Supplementary Materials of "Prompt-based Generation of Natural Language Explanations of Synthetic Lethality for Cancer Drug Discovery"

Ke Zhang^{1,2,3}, Yimiao Feng^{1,4}, Jie Zheng^{1,5,*}

 1 School of Information Science and Technology, Shanghai
Tech University, Shanghai, China

²Shanghai Institute of Microsystem and Information Technology, Chinese Academy of Sciences, Shanghai, China

³University of Chinese Academy of Sciences, Beijing, China

⁴Lingang Laboratory, Shanghai, China

⁵Shanghai Engineering Research Center of Intelligent Vision and Imaging, ShanghaiTech University, Shanghai, China

{zhangke1, fengym, zhengjie}@shanghaitech.edu.cn

1 An example of data augmentation prompt

You are a helpful assistant that rephrases text and makes sentences smooth. I will give you a sample, please rephrase the partial sentence after the word "because" of the sample, then give me 10 rephrased answers. Each answer should include the exact noun phrases which I will give you, and each answer must start with "because". The complete sample is: <u>TP53 and CDK2 have a synthetic lethality relationship</u>, because TP53 is a tumor suppressor that regulates cell cycle arrest, apoptosis and DNA repair, and CDK2 is a cyclin-dependent kinase that controls cell cycle progression and DNA replication. Therefore, inhibition of CDK2 in TP53-mutant cells results in synergistic cell death due to impaired DNA repair and increased DNA damage. The phrases are "DNA repair", "DNA damage", "cell cycle progression", "cell death".

2 Human annotation pipeline

Algorithm 1: Human annotation

```
1 Input: GenepairsCollection Q_{nb}, AnswerCollection M_{nb}, CitationCollection R_{nb}
 2 FactGenePairsCollection Q_{fact} \leftarrow \{\}
 3 FactAnswerCollection M_{fact} \leftarrow \{\}
 4 FactCitationCollection R_{fact} \leftarrow \{\}
 5 FeatureCollection F_{fact} \leftarrow \{\}
 6 HypotheticalAnswerCollection M_{hypo} \leftarrow \{\}
    for i \leftarrow 1 to len(M_{nb}) do
 7
         gene pair (u, v) = Q_{nb}[j]
 8
 9
         answer \leftarrow M_{nb}[i]
         citations \leftarrow R_{nb}[i]
10
         if AnnotatorReadandCheck(answer, citations) then
11
              features \leftarrow FeatureAnnotation(answer)
12
              Q_{fact} \leftarrow (u, v)
13
              M_{fact} \leftarrow answer
14
              R_{fact} \leftarrow citations
15
             F_{fact} \leftarrow features
16
\mathbf{17}
         else
18
              add answers to M_{hypo}
         end
19
         pairs_{new} \leftarrow AnnotatorMiningNewpairs(citations)
20
         \mathbf{if} \ \mathrm{pairs}_{\mathrm{new}} \neq \ \varnothing \ \mathbf{then}
21
              answers_{new} \leftarrow AnnotatorSummarization(citations)
22
              features \leftarrow FeatureAnnotation(answers)
23
\mathbf{24}
              Q_{fact} \leftarrow pairs_{new}
              M_{fact} answers_{new}
\mathbf{25}
              R_{fact} \leftarrow citations
26
              F_{fact} \leftarrow features
27
         end
\mathbf{28}
29 end
```

3 From a KG subgraph to a personalized KG prompt

According to the KG subgraph in Fig. 1, since RAD52 shares two functions with BRAC2's SL partner genes, we assume that RAD52 and BRAC2 also share the functions. Therefore, the KG prompt for BRAC2 and RAD52 is: <u>BRAC2</u> and <u>RAD52</u> may share common functions, including <u>DNA Damage</u> Response, DNA repair.



Figure 1: A KG subgraph for an SL gene pair (BRCA2, RAD52). Light blue nodes are the two target genes, grey nodes represent other genes that have SL relationships with BRAC2, and dark blue nodes are two gene functions.