## AlloDriver V3

## 服务器

• IP: 175.185.16.17

• 用户名: hipeson

• 密码: hipeson@123

## 数据

- 简介: 共有17130条突变数据,已平衡。其中8565为driver (阳性数据),另8565为passenger (阴性突变)。/home/hipeson/driverteam/Data/all\_balance\_17130.csv (数据在服务器上的位置)。
- all\_balance\_17130.csv每行数据格式如图:
  - 每一行相继记录了一条driver数据(;前)和一条passenger数据(;后),以;隔开
  - 每一条数据依次记录 PDB id, Chain id, PDB residue index, PDB residue (three letter), Uniprot id, Uniprot residue index, Uniprot residue (one letter), Mutation (driver or passenger),以,隔开
  - 所以6cms,A,73,THR,Q06124,73,T,T73I指 蛋白Q06124的三维结构 PDB id 6cms在A链的73号位残基Thr可突变为Ile (I),此突变为 driver。
  - 相应的蛋白三维结构已经提前下载 至/home/hipeson/driverteam/Data/PDBs。推荐使用biopython进行 处理,或对缺失数据重新下载
  - 具体数据划分可参考

https://academic.oup.com/nar/article/51/W1/W129/7132339 进行随

机8:1:1划分

6cms, A, 73, THR, Q06124, 73, T, T73I; 6cms, A, 491, PRO, Q06124, 491, P, P491F 5mcv,B,273,ARG,P04637,273,R,R273L;5mcv,A,229,CYS,P04637,229,C,C229F 2pkl,A,877,THR,P10275,878,T,T878A;2pkl,A,801,PRO,P10275,802,P,P802L 421p, A, 58, THR, P01112, 58, T, T58I; 421p, A, 33, ASP, P01112, 33, D, D33Y 2j1y,C,126,TYR,P04637,126,Y,Y126N;2j1y,B,248,ARG,P04637,248,R,R248H 1ycs, A, 179, HIS, P04637, 179, H, H179D; 1ycs, A, 160, MET, P04637, 160, M, M160T 7dhz, A, 273, ARG, P04637, 273, R, R273C; 7dhz, A, 174, ARG, P04637, 174, R, R174H 4nmm, A, 12, CYS, P01116, 12, G, G12A; 4nmm, A, 147, LYS, P01116, 147, K, K147T 5ecg, A, 179, HIS, P04637, 179, H, H179P; 5ecg, B, 133, MET, P04637, 133, M, M133V 4ark, A, 115, LEU, Q02750, 115, L, L115P; 4ark, A, 189, ARG, Q02750, 189, R, R189K 3rs2,A,13,GLY,P01112,13,G,G13D;3rs2,A,64,TYR,P01112,64,Y,Y64H 2bim, B, 197, VAL, P04637, 197, V, V197M; 2bim, B, 97, VAL, P04637, 97, V, V97D 5yu9, A, 724, GLY, P00533, 724, G, G724S; 5yu9, A, 790, MET, P00533, 790, T, T790A 4ifj,A,415,ARG,Q14145,415,R,R415H;4ifj,A,334,TYR,Q14145,334,Y,Y334H 1xkk,A,858,LEU,P00533,858,L,L858R;1xkk,A,800,ASP,P00533,800,D,D800N 3ii5,A,593,ASP,P15056,594,D,D594A;3ii5,A,462,ILE,P15056,463,I,I463S

## 模型

- 目标: 使用surface革新driver prediction蛋白表征
- 参考

https://github.com/gcorso/DiffDock/blob/dev/models/all\_atom\_score\_model.py 中build\_cross\_conv\_graph中 ATOM to RECEPTOR交互 建图进行RECEPTOR to SURFACE交互建图

• 也可完全参考

https://academic.oup.com/bioinformatics/article/40/7/btae413/7 697100 , 与我们目的一致,只是任务不同