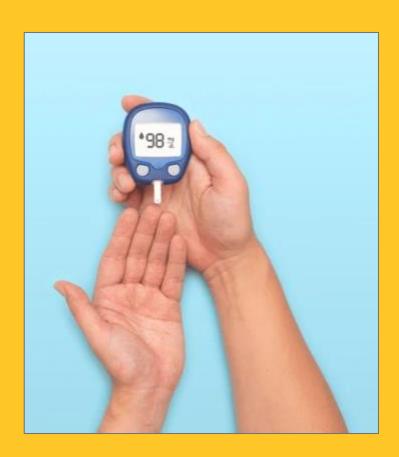
Analyzing Cardiovascular and Kidney Disease Risks Among Diverse Populations with Type 2 Diabetes Using Compartmental Modeling and the NIH All of Us Database

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Background



Diabetes Definition

- Diabetes Mellitus is a chronic metabolic disease
- The body doesn't produce enough or cannot use insulin effectively
- This leads to high blood sugar levels

High blood sugar can lead to problems including:

- Neuropathy
- Retinopathy
- Fatigue
- Kidney Disease
- Cardiovascular Disease
- Ketoacidosis (Only Type 1)
- Death

Differences in Type 1 vs Type 2 Diabetes

Table 1: Statistical comparison of Type I and Type II Diabetes detailing physical traits, risk factors, and molecular basis. ¹⁻³			
	TYPE I DIABETES	TYPE II DIABETES	
ONSET AGE	Childhood/adolescence	After 40 years of age	
PHENOTYPE	Often thin or normal weight	Often obese	
	Prone to ketoacidosis	No ketoacidosis	
INSULIN LEVELS	Absolute insulin deficiency	Relative insulin deficiency and/or resistance	
INSULIN ADMINISTRATION	Required for survival	Not required for survival	
PANCREAS	Damaged by autoimmune attack	Not damaged	
RISK FACTORS	Increased prevalence in relatives	Increased prevalence in relatives	
	Autoimmune, genetic	Obesity, physical inactivity,	
		ethnicity, impaired glucose	
		tolerance	
PREVALENCE	5-10% of cases	90-95% of cases	
TREATMENT	Insulin injections	(1) healthy diet and increased	
		exercise; (2) hypoglycemic	
		tablets; (3) insulin injections	

Diabetes Stats in the USA

Type 2 Diabetes

More than 37 million

Prevalence

1 in 10 adults

Prediabetes risk

1 in 3 adults have prediabetes

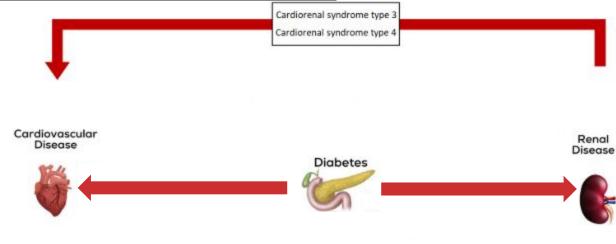
11.6%

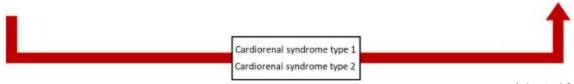
Prevalence Underrepresented groups more affected

Centers for Disease Control and Prevention (2025)

Cardiovascular and Kidney Disease

Interaction with cardiovascular complications

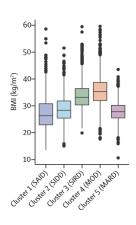


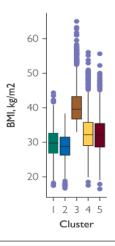


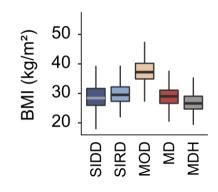
Type 2 Diabetes Subtypes

- Severe Autoimmune Diabetes (SAID)
- Severe Insulin-Deficient Diabetes (SIDD)
- Severe Insulin-Resistant Diabetes (SIRD)
- Mild Obesity-Related Diabetes (MOD)
- Mild Age-Related Diabetes (MARD)

Previous Subtype Categorization







Ahlqvist et al. (2018)

- SIDD
- SIRD
- MOD
- MARD
- SAID

Xue et al. (2023)

- SIDD
- SIRD
- MOD
- MARD
- MARD+SIRD

Sliecker et al. (2021)

- SIDI
- SIRD
- MOD
- MD
- MDH

Research Question

How are the Type 2 Diabetes Mellitus subtypes distributed among the US population and how do they contribute to cardiovascular and kidney disease risks?

Aims





Identify type 2 diabetes subtypes and analyze the prevalence of related cardiovascular and kidney complications



Aim 2

Assess the relationship between type 2 diabetes subtypes and race/ethnicity



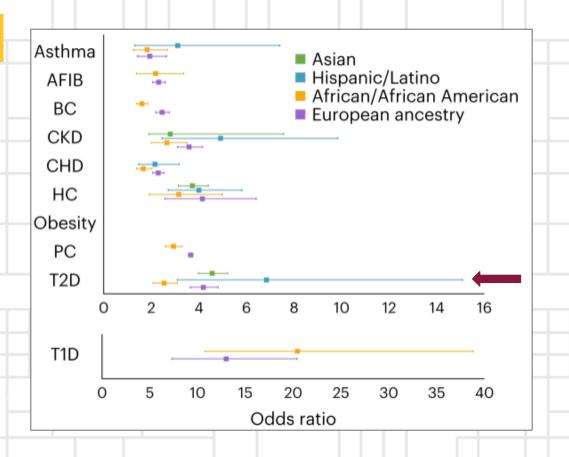
Aim 3

Model the and predict behavior of type 2 diabetes subtypes

Associated Risks Related to Race and Ethnicity

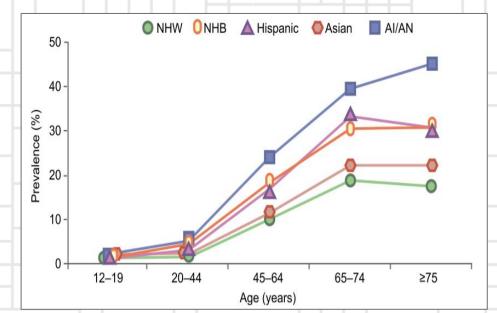
Hispanic/Latino Population at Higher Risk

- Based off genetic predisposition (GWAS)
- Hispanics have the highest risk and variation in T2DM, while Africans have the lowest risk



Prevalence Across Race and Ethnicity

- T2DM prevalence increases
 with age in all races and
 ethnicities
- Non-genetic factors can lead to higher rates of disease in groups with lower genetic risk



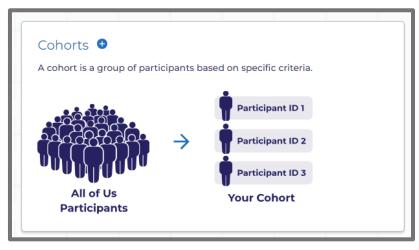
NHW = Non-Hispanic White NHB = Non-Hispanic Black Al/AN = American Indian/Alaska Native

All of Us Database

All of Us Initiative and Database

- NIH Biomedical Data Resource (US
- Participants)
- ² 864,000+ Participants
- Cloud based platform for data analysis
- Different tiers of access
 - Public, Registered, Controlled
- 5 All participants have given consent for certified researchers to access their data





Certification

- Avoiding Stigma and Stigmatizing Research
- Interaction between Biology and Society
- Group Harms and Cultural Competence
- 4 Social Responsibility in Research









Subtypes and Clustering

Importance of Clustering and Subtypes

- 1 Subtypes Have Different Characteristics
 - Characteristics can impact complications
 - Kidney Function (Creatinine and eGFR)
 - Heart Disease/Stroke (HDL)
 - Elevated blood sugar levels (HBA1c)
 - Other Health Conditions (BMI, Age Onset)

Personalized Treatment of T2DM and Complications

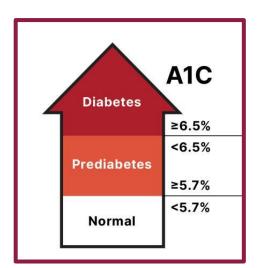
- Differing risks can mean different treatments per cluster
- Subtype identification important



Final Cohorts



- 1 Cohort 1 Nondiabetic Control
 - Include if:
 - A1c below 5.7%
 - Exclude if:
 - T2DM or T1DM diagnosis
 - Cardiovascular or kidney complications



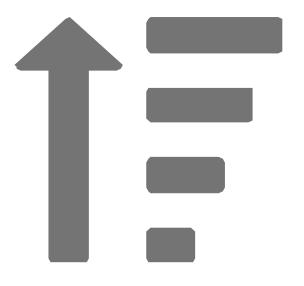
Cohort 2 - Prediabetes and T2DM

- Include if:
 - Any measurements in clustering variables (A1c, BMI, HDL, Creatinine) AND T2DM/Prediabetes Diagnosis
- Exclude if:
 - Cardiovascular or Kidney complications before diagnosis
 - T1DM Diagnosis
 - Pregnancy related diabetes

Clustering Tendency - Hopkins Statistic

1 Hopkins Statistic

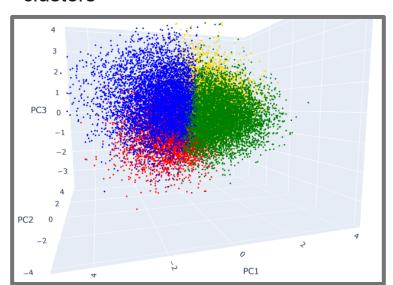
- Measures how likely the data is to be able to be clustered meaningfully
- Looks at the differences between our data and a uniformly distributed dataset
- Values closer to 1 indicate that our data is more likely to be clustered
- Our Hopkins Value: ~0.9989



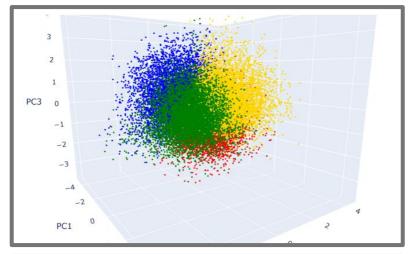
3D Clustering Graph

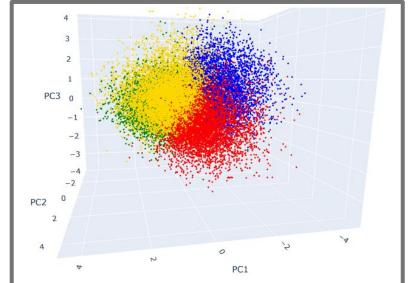
First three Principal Components

- 33.00% + 23.84% + 17.99% = 74.83%
- Stronger separation of clusters



- 1 SIDD
- 2 SIRD+MARD
- 3 MOD
- 4 MDH





Identifying Subtypes

Which clusters correspond to which subtypes?

- Cluster 1 Severe Insulin Deficient (SIDD)
- Cluster 2 Severe Insulin Resistant + Mild Age Related (SIRD+MARD)
- Cluster 3 Mild Obesity Related (MOD)
- Cluster 4 Mild Diabetes with high HDL cholesterol (MDH)

Median table of characteristics for each cluster. Important to note that each observation is an average of participants' measures

Cluster	Age Onset	BMI	A1c	eGFR	HDL
1 (SIDD)	54	32.348	8.054	93.714	41.750
2 (SIRD+MARD)	<mark>66</mark>	31.754	6.736	66.709	40.667
3 (MOD)	<mark>47</mark>	39.276	6.273	99.741	42.523
4 (MDH)	63	29.579	6.200	85.409	58.000

Cluster Stability - Mean Jaccard Coefficients

Mean Jaccard Coefficient per cluster

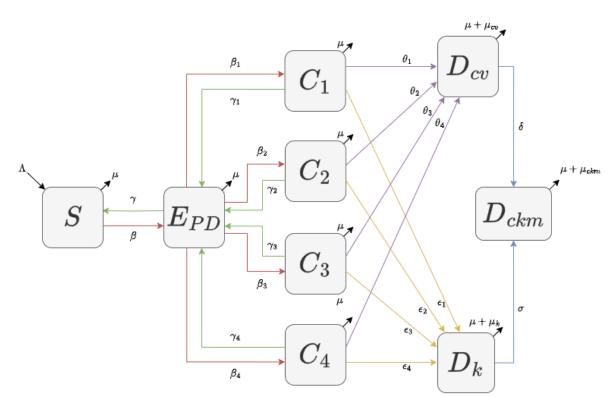
- Measures the similarity of points within the clusters
- Resamples original data to create new datasets which are then clustered
- Take the mean of all iterations
- Used 2000 resamplings
- Values closer to 1 indicate stronger stability

Jaccard similarity means for each cluster considering 2000 bootstraps. Coefficients range between 0 and 1. Typically, numbers above 0.75 are considered stable Anjana et al. (2020)

Cluster	Jaccard Similarity Mean	
1 (SIDD)	0.9123	
2 (SIRD+MARD)	0.9310	
3 (MOD)	0.9807	
4 (MDH)	0.8869	

Modeling

Current Model



S(t): Susceptible

E_{PD}(t): Prediabetic

C_i(t) for i=1,2,3,4: Diabetic Clusters

 $D_{cv}(t)$: Diabetes with a cardiovascular complication

 $D_k(t)$: Diabetes with a kidney complication

D_{ckm}(t): Diabetes with a cardiovascular and kidney complication

Model

$$\frac{dS}{dt} = \Lambda - \beta S + \gamma E_{PD} - \mu S,\tag{1a}$$

$$\frac{dE_{PD}}{dt} = \beta S + \gamma_1 C_1 + \gamma_2 C_2 + \gamma_3 C_3 + \gamma_4 C_4 - (\beta_1 + \beta_2 + \beta_3 + \beta_4 + \gamma + \mu) E_{PD},$$
 (1b)

$$\frac{dC_1}{dt} = \beta_1 E_{PD} - (\mu + \gamma_1 + \theta_1 + \epsilon_1)C_1,\tag{1c}$$

$$\frac{dC_2}{dt} = \beta_2 E_{PD} - (\mu + \gamma_2 + \theta_2 + \epsilon_2) C_2, \tag{1d}$$

$$\frac{dC_3}{dt} = \beta_3 E_{PD} - (\mu + \gamma_3 + \theta_3 + \epsilon_3)C_3,\tag{1e}$$

$$\frac{dC_4}{dt} = \beta_4 E_{PD} - (\mu + \gamma_4 + \theta_4 + \epsilon_4)C_4,\tag{1f}$$

$$\frac{dD_{CV}}{dt} = \theta_1 C_1 + \theta_2 C_2 + \theta_3 C_3 + \theta_4 C_4 - (\delta + \mu + \mu_{cv}) D_{CV}, \tag{1g}$$

$$\frac{dD_K}{dt} = \epsilon_1 C_1 + \epsilon_2 C_2 + \epsilon_3 C_3 + \epsilon_4 C_4 - (\sigma + \mu + \mu_k) D_K, \tag{1h}$$

$$\frac{dD_{CKM}}{dt} = \delta D_{CV} + \sigma D_K - (\mu + \mu_{ckm}) D_{CKM}. \tag{1i}$$

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Mathematical Analysis

Proposition

The closed set

$$D = \{ (S, E_{pd}, C_1, C_2, C_3, C_4, C_5, D_{cv}, K, D_{ckm}) \in \mathbb{R}^{10}_+ : N \le N^* \}$$

is positively-invariant and attracting.

Here,

$$N^* = \Lambda/\mu$$

is the asymptotic value for the supersolution N.

Mathematical Analysis

Equilibrium Point

Assuming compartments $C_{1,2,3,4,5}$ are condensed into one compartment C_i , then our model has one interior positive equilibrium point $(S^*, E_{PD}^*, C_i^*, D_{CV}^*, K^*, C_{KM}^*)$. By setting

$$\frac{dS}{dt} = \frac{dE_{PD}}{dt} = \frac{dC_i}{dt} = \frac{dD_{CV}}{dt} = \frac{dK}{dt} = \frac{dD_{KM}}{dt} = 0,$$

we get the following equilibrium

$$S^* = \frac{\lambda \left(\beta_i(\epsilon_i + \mu + \theta_i) + (\gamma + \mu)(\gamma_i + \epsilon_i + \theta_i + \mu)\right)}{\beta_i(\theta_i + \mu + \epsilon_i)(\beta + \mu) + \mu(\gamma_i + \theta_i + \mu + \epsilon_i)(\beta + \gamma + \mu)}$$

$$E_{PD}^* = \frac{\beta \lambda (\gamma_i + \theta_i + \mu + \epsilon_i)}{\beta_i (\theta_i + \mu + \epsilon_i)(\beta + \mu) + \mu (\gamma_i + \theta_i + \mu + \epsilon_i)(\beta + \gamma + \mu)}$$

$$C_i^* = \frac{\beta \beta_i \lambda}{\beta_i (\theta_i + \mu + \epsilon_i)(\beta + \mu) + \mu(\gamma_i + \theta_i + \mu + \epsilon_i)(\beta + \gamma + \mu)}$$

$$D_{CV}^* = \frac{\beta \beta_i \theta_i \lambda}{\left(\beta_i (\theta_i + \mu + \epsilon_i)(\beta + \mu) + \mu(\gamma_i + \theta_i + \mu + \epsilon_i)(\beta + \gamma + \mu)\right) \left(\delta + \mu + \mu_{CV}\right)}$$

$$K^* = \frac{\beta \beta_i \epsilon_i \lambda}{\left(\beta_i (\theta_i + \mu + \epsilon_i)(\beta + \mu) + \mu(\gamma_i + \theta_i + \mu + \epsilon_i)(\beta + \gamma + \mu)\right)(\mu + \mu_K + \sigma)}$$

$$C_{KM}^* = \frac{\beta \beta_i \lambda \left(\delta \theta_i (\mu + \mu_K) + \delta \sigma(\epsilon_i + \theta_i) + \epsilon \sigma(\mu + \mu_{CV}) \right)}{\left(\beta_i (\theta_i + \mu + \epsilon_i) (\beta + \mu) + \mu (\gamma_i + \theta_i + \mu + \epsilon_i) (\beta + \gamma + \mu) \right) \left(\mu + \mu_{CKM} \right) \left(\delta + \mu + \mu_{CV} \right) \left(\mu + \mu_K + \sigma \right)}$$

This equilibrium always exists and is stable (by using Routh-Hurwitz criterion)

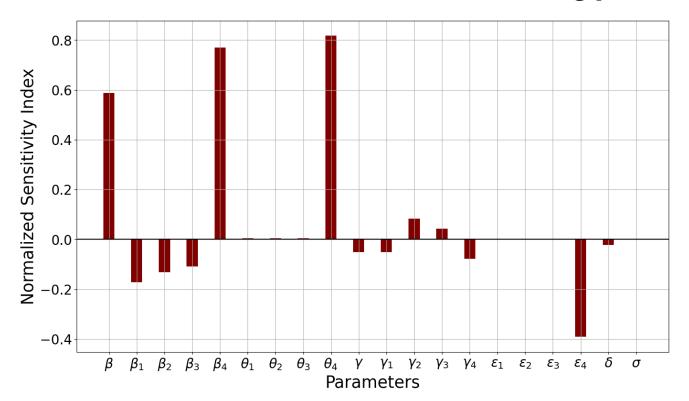
Results

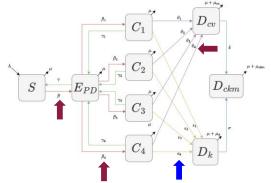
Our Fitted Parameters

Parameter	Description	Value	Units	References
Λ	Recruitment rate	987.015	people·month ⁻¹	Estimated
β	Transfer from susceptible to prediabetic	0.009802	month ⁻¹	Estimated
γ	Recovery from prediabetic to susceptible	0.003767	month ⁻¹	Estimated
μ	Natural death rate	0.01271	$month^{-1}$	CDC
γ_i	Recovery from clusters to prediabetic	[Expanded in following table]	month ^{−1}	Estimated
β_i	Transition from prediabetic to clusters	[Expanded in following table]	month ^{−1}	Estimated
$ heta_i$	Transition to diabetes with cardiovas- cular complications	[Expanded in following table]	month ⁻¹	Estimated
μ_{CV}	Death rate with cardiovascular compli- cations	0.0015072541	month ⁻¹	Xue et al. (2023)
$\mu_{ m K}$	Death rate with kidney complications	0.0036783	month ^{−1}	Zhao et al. (2025)
μ_{CKM}	Death rate with CKM complications	0.007815	month ^{−1}	Zhao et al. (2025)
ϵ_i	Transition to diabetes with kidney disease	[Expanded in following table]	month ⁻¹	Estimated
δ	Progression from CV to CKM	0.0003181	month ^{−1}	Estimated
σ	Progression from kidney to CKM	0.0003181	month ⁻¹	Estimated

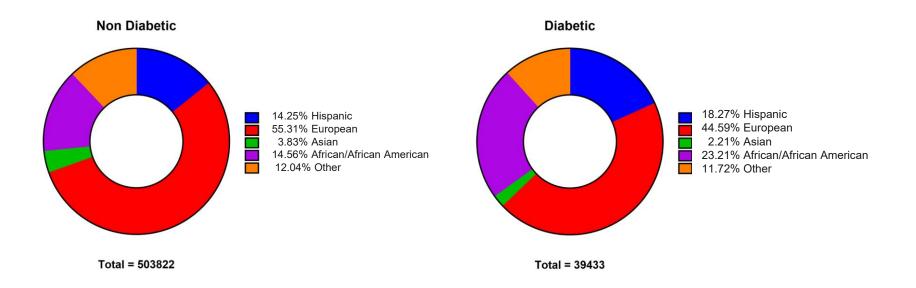
Parameter	Value	Units
β_1	0.01935	month ^{−1}
β_2	0.01540	month ^{−1}
β_3	0.00785	month ^{−1}
β_4	0.01011	month ^{−1}
θ_1	0.000013	month ^{−1}
θ_2	0.000017	month ⁻¹
θ_3	0.000017	month ⁻¹
θ_4	0.00619	month ^{−1}
ϵ_1	0.000047	month ^{−1}
ϵ_2	0.000065	month ^{−1}
ϵ_3	0.000088	month ⁻¹
ϵ_4	0.01426	month ⁻¹
γ_1	0.02103	month ^{−1}
γ_2	0.02179	month ^{−1}
<i>γ</i> ₃	0.00847	month ⁻¹
γ_4	0.00372	month ⁻¹

Sensitivity Analysis for D*_{CV}

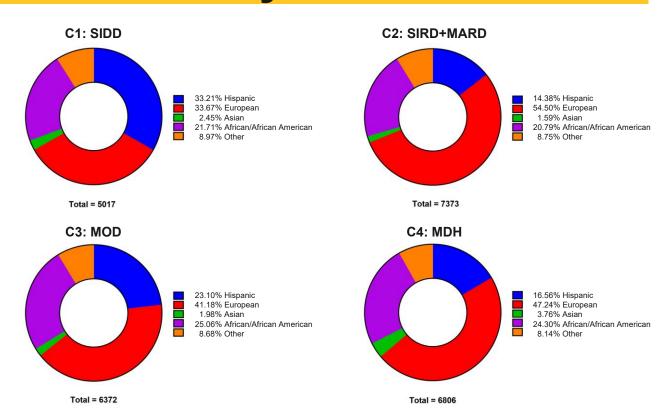




Type 2 Diabetes by Race/Ethnicity (All of Us)



Race/Ethnicity in Each Cluster



Conclusions and Future Studies

Selected Conclusions

- Four distinct T2DM subtypes were identified using K-means clustering:
 - Severe Insulin Deficiency Diabetes (SIDD)
 - Severe Insulin Resistant + Mild Age Related (SIRD+MARD)
 - Mild Obesity Related (MOD)
 - Mild Diabetes with high HDL cholesterol (MDH)
- Subtype classification was associated with different risks supporting the need for personalized management strategies
- Race and ethnicity influenced subtype distributions suggesting genetic and potential sociodemographic contributions to subtype risk
- 4 The model could be used as a tool for predicting disease progression allowing tailored interventions based on subtype and risk factors



Future Work

- 01 Improve the model
 - Currently captures general trends
 - Want more accurate predictions
- 03 Undiagnosed Individuals
 - Current data analysis relies on diabetes diagnosis
 - Considering them increases model accuracy

- **More complications**
 - Retinopathy and Neuropathy in clusters with high HBA1c
- Model with Race/Ethnicity and Genetics
- Include race/ethnicity and genetic predisposition in model parameters
- Focus more on Hispanic population

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We gratefully acknowledge *All of Us* participants for their contributions, without whom this research would not have been possible. We also thank the National Institutes of Health's *All of Us Research Program* for making available the participant data and cohort data examined in this study. This study used data from the *All of Us* Research Program's Controlled Tier Dataset version 8, available to authorized users on the researcher workbench



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Supplementary Materials

Data Cleaning

What we did

- 1. Calculated Age at Onset
- Calculated eGFR from Creatinine
- 3. Excluded outliers
 - Domain knowledge
 - Box plots and quartiles
- 4. Calculated averages of measurements 4. Person ID and measurement value for each person

What we used

- 1. Person ID, DoB, condition start
- 2. Person ID, measurement time and value, DoB, sex at birth
- 3. Measurement value, measurement units

Conditions Data

- Person ID
- Condition name
- Condition start time

Demographic Data

- Person ID
- Date of Birth
- Sex at birth
- Race/Ethnicity

Measurement Data

- Person ID
- Measurement name
- Measurement value
- Measurement time
- Measurement Unit

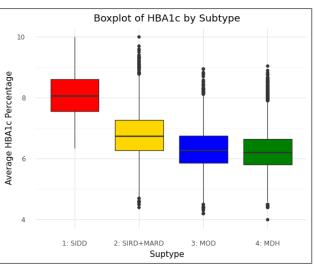
Mathematical Analysis

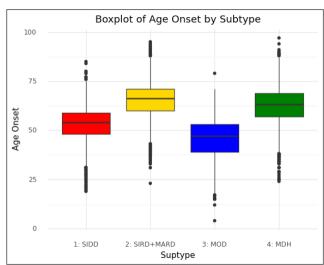
Equilibrium Point

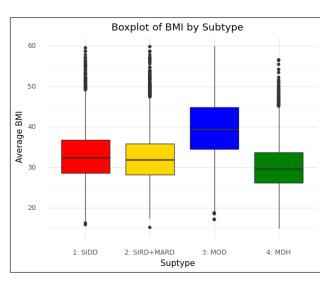
$$J(S^*, E_{PD}^*, C_i^*, D_{CV}^*, K^*, C_{KM}^*) = \begin{bmatrix} -\beta - \mu & \gamma & 0 & 0 & 0 & 0 \\ \beta & -\beta_i - \gamma - \mu & \gamma_i & 0 & 0 & 0 \\ 0 & \beta_i & -\gamma_i - \epsilon_i - \theta_i - \mu & 0 & 0 & 0 \\ 0 & 0 & \theta_i & -\delta - \mu - \mu_{CV} & 0 & 0 \\ 0 & 0 & \epsilon_i & 0 & -\mu - \mu_{K} - \sigma & 0 \\ 0 & 0 & \delta & \sigma & -\mu - \mu_{CKM} \end{bmatrix}.$$

$$(3)$$

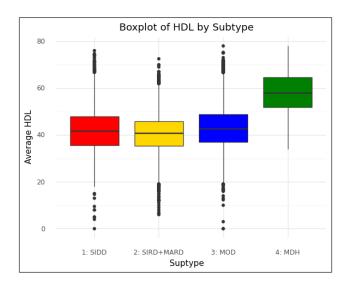
Identifying Subtypes

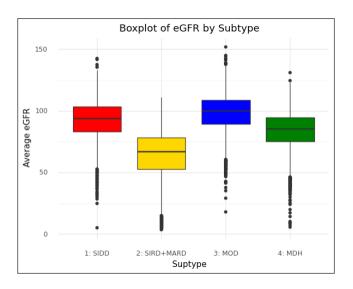






Identifying Subtypes





Mathematical Analysis

Equilibrium Point

$$J^* = \begin{bmatrix} -\beta - \mu & \gamma & 0 \\ \beta & -\beta_i - \gamma - \mu & \gamma_i \\ 0 & \beta_i & -\gamma_i - \epsilon_i - \theta_i - \mu \end{bmatrix}$$

Stability proven by Routh-Hurwitz criterion.

Mathematical Analysis

Equilibrium Point

$$J^* = \begin{bmatrix} -\beta - \mu & \gamma & 0 \\ \beta & -\beta_i - \gamma - \mu & \gamma_i \\ 0 & \beta_i & -\gamma_i - \epsilon_i - \theta_i - \mu \end{bmatrix}$$

Stability proven by Routh-Hurwitz criterion.

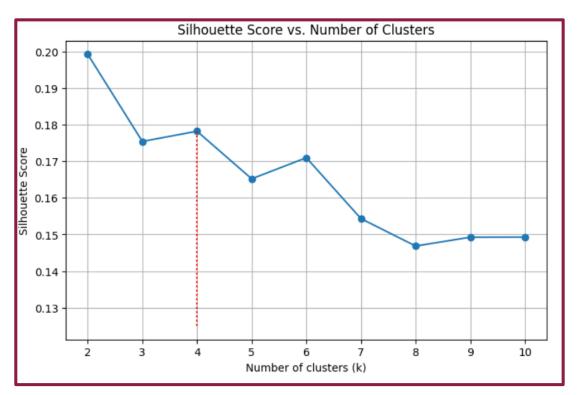
Clustering

K-means Clustering

- Participant Averages
- Sklearn kmeans
- N = 25,568
- HbA1c, BMI, Age at Onset, eGFR, HDL

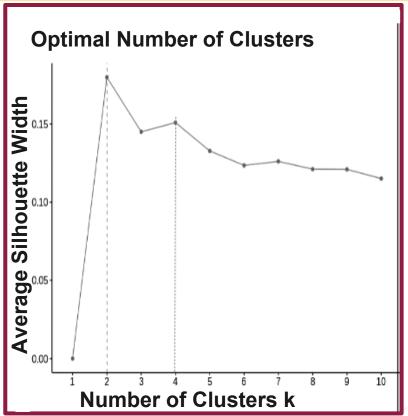
2 Silhouette Method

- Shows optimal number of clusters
- All previous studies we have looked at found 4-5 clusters
- Precedent for using second highest silhouette score



Anjana et al., 2020 Type 2 Diabetes Subtypes in Asian and Indian Populations

- General Findings
 - 7 Clustering variables
 - 4 replicable clusters
 - N=19,084
 - MARD, SIDD, IROD, CIRDD
 - New ones are combinations of ones from other papers
- 2 Silhouette Method
 - Despite 2 being higher, they chose k=4



2 Cluster Medians to Compare

Cluster	Age Onset	ВМІ	A1c	eGFR	HDL
1*	65	30.4000	6.55	76.308	48.000
2*	49	36.768	6.80	98.422	42.000

*Note: Cluster 1 and 2 here *do not* directly correspond to cluster 1 and 2 in other slides

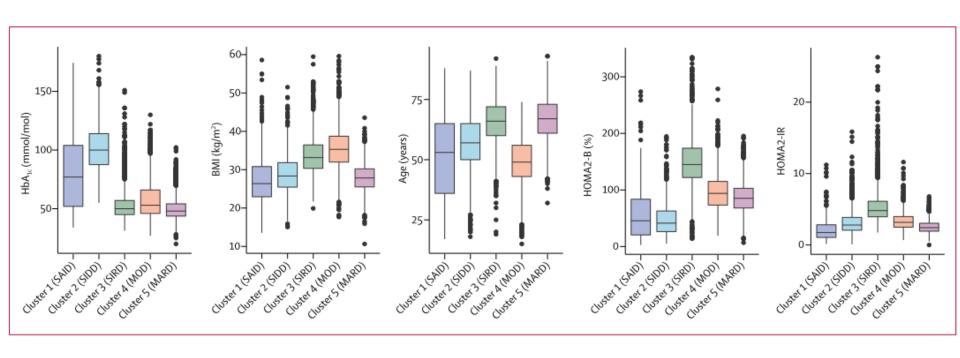
Our Cluster Medians to Compare

Which clusters correspond to which subtypes?

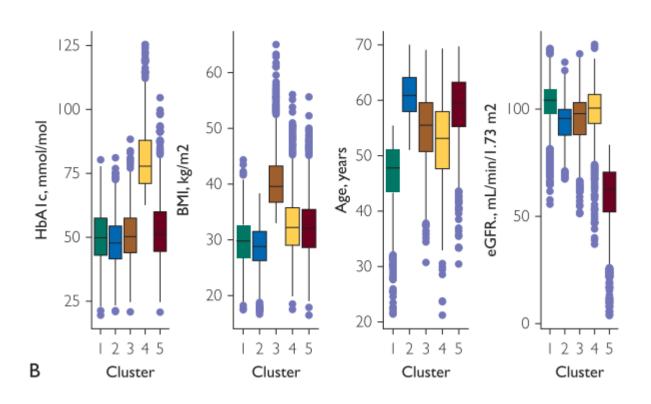
- Cluster 1 Severe Insulin Deficient (SIDD)
- Cluster 2 Severe Insulin Resistant + Mild Age Related (SIRD+MARD)
- Cluster 3 Mild Obesity Related (MOD)
- Cluster 4 Mild Diabetes with high HDL cholesterol

Cluster	Age Onset	ВМІ	A1c	eGFR	HDL
1	54	32.348	8.054	93.714	41.750
2	<mark>66</mark>	31.754	6.736	66.709	40.667
3	47	39.276	6.273	99.741	42.523
4	63	29.579	6.200	85.409	58.000

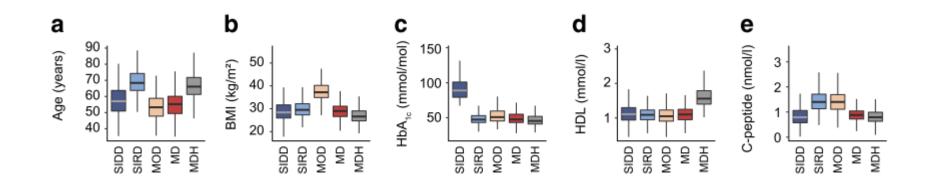
Ahlqvist Medians to Compare



Xue Medians to Compare



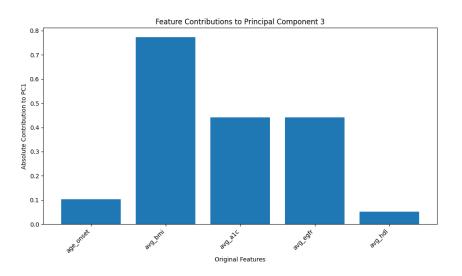
Sliecker Medians to Compare

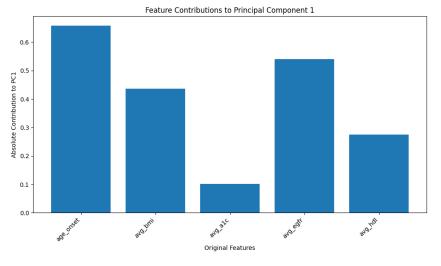


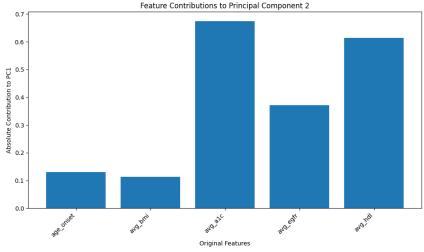
PC Contributions

First three Principal Components

• 33.00% + 23.84% + 17.99% = 74.83%





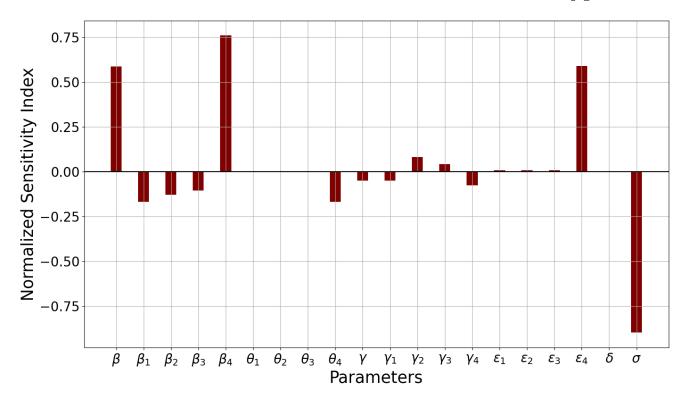


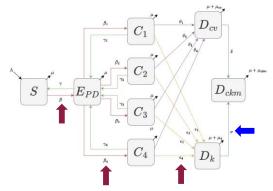
eGFR = $142 \times \min(SCr/\kappa, 1)^{\alpha} \times \max(SCr/\kappa, 1)^{-1.200} \times 0.9938^{Age} \times 1.012$ [if female]

Abbreviations/units

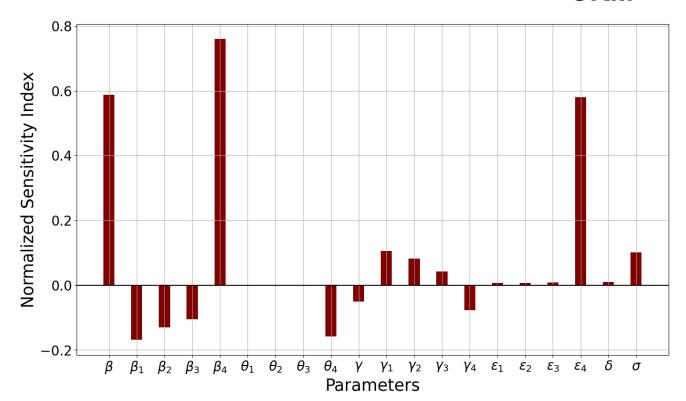
- eGFR = estimated GFR in mL/min/1.73 m²
- SCr = standardized serum creatinine in mg/dL
- $\kappa = 0.7$ (females) or 0.9 (males)
- $\alpha = -0.241$ (females) or -0.302 (males)
- min = indicates the minimum of SCr/κ or 1
- max = indicates the maximum of SCr/κ or 1
- age = years

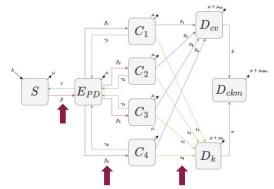
Sensitivity Analysis for D*_K

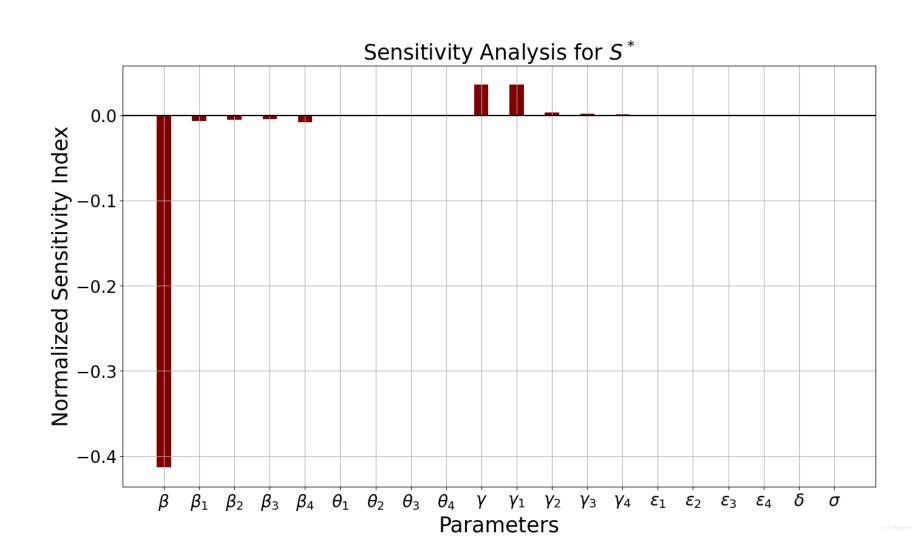


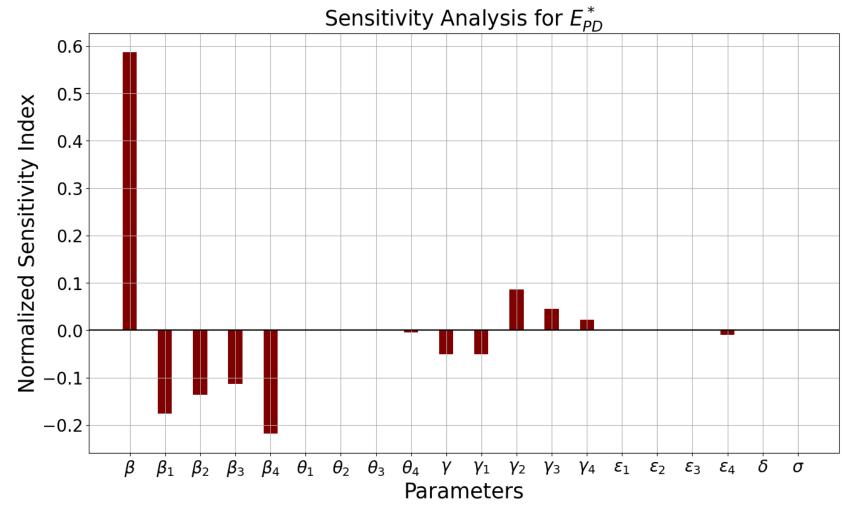


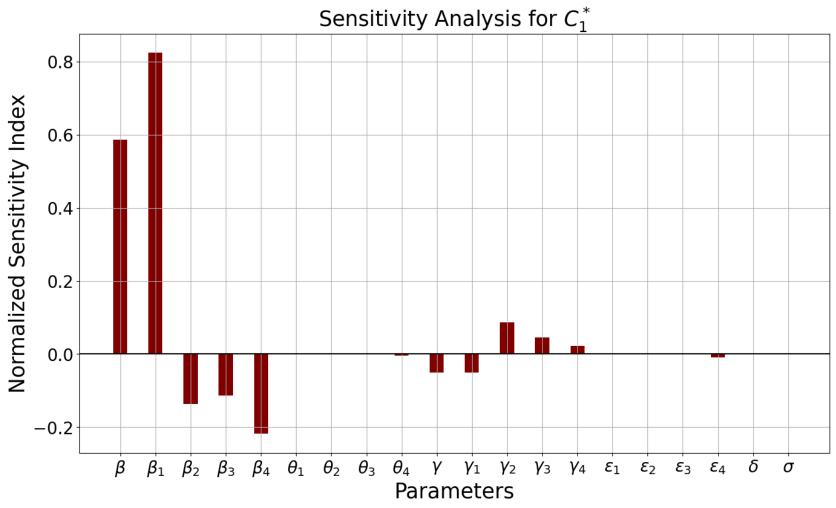
Sensitivity Analysis for D*_{CKM}

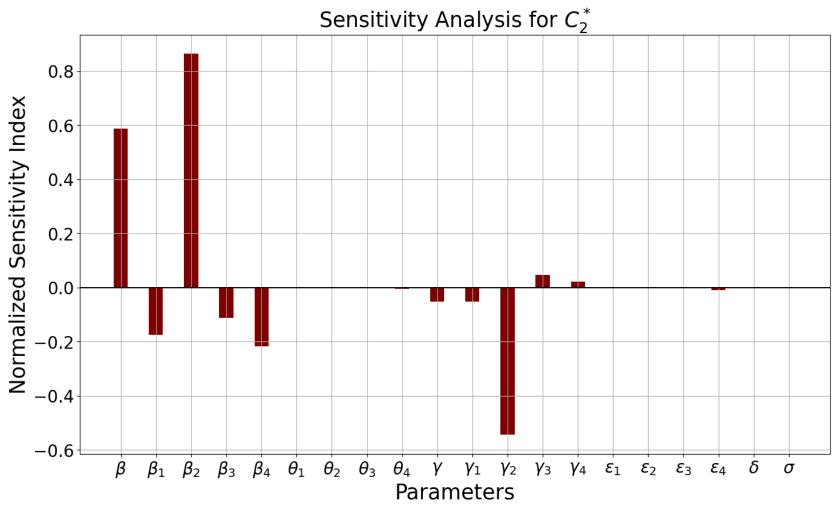


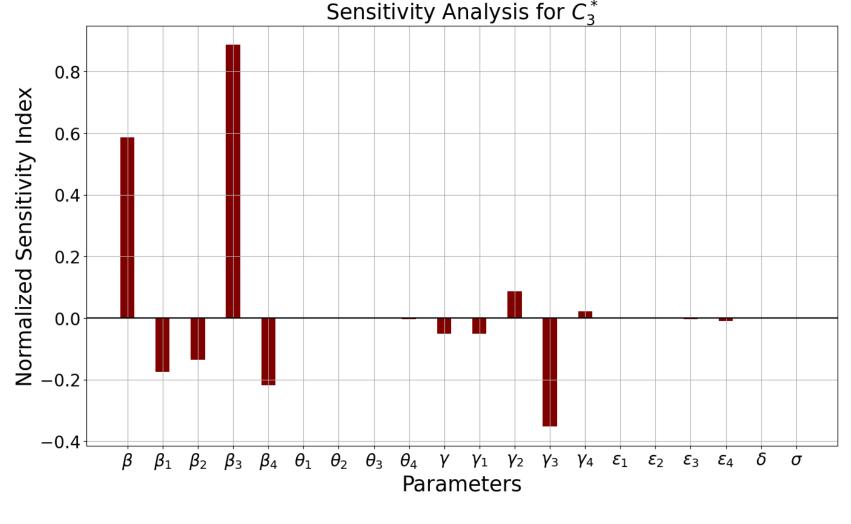


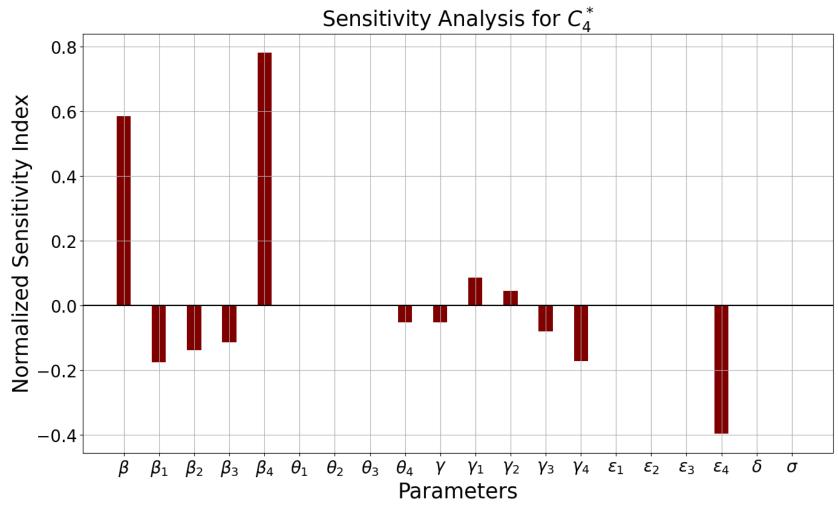


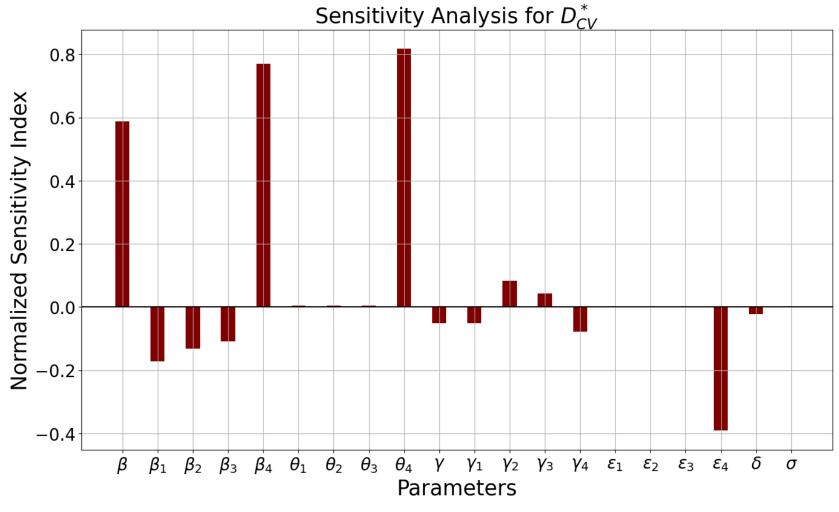


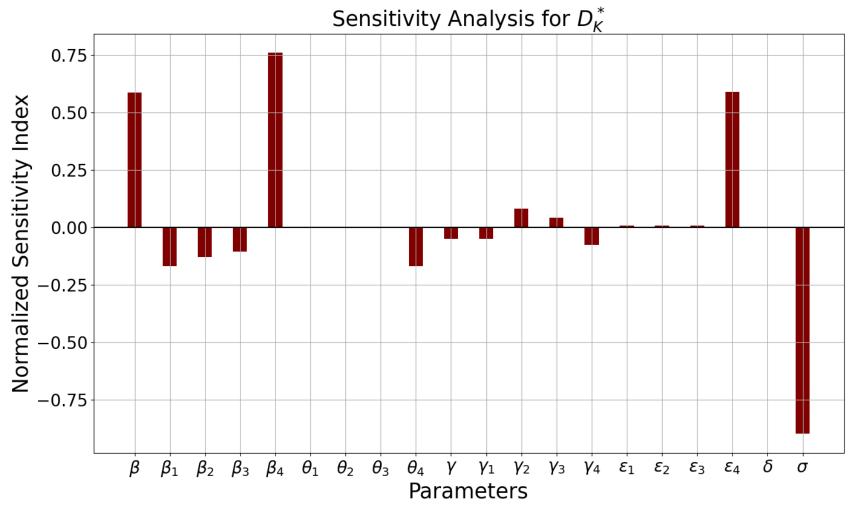


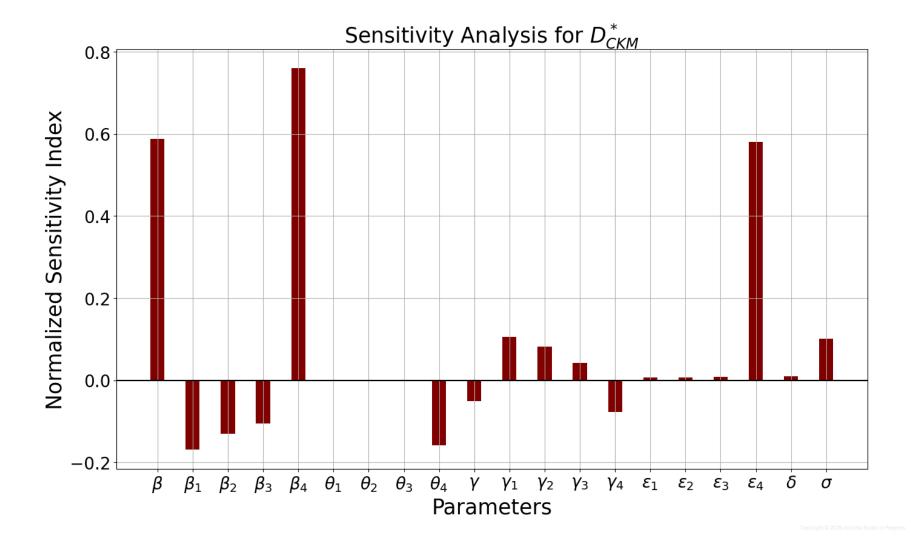










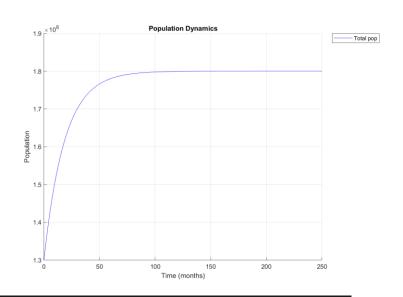


Preliminary results

Boundedness

From the assumption that μ_{cv} , μ_k , and μ_{ckm} are minimized, then $\frac{dN}{dt} = \Lambda - \mu N$. Thus,

$$\limsup_{t\to\infty} N(t) = \frac{\Lambda}{\mu}$$



Preliminary results

Positive Invariance

Starting at

$$\frac{d}{dt}S(t) = \Lambda + \gamma E_{pd}(t) - \beta S(t) - \mu S(t)$$

by integrating by integration factor, we get

$$\Psi(t)S(t) - \Psi(0)S(0) = \int_0^t \Psi(t')(\Lambda + \gamma E_{pd}(t')dt')$$

Then,

$$S(t) = \Psi(t)^{-1} \left(\int_0^t \Psi(t) (\Lambda + \gamma E_{pd}(t)) dt + S(0) \right) > 0$$

where

$$\Psi(t) = e^{(\beta + \mu)t}$$

Preliminary results

Equilibrium Point

$$J(S^*, E_{PD}^*, C_i^*, D_{CV}^*, K^*, C_{KM}^*) = \begin{bmatrix} -\beta - \mu & \gamma & 0 & 0 & 0 & 0 \\ \beta & -\beta_i - \gamma - \mu & \gamma_i & 0 & 0 & 0 \\ 0 & \beta_i & -\gamma_i - \epsilon_i - \theta_i - \mu & 0 & 0 & 0 \\ 0 & 0 & \theta_i & -\delta - \mu - \mu_{CV} & 0 & 0 \\ 0 & 0 & \epsilon_i & 0 & -\mu - \mu_{K} - \sigma & 0 \\ 0 & 0 & \delta & \sigma & -\mu - \mu_{CKM} \end{bmatrix}.$$

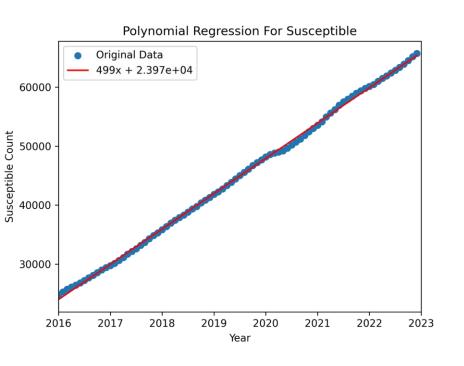
$$(3)$$

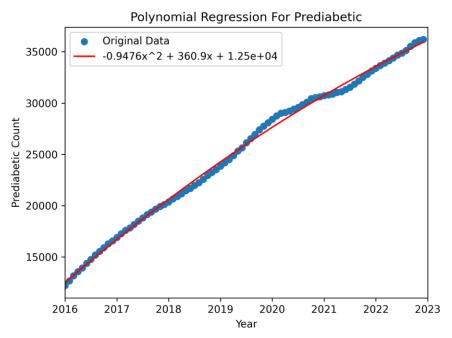
Preliminary results

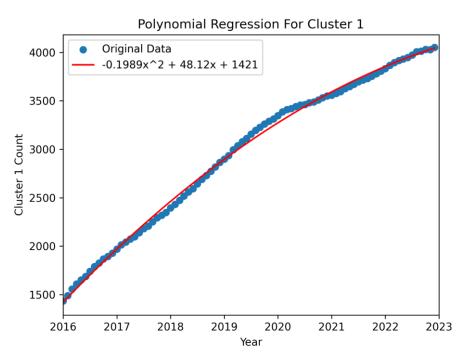
Equilibrium Point

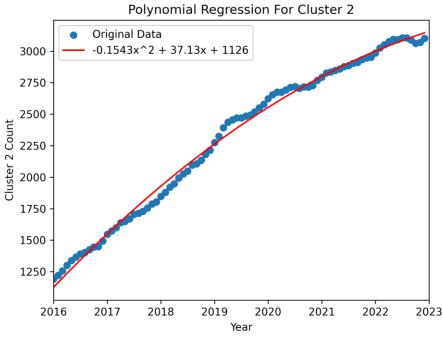
$$J^* = egin{bmatrix} -eta - \mu & \gamma & 0 \ eta & -eta_i - \gamma - \mu & \gamma_i \ 0 & eta_i & -\gamma_i - \epsilon_i - heta_i - \mu \end{bmatrix}$$

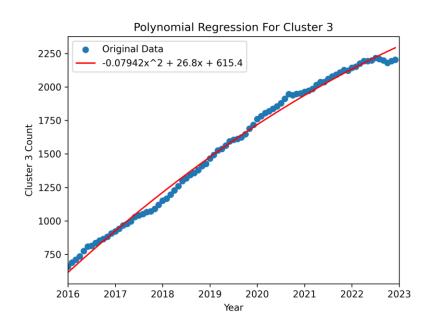
Stability proven by Routh-Hurwitz theorem.

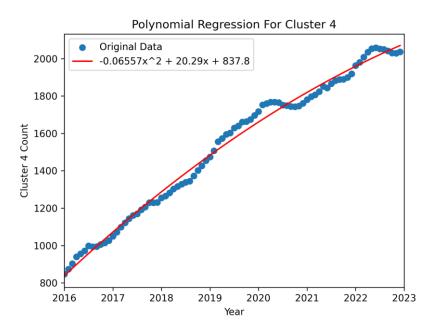


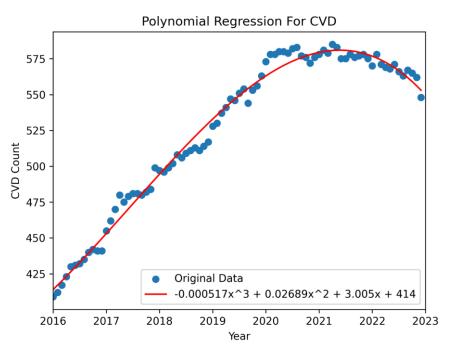


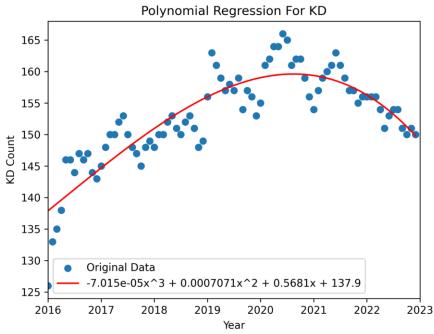


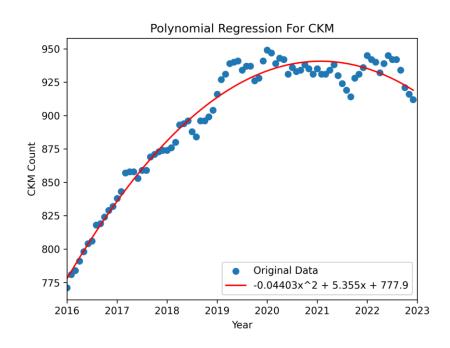






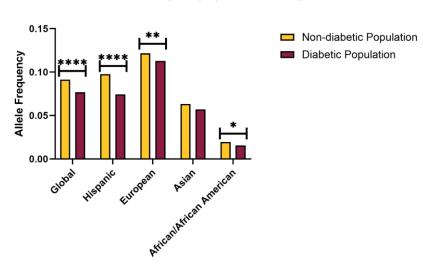




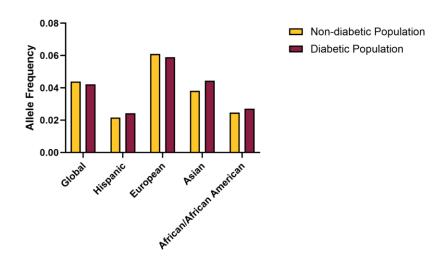


Allele Frequencies PPARG

PPARG rs1801282 Allele Frequency by Race/Ethnicity



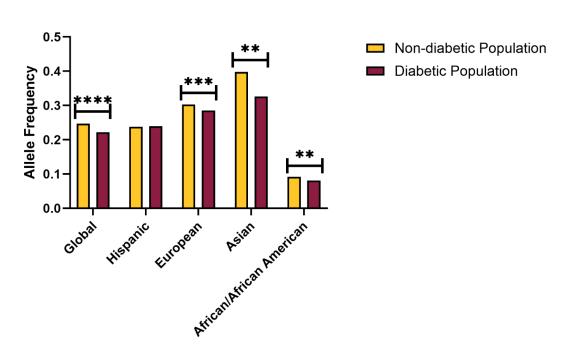
PPARG rs17036101 Allele Frequency by Race/Ethnicity



Allele Frequencies

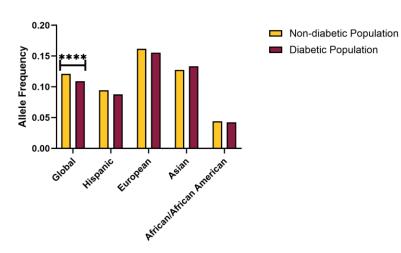
SLC30A8

SLC30A8 rs13266634 Allele Frequency by Race/Ethnicity

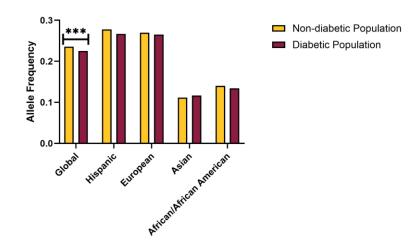


Allele Frequencies CAPN10

CAPN10 rs2975760 Allele Frequency by Race/Ethnicity

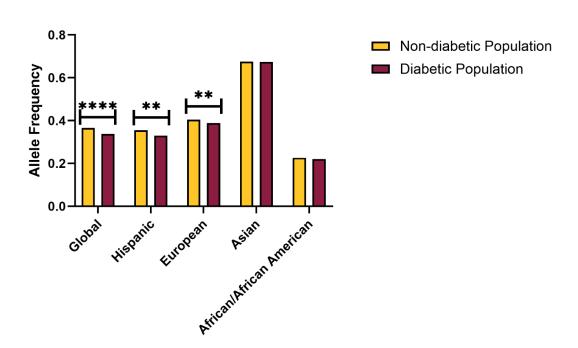


CAPN10 rs3792267 Allele Frequency by Race/Ethnicity



Allele Frequencies HHEX/IDE

HHEX/IDE rs1111875 Allele Frequency by Race/Ethnicity



Relative Error

Per Cluster

	error_c1	error_c2	error_c3	error_c4
0	0.036609	0.051199	0.074788	0.000433
1	0.036478	0.050548	0.073827	0.008182
2	0.037020	0.048663	0.073920	0.019918
3	0.036751	0.045114	0.073013	0.021411
4	0.035935	0.050381	0.070196	0.022008
5	0.040320	0.056263	0.077616	0.008893
6	0.044905	0.071182	0.099879	0.003380
7	0.050198	0.078415	0.117229	0.006519
8	0.055528	0.083127	0.133252	0.012917