CANCER PATIENTS

CONTROLS

ACTCGATACTGCATGCAAACCCATGCCATCATTCAGTCATACATGCCAACTTGACCTAGACACTGCATGACTGACTGACTACTGACTGCATGCATGGGGCACAGATCGACACGACTGTGACCGAAGCGATCGATGCGTACGATCGACGATGACGCATG

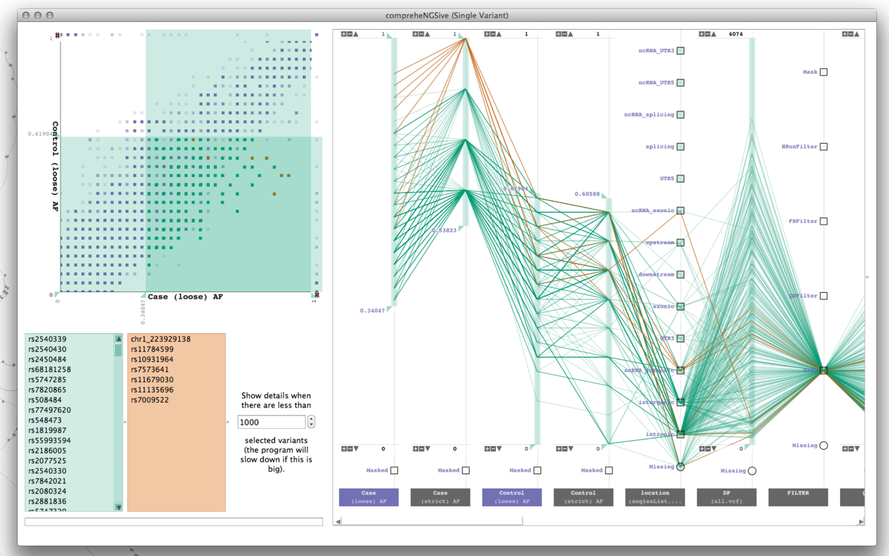
**#1** **Next-Generation Sequencing is a new technology that lets scientists access a person's entire genome. Short pieces of DNA are read, and specialized algorithms stitch them together. In terms of money, it's much cheaper than previous methods. In terms of complexity, it's much trickier to analyze.**

**#2** **Assuming we have quality data for everyone in a study, we have another problem: of the roughly 15 million variations from person to person (three are shown here), which ones could be causing or contributing to disease?**

EXPLORING THE BIOLOGICAL DATA

# EXPLOSION

ALEX BIGELOW, MIRIAH MEYER, NICOLA CAMP




**#3** **Genetic epidemiologists can also leverage family pedigrees to refine their search of the genome. Another ongoing project in collaboration with the Utah Population Database aims to make complicated pedigrees (like this one of 6770 people) easier to use in analysis.**

**#4** **compreheNGSive is a tool Alex Bigelow (SCI) and Nicola Camp (U of U Genetic Epidemiology) are developing using design study methodology to tackle the NGS issue. Statistics, annotations, and quality scores for each variant are visualized and filtered interactively.**