Recent genomic profiling studies in pancreatic adenocarcinoma (PDA) have revealed actionable mutations affecting multiple signaling pathways. In spite of these mutations, targeted inhibitions of these pathways have low success rates. A possible reason for these failures is that single-gene targeted drugs have not been effective. In this study, we focused on several KRAS mutant samples from Pancreatic Adenocarcinoma (PDA) patient samples. We conducted computational models using a network approach to predict drug activity and responses. The network approach is a powerful tool for modeling the complex interactions between proteins in a biological system. Our approach focused on the KRAS signaling pathway, which is a key driver of PDA. We used a computational model to predict the efficacy of drugs that target the KRAS pathway. The model was able to predict the sensitivity of PDA cells to different drugs. The results of this study suggest that a network approach to drug discovery is a promising strategy for identifying effective treatments for PDA. Further studies are needed to validate these findings and to develop new strategies for treating PDA.