Abstract: The recognition that significant genetic and phenotypic differences exist between cancerous and normal cells, and that every person’s cancer is unique, has led to the development of a vast array of cancer targeted drugs and imaging agents. However, genetic, molecular and physiological heterogeneity within cancers represent significant challenges to the success of many cancer targeted drugs/agents. More quantitative molecular imaging methods capable of accurately assessing the heterogeneity of molecular expression and targeted drug efficacy in vivo will be critical to overcoming these challenges, and could significantly enhance cancer detection, diagnosis, surgical guidance, and personalized/precision therapy. True quantification in molecular imaging is obfuscated by many factors, including: (1) imaging system factors (i.e., factors that affect how accurately the concentration of imaging agent is reproduced), and (2) imaging agent “kinetic” factors (i.e., factors that affect how well the imaging agent distribution describes the distribution of the targeted biological molecule). Over the last decade, our group has been spearheading efforts to overcome these factors using so-called “paired-agent” imaging methods that were first proposed in the 1950s but required imaging system advancements that were not widely available until around 2010. This presentation will provide an overview of the principles and complexity of paired-agent imaging, with a focus on some examples of clinical applications that are under development.

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