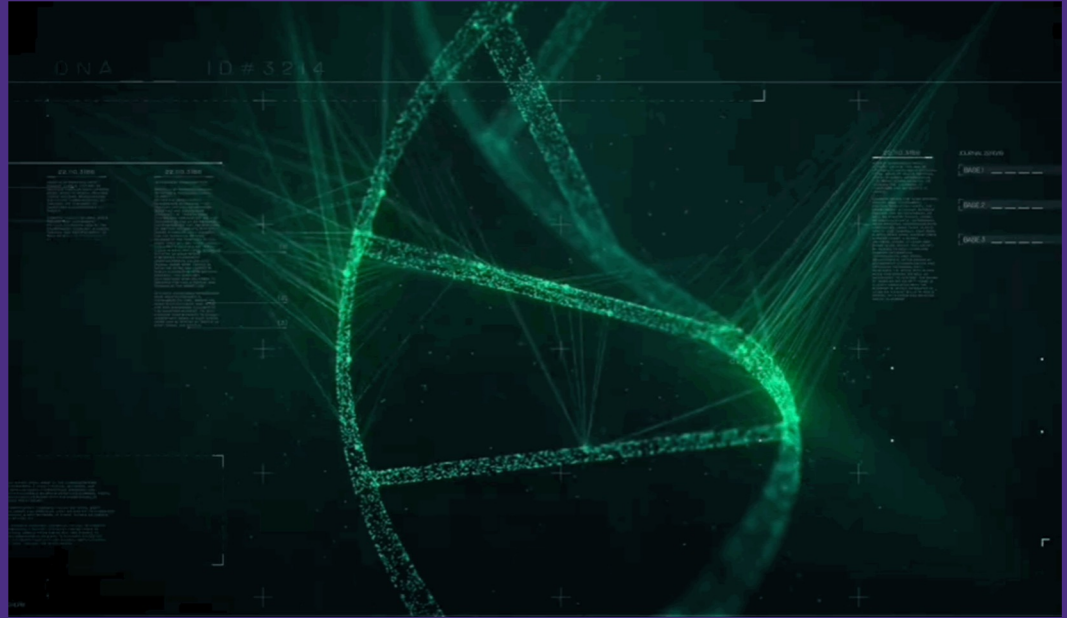


# UltraGene



Presented by: Cristian, Dana, KC, Zi

***BE BOUNDLESS***

**W**

# Background

## <Problems>

It's hard to understand the meaning behind 23andME gene raw data.

#	rsid	chromosome	position	genotype
rs12564807	1	734462	AA	
rs3131972	1	752721	AG	
rs148828841	1	760998	CC	
rs12124819	1	776546	AG	
rs115093905	1	787173	--	
rs11240777	1	798959	AG	
rs7538305	1	824398	--	
rs4970383	1	838555	CC	
rs4475691	1	846808	CC	
rs7537756	1	854250	AA	
rs13302982	1	861808	GG	
rs55678698	1	864490	CC	
i6019299	1	871267	CC	
rs1110052	1	873558	TT	
rs147226614	1	878697	GG	
i6019302	1	881843	GG	
rs2272756	1	882033	GG	
rs67274836	1	884767	AG	
i6019303	1	888554	CC	
rs13302945	1	889159	CC	
i6019304	1	889182	GG	
i6019305	1	891343	GG	
rs13303106	1	891945	GG	
i6019306	1	894379	GG	
rs13303010	1	894573	AA	
i6019308	1	897792	CC	
i6019309	1	898082	AA	
rs6696281	1	903104	CC	
i6019310	1	905681	CC	
i6019311	1	906114	CC	
i6019312	1	907666	--	
i6060381	1	909238	GG	
rs2340592	1	910935	GG	
rs13303118	1	918384	GT	
rs78164078	1	921071	GG	
rs6665000	1	924898	AA	
rs2341362	1	927309	CC	

# Background

## <Solution>

We provide customer with a platform to conduct searches and comparisons to identify high-risk genes.

## Matches with AI and experiment.

	position	Alt	Ref	Functional score
0	37,807,852	G	T	-0.46
1	37,807,852	G	T	-0.46

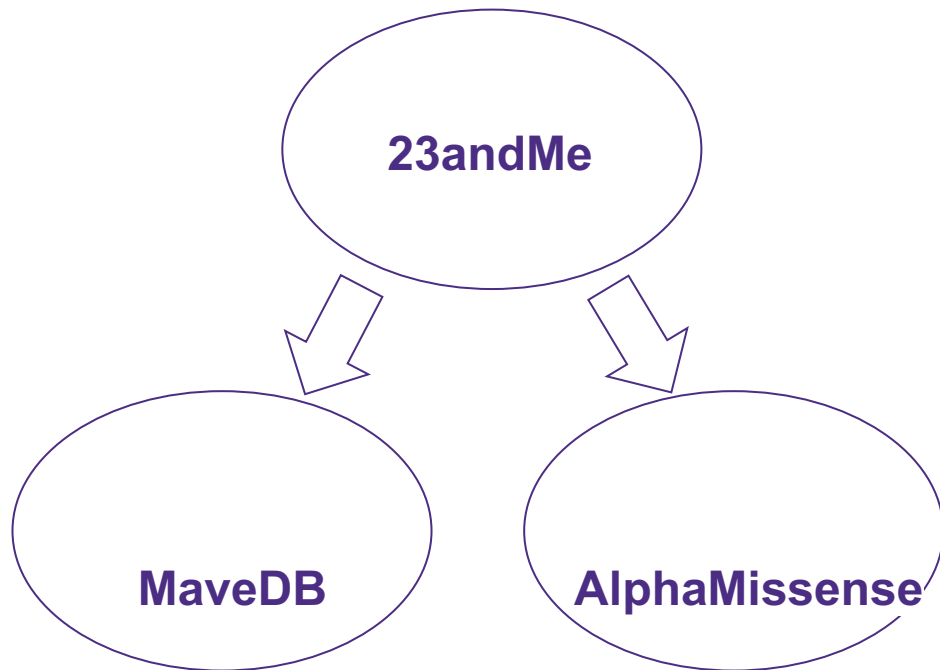
# User Story

Michael got his genetic report from 23andMe and is eager to find out his personal genetic information and family genetic history.

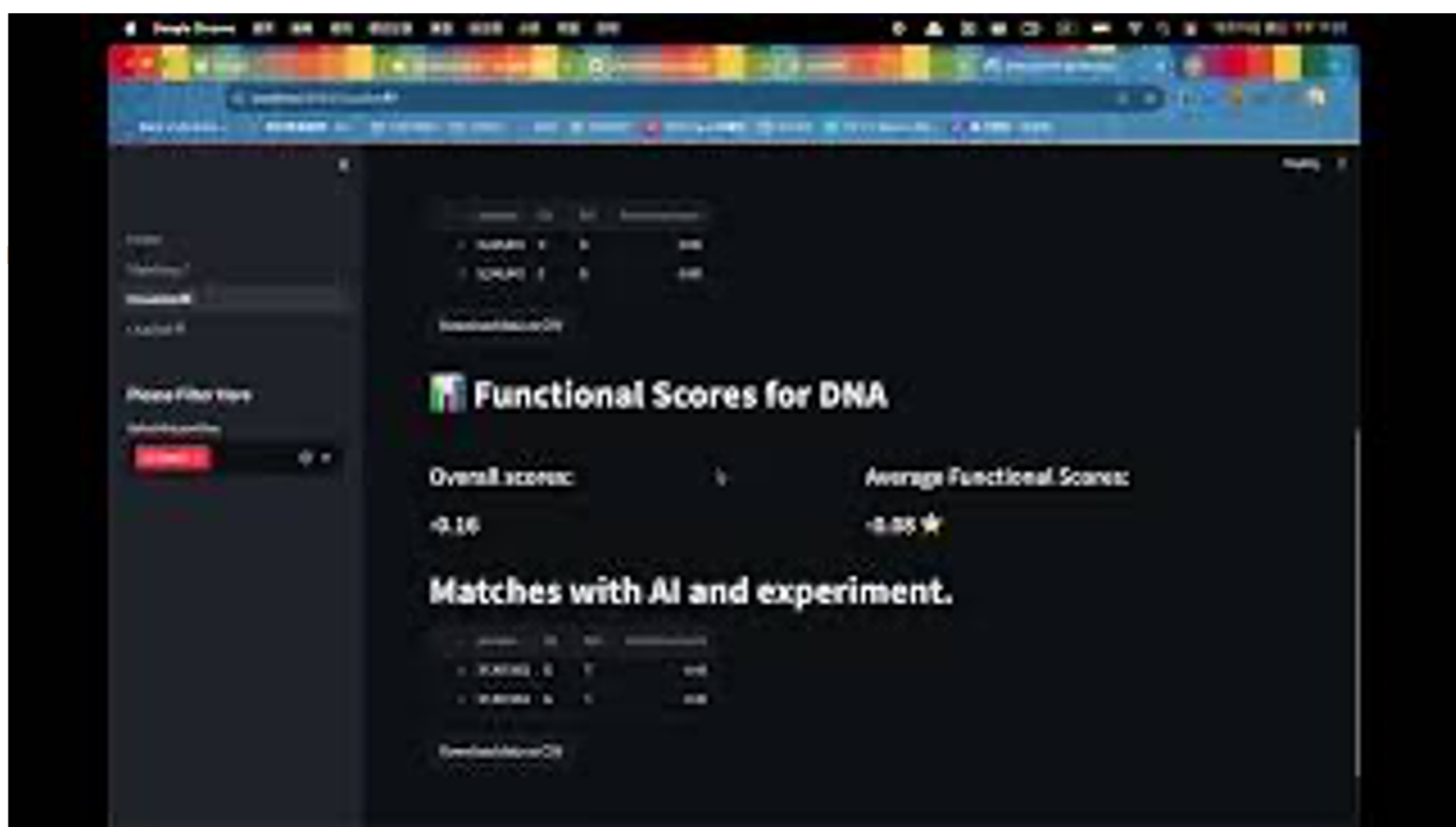
UltraGene can simplify the complexity of genetic analysis, uncover potential genetic anomalies in a user-friendly manner.



# Intro to UltraGene



UNIVERSITY *of* WASHINGTON





# Results & highlight

## Information obtained from UltraGene:

- gene position
- functional score
- FAQ with chat bot
- identifies and suggests the most dangerous DNA positions



# Future work

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- **Incorporation of Additional Databases ( aim for Open Source ) :**
  - **EX - data on genetic inheritance patterns Autosomal Dominant vs Recessive (*i.e., 1 or 2 copies of the gene need to be defective to cause disease*)**
- **Support for Multiple Data Formats:**
  - **Expand the data input compatibility to accept various formats (ex. WGS, Exome )**
  - **Move beyond exclusive support for 23andMe SNP Chip data.**