**Introduction**

* Clear cell renal cell carcinoma- most common form of kidney cancer, high tendency for metastasis
* Common solid tumour, currently renal cell carcinoma accounts for 2% of cancer diagnoses and deaths worldwide (<https://acsjournals.onlinelibrary.wiley.com/doi/full/10.3322/caac.21492>), 76% 5-year survival rate in US making it deadliest urological cancer (Epidemiology of Renal Cell Carcinoma)
* Valuable to determine expression factors correlated ith malignancy
* Has been recently elucidated in microarray study that neuronal pentraxin2 (NPTX2) is overexpressed in ccRCC cancer cells and contributes to migration and cancer viability, but should be possible for scientists to investigate other significant genes without repeating parts of the analysis themselves
* Additionally, valuable for non-bioinforamtics experts to still be able to browse gene expression datasets without downloading and analyzing themselves
* Such a browser has been created for colon cancer <https://www.colonomics.org/data-browser/expression-browser/>, and liver cancer <https://webs.iiitd.edu.in/raghava/cancerliver/> but none could be found for renal studies
* Objective – to create a web interface which allows users to query genes differentially expressed in renal cell carcinoma
* **Interface and methodology**
* Preprocessed renal Affymetrix expression dataset downloaded from <https://sbcb.inf.ufrgs.br/cumida>. Probe information such as gene symbol and name, GO terms, fold changes and t-test statistics will be determined in Bioconductor, then all information loaded into mySQL database.
* Schema:
* Sample: sample\_id, class
* Expression: sample\_id, probe\_id, value
* Gene: probe\_id, gene\_symbol, gene\_name, p\_value, fold\_change,
* Ontology: probe\_ID, GO\_term
* On main page, users will be able to search by gene name, gene symbol or GO term. Will have a small list of ~10 highly associated genes and p-values to give users ideas about what to search
* Once form element in html is filled (document is ready), Javascript will detect and send term to python cgi script through ajax. Script will query mysql database using mysql.connector module, then return results. Results will be displayed in table on search page.
* Result page: avg, std expression in control and affected, fold change, stacked histogram, violinplot or boxplot of control vs affected expression, t-test result p-value
* Also show gene’s GO terms
* Be able to click on GO terms to automatically search genes which share this term
* Always have the search bar at the top or a return to search page