**Introduction**

Small tumours survive by drawing on oxygen and nutrients supplied from the nearest existing vasculature. Once a tumours size exceeds 1-2 mm3, it can no longer survive based on the diffusion limit of oxygen and nutrients. In order to continue growing, the tumour and starts an angiogenic process to build its own vasculature to sustain its supply of oxygen and nutrients. Tumour vasculature consists of vessels recruited from pre-existing networks as well as angiogenic vessels and differs significantly from healthy vasculature on both a micro (vessel properties) and a macroscale (network geometry).

There has been some work done into analyzing tumour vessels from a network perspective. Skinner *et al.* reported higher frequency of branching within tumour vasculature compared to healthy vasculature. [23] These findings were expanded by *Less et al.* who directly studies the branching patterns of tumour vasculature and found that two different types of branching patterns. The first was characterised by decreasing vessel diameter and length in successive generations of vessels. The second was characterised by fluctuations in both radius and length across higher degrees of branching. They reported the presence of loops in the vasculature and categorised them into “self loops”, which are loops between two points consisting of just two vessels and “true loops” which are loops consisting of multiple vessels. Pries *et al.* in2010suggested based on the above properties that this can give rise to a “shunt problem” in the tumour vasculature, whereby low resistance, short paths divert blood away from longer paths.

**Dataset**

From the Walker-Samuel Lab at UCL, we obtained two different networks for tumours for colorectal adenocarcinomas. The first network is that of an LS174T mouse model that is known to have lower vascular density and

Previous work on these models established that …

**Aims:**

For this project we have the following aims:

1. Explore structural difference between SW1222 and LS174T tumours through graphlet and motif analysis
2. Identify the presence, or lack thereof, of recurring roles and different communities / clusters of nodes in the different tumour types with the target of linking that back to the relevant oncological physiology
3. Compare

* Background
  + Introduce tumour microenviroment and the problem
* Motivation
  + What work has been done on this problem, why is it interesting and what questions are we asking
* Dataset:
  + Description of the two graphs that we already have
    - Number of nodes
    - Number of edges
    - What scalar values we poses on them?
* Challenges
  + Limited data
  + Noisy biological data
  + Rat model / not human
  + Lack of compute resources
  + The project is exploratory / no intial quanitive metrics for success
* Aims:
  + Identify key differences based on initial finding in the paper
  + Graphlet and motif analysis
  + Null model analysis
  + Community detection
  + Whatever the hell shenoi writes about