

# PepperPathway: Visualizing Proteins of Influence in Cancer Pathways

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## Objectives

To produce an accessible program with the purpose of:

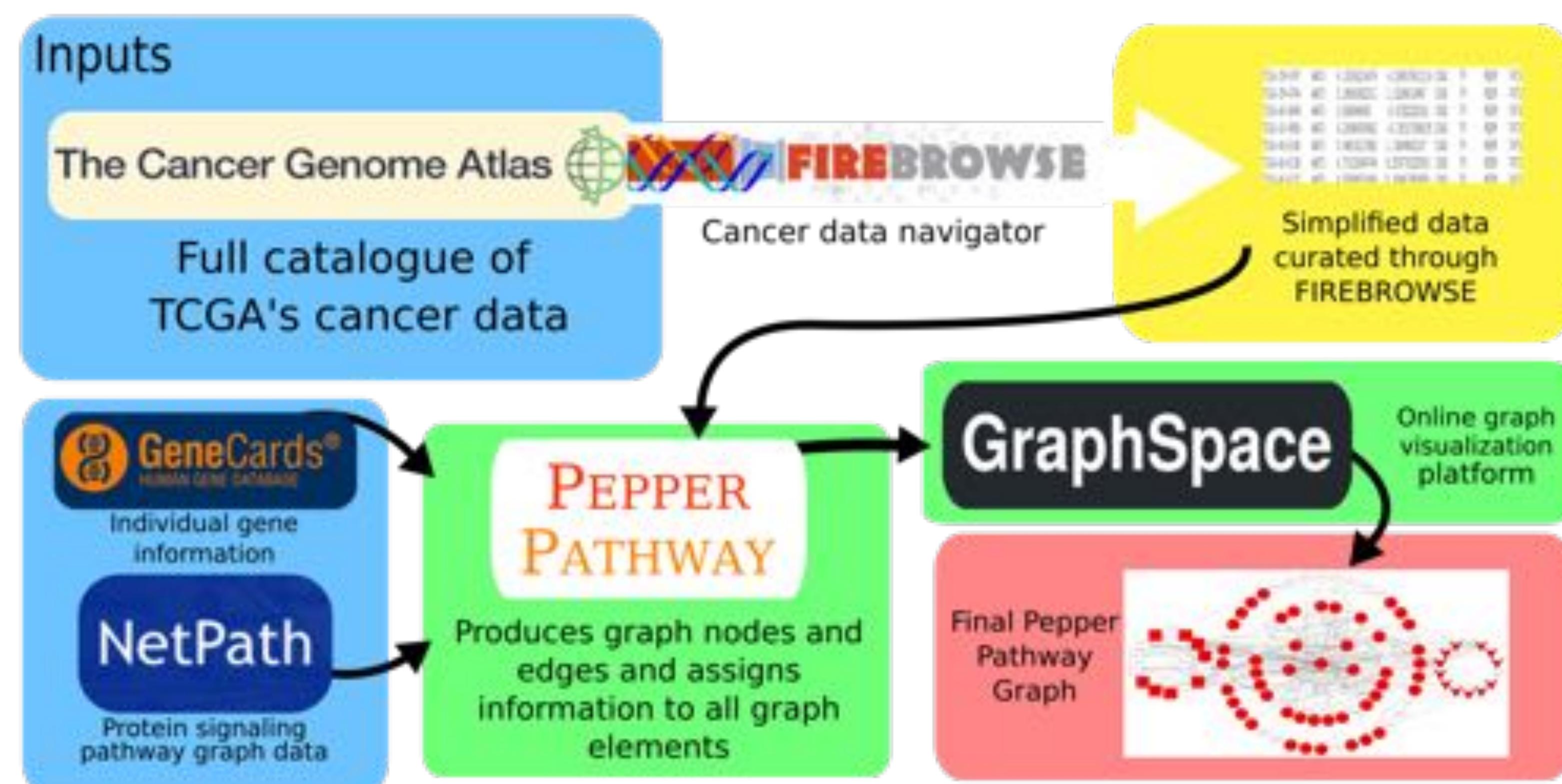
- Pulling quantitative data from The Cancer Genome Atlas for any number of desired proteins across multiple protein signaling pathways.
- Visualizing data and statistical analysis in a meaningful way with the GraphSpace graphical platform.

## Introduction

Clinical data relevant to cancer research has accumulated at an incredible rate, and a significant portion of that data has been collected in public databases such as The Cancer Genome Atlas (TCGA). Computational approaches permit us to analyze information of particular proteins in certain cancer contexts across vast swathes of clinical data. To aid researchers in providing multiple avenues to visualize cancer data, I present PepperPathway.

## Methods

Information from the TCGA [1] was pulled using the Broad Institute's Firehose project [2], and protein signaling pathway data comes from NetPath [3]. The desired information is processed through statistical analyses of the user's choice, and then visualized using the online platform GraphSpace [4] to produce a meaningful graph showcasing analyzed cancer data directly upon a protein signaling pathway.



## Contact Information

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## Example Result



An example visualization showing proteins from the Wnt pathway with data from patients with colon adenocarcinoma (COAD). For this case, per protein typically 41 healthy tissue samples are paired with 45 tumor tissue samples from the same patient are analyzed. Red nodes denote a significance ( $p < 0.01$ ) according to a t-test for mRNA expression between healthy tissues and COAD tissues.

## Example Interpretations

These example proteins from the network above showcase four possible ways to interpret information from PepperPathway. Information was gathered from GeneCards [5].

Protein (Prediction)	Description
APC (Known)	A negative regulator for beta-catenin (CTNNB1) and found to interact with E-cadherin, this protein affects cell adhesion. It is clearly implicated as an affected cancer protein for COAD, and classified as such by PepperPathway.
PRKACA (Likely)	A protein responsible for phosphorylating cAMP dependent proteins involved in differentiation, proliferation, and apoptosis. Abnormal expression has been found in tumor samples, but not implicated to be significant specifically for COAD. Classified as significant by PepperPathway, it may be worth investigating for COAD influence.
FZD4 (Novel)	A receptor for Wnt proteins, and coupled to the beta-catenin pathway. It has not been classified as a cancer protein before PepperPathway. May be influential in COAD development, but has not been previously investigated.
FZD9 (Known)	A receptor for Wnt proteins, and coupled to the beta-catenin pathway. It is not classified as a cancer protein, and PepperPathway.

## References

- [1] The Cancer Genome Atlas Network, *Nature* 2012 (TCGA).
- [2] Broad Institute TCGA Genome Data Analysis Center, downloaded Jan 2016 (Firehose).
- [3] Kandasamy et al., *Genome Biology*, 2010 (NetPath).
- [4] Bharadwaj et al., *Bioinformatics* 2017 (GraphSpace).
- [5] Lancet et al. *Trends in Genetics*, 1997 (GeneCards).

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