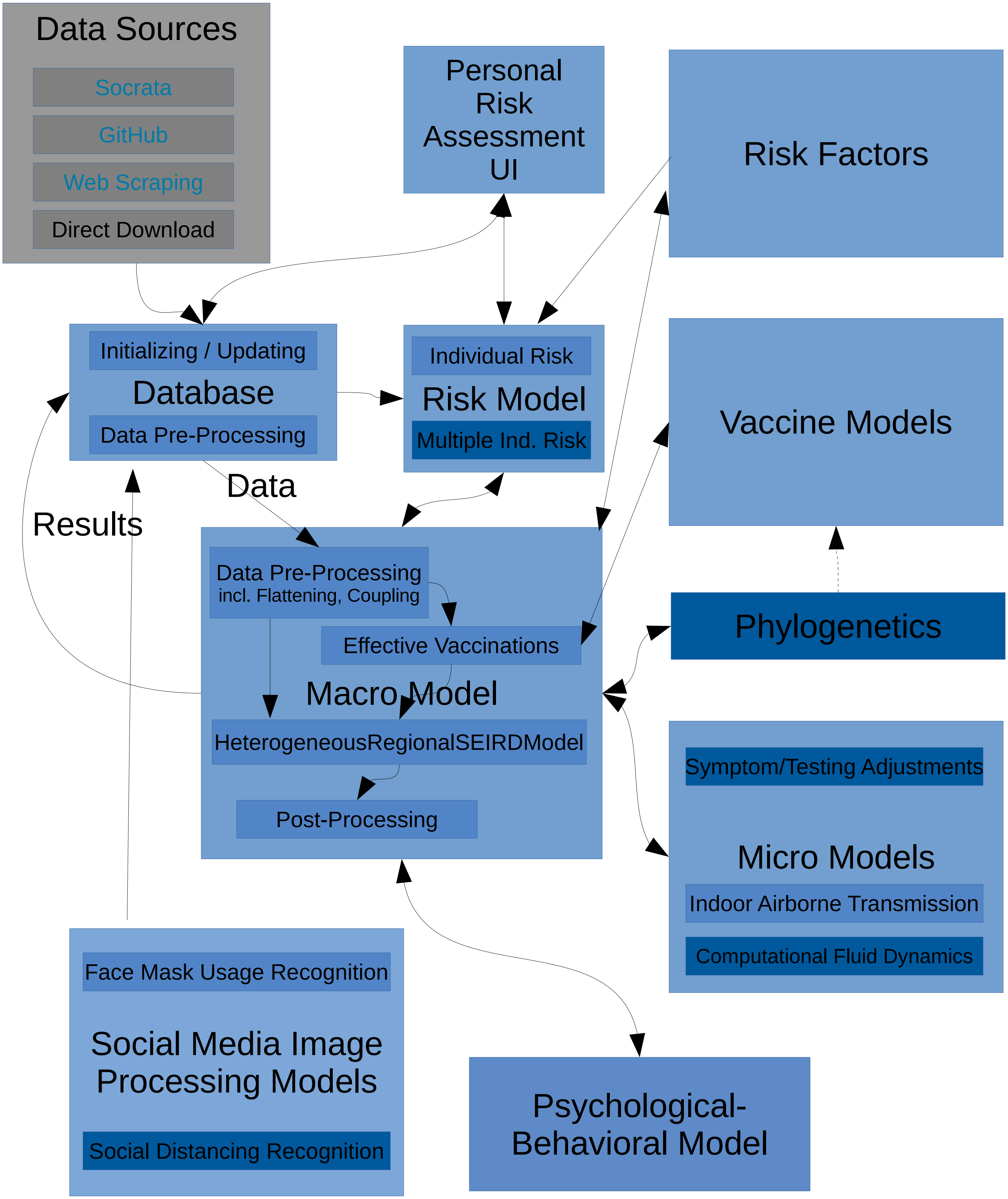
Data Sources
Socrata
GitHub
Web Scraping
Direct Download
Personal Risk Assessment UI
Risk Factors
Initializing / Updating
Database
Data Pre-Processing
Individual Risk
Risk Model
Multiple Ind. Risk
Vaccine Models
Data
Results
Data Pre-Processing
incl. Flattening, Coupling
Effective Vaccinations
Macro Model
HeterogeneousRegionalSEIRDModel
Post-Processing
Phylogenetics
Symptom/Testing Adjustments
Micro Models
Indoor Airborne Transmission
Computational Fluid Dynamics
Face Mask Usage Recognition
Social Media Image Processing Models
Social Distancing Recognition
Psychological-Behavioral Model

Data Sources: Public health departments' and other organizations' studies, reports and datasets with data pertinent to risk, such as vaccination & case statistics, and demographics. In the future, aggregate travel/commuting data and data from social media may be added.

Personal Risk Assessment UI: The user interface for inputting individual-specific data to the Risk Model and receiving the individual-specific risk assessment result from it.

Risk Factors: Module for handling predetermined factors affecting risk such as predisposing health conditions, age, race/ethnicity, sex, previous infection, etc.

Database: Storage of most of our pertinent data and information in a convenient, computer-accessible form for retrieval and analysis. The database does the initial data preprocessing before handing off to the Macro Model for further processing.

Risk Model: Our probabilistic-based model of individual risk of infection and death, and, in the future, hospitalization and Long COVID.

The model will include multiple individual risk assessments so that for multiple people who interact with each other, the component of individual risk due to this interaction will be identified in each individual's risk.

Vaccine Models: Our models of the effect of *vaccine product/type* and *time-since-vaccination* on the risk of an individual's chances of being infected, of being hospitalized, or of dying from COVID-19.

Macro Model: Our population-scale model of disease spread, which is based on a commonly-used epidemiological model type named "SEIRD" (**S**usceptible, **E**xposed, **I**nfected, **R**ecovered, **D**eceased).

However, our model is stochastic in contrast to the traditional ordinary-differential-equation model, and we also model select individuals with their movements between regions. For increased realism, we incorporate heterogeneity of demographic groups within each region, between regions and over time.

Macro Model Pre-/Post-Processing converts the hierarchical data to/from flat tensors used by underlying models and translates the mobility data of individuals and/or groups into dynamic coupling factors.

Effective Vaccinations: The equivalent number of hypothetical, perfectly-effective vaccinations in each population for each outcome (e.g., infection or death) at each time. (This consolidates *Vaccine Models' results* and *vaccination history data* without compromising Risk or Macro Model results.)

Phylogenetics: (Future) Dynamically model each variant separately to better account for the impact of multiple active variants of COVID-19.

Micro Models: Mechanistic models for infection transmission between individuals, currently just for indoor airborne transmission through aerosolized droplets from infected people. In the future, plan to add a computational fluid dynamics model.

Social Media Image Processing Models: Models that will take photo information from social media to estimate disease-spread-influencing behavior such as mask-wearing and social distancing. Please see more about our Face Mask Usage Recognition Model component.

Psychological-Behavioral Model: currently a conceptual model that we will develop to predict how relevant behaviors (e.g., mask usage, vaccine uptake) will change within the population.