gambling Task is used to evaluate real-life decision-making (Bechara 1994) with the open-source PEBL software suite (http://pebl.sourceforge.net/battery.html).

**Optimism Bias**

Second, the Thinking Fast and Slow study investigates optimism bias and overconfidence. The study reviews the previously-mentioned reward processing SNPs and the oxytocin receptor polymorphism (OXTR rs53576 (Saphire-Bernstein 2011, Kogan 2011, Rodrigues 2009)) for positive mindset. Genomic propensity is evaluated against phenotypic tests. Three phenotypic instruments are used to test overconfidence, Schowmaker's Confident Decision Making test (Russo 1989), Blavatskyy's Experimental Test of Overconfidence (Blavatskyy 2008), and Critch's Credence Game (http://www.acritch.com/credence-game/).

**"Fight or Flight" Response**

A third element is examined in the Thinking Fast and Slow study, as the study's name suggests, genetic predisposition towards fast (e.g.; immediate gut response) or slow (e.g.; relaxed and deliberative) thinking. This is evaluated through an analysis of adrenergic SNP polymorphisms generally responsible for regulating the hormone epinephrine and the neurotransmitter norepinephrine which are related to the "fight or flight" response. Specific SNPs are reviewed such as ADRB1 rs1801252, ADRB2 rs1042711-rs1042718 and rs180088, and ADRB3 rs4994 (Dorn 2010). Phenotypic tests to evaluate the corresponding degree of arousal in the sympathetic nervous system are used: the Fight-or-Flight Response Test (Samelson 2009) and the Fight or Flight Questionnaire (http://www.fightorflighttherapy.com/questionaire.html).

**Genomics and IQ**

A fourth dimension of Thinking Fast and Slow may be investigated. While acknowledging the many contentious aspects of a purported linkage between genomics and intelligence, recent studies have found links between different measures of brain volume and intelligence which could be replicated and investigated further. Hippocampal volume, intracranial volume, and total brain volume correspond respectively to 12q24.22 rs7294919, HMGA2 rs10784502, and DDR2 rs10494373 (Stein 2012). Hippocampal volume was further associated with cognitive capabilities and decline in the process of aging, specifically MSRB3-WIF1 rs17178006, HRK-FBXW8 rs7294919, DPP4 rs6741949, and ASTN2 rs7852872 (Bis 2012). Standardized instruments for capturing intelligence quotient (IQ) are employed for phenotypic data collection. As with other descriptive genomics studies, the outcome is not deterministic information and positive interventions are possible. For example, individuals finding that they have unfavorable polymorphisms relating to brain volume might be inspired to undertake more rigorous brain training exercises as a result.

## Conclusion

As health and biology move into the big data era, integrating health information streams such as traditional medical data, 'omics' data (genomics, etc.), and quantified self daily analytic data could become an increasingly important standard investigative method. The pace is such that the next wave of big data challenges is already starting to arrive – problems related to having too much data, signal-to-noise obfuscation, and the ability to intelligently select data stream segments for relevant correlations.

Many non-inconsequential steps are required for true progress into the era of health and biology as an information science and for the realization of preventive medicine. One issue is making data available, for example in the form of large publicly-accessible biobanks. Political, regulatory, and cost concerns are paramount. Acknowledging the potential practical impossibility of protecting anonymity, mechanisms and safeguards can be employed so that willing individuals can contribute their own data. Like the Wikipedia, as asset can be created with less than 1% participation that is nevertheless a valuable - and available - public good for all. The lack of large open-source phenotypic data sets is perhaps the biggest barrier to

the execution of preventive medicine. It is not yet possible to see at a large-data scale how pathologies develop longitudinally. Once these data become available, they can be merged with other health data streams to seek an understanding of disease development and eventually prevention using both straightforward machine-learning algorithms, and sophisticated quantitative risk models from investment management, insurance, and finance.

Not only are health and biology re-organizing into information sciences, but it is also starting to be possible to examine biological phenomena as they truly are, as part of larger systems of complexity and ecology. This means that more nodes of granularity in data association are sought in the data analysis plane beyond the basics of correlation and causation. Here the two study protocols outlined investigate cognitive performance at the more systemic ecological level by integrating big health data streams to examine potential linkage between personal genomic profiles, cognitive performance, and intervention.

**Future Directions**

With the potentially fast-arriving wearable electronics platform (smartwatches, disposable patches, augmented eyewear, etc.), it could become possible to unobtrusively collect vast amounts of biometric and neurometric data. What emerged as the early Quantified Self, painstakingly collecting daily-analytic data, is giving way to a much more aware and automated Quantified Self 2.0, a *Qualified Self* who interacts directly with data as an exosense (Swan 2013). In the future, each individual may have a data-driven personal health information climate that makes real-time suggestions regarding all manner of physical and mental performance. It could be possible to quantify a wide variety of states of subjective experience including creativity, flow state, relaxation, intuition, epiphany, engagement, productivity, and fulfillment – in short, all possible emotions and mental states. Merging biometric and brain-mapping data with lifelogging information could create vivid and profound maps of human experience.

Emotion has already been made discrete as the human labeling that occurs from the measurable biophysical response called affect (Russell 1999). Potentially quantified with neurobiometrics, neurophysiological responses could be refined into different classes of behaviors per affect level and type, and have interesting corresponding broadcast mechanisms and interventional responses suggested by personal health information climates. There could be a need to re-lexicon the current narrowband terms for types of emotions as all neurophysiological behavior is understood more granularly.

The potential ability to apply objective metrics and quantitative definitions to mental processes and emotion has attendant privacy and security issues, and societal implications. Neuro data privacy rights and biometric data security are the kinds of concerns that might arise, especially if technology advancement means the increasingly facile detection of physical and mental states of others. On the other hand, perhaps a society with less deception is one that is more advanced. Objective biometric and neurometric data collection and its potential broadcast might mean that it is much easier to build mental models of others' thoughts and behaviors. Seeing the permissioned real-time neurobiometric broadcast of the data of others could certainly be a new tool in mentalization (the process of attributing meaning to actions based on perceived intentional mental states (Salters-Pedneault 2008)), and could have a significant societal impact in making communication and collaboration more effective. Finally, objective biometrics might help not only in a new understanding of emotion, mental states, and human interaction, but also in addressing currently intractable scientific problems like consciousness.

## Conflicts of Interest

The author is the founder of DIYgenomics.

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