



presented by

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AMIRA

Aggregated
Medical Information for
Research & Analysis

Determining Therapeutic Efficacy
via crowd-sourced data and crowd-sourced data science
for our collective battle against NF2

A Proposal to the SVAI NF2 Genomics Hackathon Panel
Google Launchpad San Francisco, 25 June 2017

Everyday, selfless individuals
donate bone marrow to help those
with leukemia and lymphoma.

**WOULD INDIVIDUALS
DONATE THEIR**

DATA

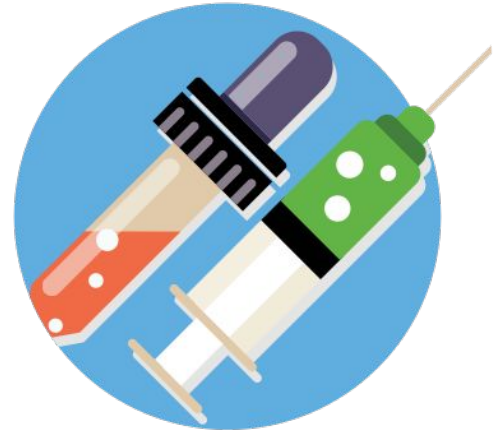
**FOR THE FIGHT
AGAINST NF2?**



Why Data?

Therapeutic efficacy is not universal, it depends on *a variety of attributes* as simple as gender and ethnicity and as complex as various trace levels in blood.

NF2 treatments need to be reviewed so the **best** treatment is given to each patient based on their **individual attributes (Precision Medicine)**. This should be multifaceted -- genetic (as Onno Faber is doing) as well as nutritional, behavioral, geographic, and clinical.



What Data Specifically?

→ Environmental and Lifestyle

Geography, local condition indicators, timeline of vitals, activity level, drug abuse, etc.

→ Symptoms

Hearing loss, ringing in the ears, and balance problems.

→ Nutrition

Vitamin and mineral levels will affect response to treatment. For example, B12 is essential for the preservation of the myelin sheath. Vegans, smokers, and drinkers experience decreased B12 levels and poor health outcomes -- *that have nothing to do with the efficacy of medications*. With nutritional data we can segment out such cases, and more subtle ones also.

→ Treatment Course and Outcomes

This forms the ground-truth that models will **calibrate to** and **test against**.

→ Genetic Information

Collection of individual genomic data along with any NF2 mutation variants. This is essential for tumor targeting.

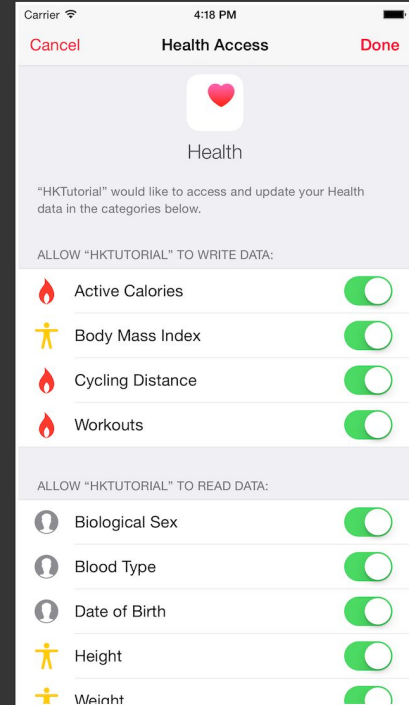
What Data Sources?

- Apple HealthKit
- Google Fit
- Samsung Health
- Nokia/Withings Health Mate
- 23andMe, deCODEme, FamilyTreeDNA via OpenSNP
- MyFitnessPal
- Shimmer
- iHealth
- Personal Genome Project
- PHR/EMR (e.g., Cerner, Epic)



How can we *widen the pool* of data contributors?

- Piggy-back on standard authorization services
- Mobile phone driven initiation
- One-click easy enrollment and contribution
- Ensure trust via independent third party
- CRA/CRM outreach to encourage participation
- Use common growth hacking techniques to *truly change the world*



How can we *widen the pool* of data scientists?

- Data pipelines with auto-downloadable training/test sets
- Ever-expanding training sets on existing pipeline
- Data repackaged into ready-consumable formats (csv, python pickles, numpy, *etc.*)
- Simple blind inference validation
- Use already present community (Kaggle)
- Outreach to C.S. departments to encourage this particular challenge

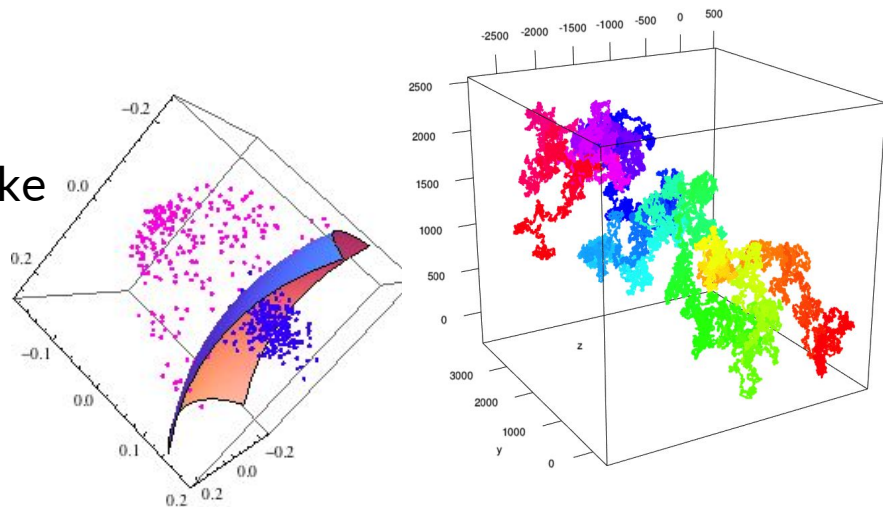
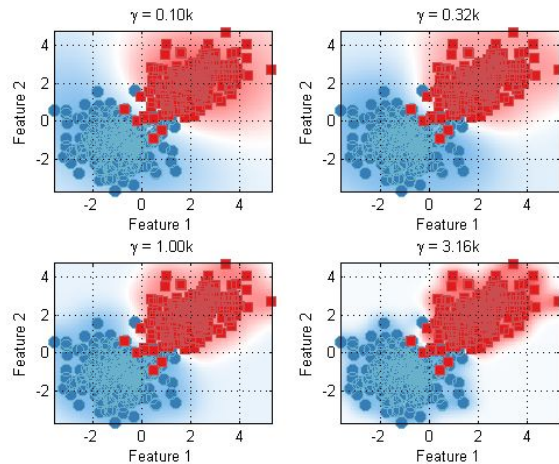


The Objective

Our objective is to classify patients into segments which will or will-not benefit from particular experimental treatments. Further, we aim to find a minimal set of attributes which drive these segments.

We will achieve this using machine learning: segmentation and classification techniques like logistic regression, support vector machines, random forest decision trees, etc.

Our first step will be to set up fully functional notebooks demonstrating this.



A scatter plot illustrating a classification problem in a 2D space defined by axes X_1 (horizontal) and X_2 (vertical). The plot shows two classes of data points: red dots and black dots. The background is filled with a grid of small dots, colored red or black, representing the predicted class for each point in the space. Two solid lines, one red and one black, represent the decision boundaries separating the two classes. The red boundary is generally located to the left of the black boundary, indicating a separation between the two classes based on the X_1 coordinate.

Key Approaches Proposed: Support Vector Machines, K-Nearest Neighbors, Logistic Regression, Principal Component Analysis, and Deep Learning if sufficient data possible.

A photograph of the Golden Gate Bridge in San Francisco, taken from a low angle looking up at one of the towers. The bridge is silhouetted against a bright orange and yellow sunset sky. The water below is calm, reflecting the light. In the distance, the city skyline and hills are visible under a clear blue sky.

Building Bridges

AMIRA is a “**concentrator model**” -- we want to take many of the groups’ impressive work we’ve seen this weekend and offer a **facility to concentrate** their downstream features into an **experimental therapeutic model translating into more precise studies**.

In essence, we’re proposing an overarching effort that includes Onno’s efforts around genetic profiles fused with other silos.

We hope to promote an adaptable infrastructure for scientists across disciplines (e.g., computer science + medical) to come together.

The background features a network of green and blue lines with circular nodes containing various icons: a tooth, a pill, a DNA helix, a microscope, a clipboard with a plus sign, a water drop, a flask, and a heart with a pulse line.

Getting out of the way

We do not wish to be constrained by tools. We want consumption to be turn-key so anyone can use any tool to contribute data driven insights and drive progress.

However, we can make it easier with templates and starter material to get people going, e.g., **python**, **scikit-learn**, **numpy**, and **Jupyter**.

Our A-Team

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What is possible with determined partners?

October 2017

Android & iPhone app with one-click data donation & anonymization from popular health data services

December 2017

Integrations to genomics research outputs into central pipeline

2017-Q3

2017-Q4 and Beyond

November 2017

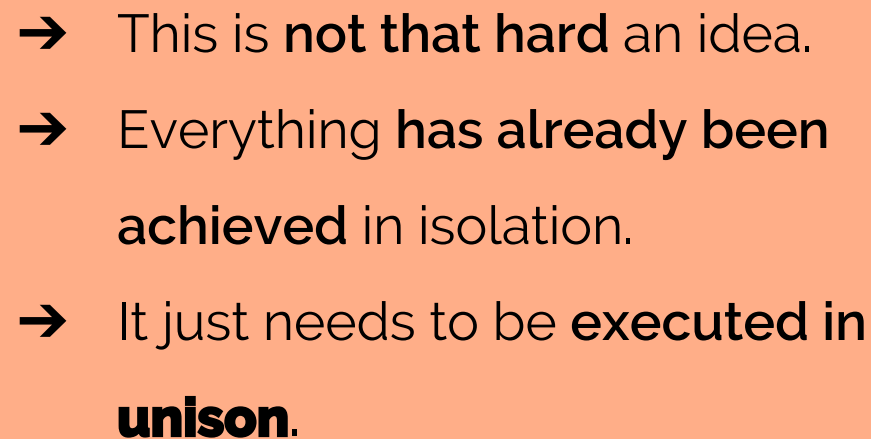
Data pipeline and Jupyter-ready machine learning analysis templates:
users hit the ground running

Beyond

More data sources
More turnkey
More templates
Other conditions (economy of scale)

So what is **the ask?**

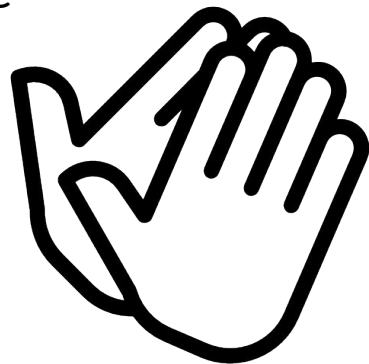
- *we don't* want money
- **we need** everyone, especially patients to donate data
- **we need** an independent trustworthy organization to serve as the data concentrator & anonymizer
- **we need** Kaggle/Google to host the data and blind set verification so the public can participate
- **we need** enthusiasts like you to build models to segment attributes driving therapeutic efficacy



CONTACT US IF YOU CAN HELP

Acknowledgements

- Silicon Valley Artificial Intelligence and Peter Kane
- Onno Faber and NF2 Project
- The Hackathon Mentors and Judges
- Google for the cloud computing credits
- Kaggle for their superb platform (*hint, hint!*)
- NF2 Tumor Genomics Hackathon Sponsors:



Google
Genomics



RECURSION
pharmaceuticals

Contact Us, *Let's Make it Happen*

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