1158-92-135 **Johannes G. Reiter*** (johannes.reiter@stanford.edu). *A mathematical model of ctDNA shedding predicts tumor detection size.*

Early cancer detection aims to find tumors before they progress to an incurable stage. We developed a stochastic mathematical model of tumor evolution and circulating tumor DNA (ctDNA) shedding to investigate the potential of ctDNA-based cancer early detection tests. We inferred ctDNA shedding rates of early stage lung cancers and calculated that a 15 mL blood sample contains on average only 1.5 genome equivalents of ctDNA for lung tumors with 1 billion cells (size of ≈ 1 cm^3). We considered two clinically different scenarios: cancer screening and cancer relapse detection. For monthly relapse testing with a sequencing panel covering 20 tumor specific mutations, we found a median detection size of 0.24 cm^3 corresponding to a lead time of 160 days compared to imaging based relapse detection. For annual screening, we found a median detection size of $2.8 - 4.8$ cm^3 depending on the sequencing panel size and on the mutation frequency. The expected detection sizes correspond to lead times of $390 - 520$ days compared to current median lung tumor sizes at diagnosis. This quantitative framework provides a mechanistic interpretation of ctDNA based cancer detection approaches and helps to optimize cancer early detection strategies. (Received February 27, 2020)