# **Study Title**

Using an Office-Based Screening Program of 300,000 Individuals to Predict Alpha-1 Antitrypsin Deficiency

# **Background**

Alpha-1 antitrypsin deficiency (AATD) is a rare genetic disease due to an inherited mutation in the alpha-1 antitrypsin (AAT) protease inhibitor (PI) of the enzyme elastase, which can lead to increased risk of pulmonary and hepatic disease.1 The normal allele is termed “M”; whereas, the most common abnormal alleles are “Z” and “S” respectively. The allelic homozygous PI\*ZZ accounts for 95% of persons with AATD.2 It is estimated that 1 in 5,097 individuals in the United States have AATD, and it accounts for 1-2% of all chronic obstructive pulmonary disease (COPD) cases.2,3

The World Health Organization, American Thoracic Society, and European Respiratory Society recommend testing of all individuals with COPD for AATD.4-6 However, there is significant time and cost associated with testing more than an estimated 174 million persons globally, and there is low uptake of this recommendation in clinical practice.7

A more focused approach to who should be screened is desirable. Strategies have been developed to enhance detection using case-finding methods, for example, respiratory therapist identifying patients with fixed airway obstruction and providing information and free testing samples for AATD.8 Creating automatic alerts in the electronic medical record to screen for AATD has also been employed.9,10 There is also literature describing serum AAT to predict PI\*ZZ genotype.11,12

The University of Florida Alpha-1 Antitrypsin Genetic Laboratory has screened over 300,000 patients since 2003 for AATD. Screening is offered free to patients and collects information such as gender, race, date of birth, smoking history, liver disease history, and respiratory disease history.

We hypothesize that reviewing a large database of screened patients would identify the effect of certain patient characteristics to yield an abnormal serum AAT level and genotype. We would like to use machine learning to evaluate this database and develop a model to predict the likelihood of having or risk stratify an abnormal serum AAT genotype.

# **Objectives**

* Use machine learning to evaluate this office-based screening program database and develop a model to predict the likelihood of having or risk stratify an abnormal serum AAT genotype

# **References**

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