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| **Class : generate\_ppt\_content.py**  **[Module to generate all slides content]** |
| Methods:  \_init\_(db\_path)  .het\_homo(vec)  .generate\_info\_dict(info)  .get\_dict\_valur(key)  .clean\_pheno(pheno)  .clean\_exac\_val(exac)  .generate\_key\_dictionary()  .generate\_content(df\_rec)  .clean\_phenotypes(pheno\_list)  .subject\_slide\_content(var\_df) |
| Called program:  screen\_shots.py  get\_web\_content.py  Database.py |

**Class diagram**

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| **Class: Database.py**  **[Module to save web scraped content to a sqlite Database]** |
| Methods:  \_init\_(database)  .create\_table(table\_name,table\_cols)  .insert\_records(record)  .get\_records(gene)  .get\_gene\_list()  .close\_db\_connection()  .db\_commit()  .db\_refresh()  .db\_update(gene,new\_rec) |
| Called program:  None |

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| Class : **screen\_shots.py** |
| Methods:  \_init\_(gene,home path)  .gene\_summary\_gen()  .gene\_exac\_gen() |
| Called program:  None |

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| Class : **Database\_refresh.py**  **[Module to refresh DB periodically]** |
| Methods:  \_init\_(dbpath)  .search\_web(gene) |
| Called program:  Database.py  get\_web\_content.py |

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| Class : **annotate\_variants.py**  **[Module to annotate variants]** |
| Methods:  \_init\_(ip\_var\_file, op\_vcf\_name, op\_path) |
| Called program:  NA |

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| **Class : process\_annotated\_vcf.py**  **[Module to process annotated vcf]** |
| Methods:  \_init\_(zip filename)  .process() { returns processed data frame} |
| Called program:  NA |

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| **Class : fill\_ppt\_with\_content.py**  **[Module to fill ppt with content]** |
| Methods:  \_init\_(content\_dict)  .subject\_slide(subslide,data\_frame)  .slideone(slide1)  .process\_disease(Disease)  .slidetwo(slide2)  .pheno\_print(pheno) |
| Called program:  NA |

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| Class : **run\_tool.py**  **[Module to run tool]** |
| Methods:  main(ip\_vcf,rep\_name,op\_rep,db\_path) |
| Called program:  process\_annotated\_vcf.py  generate\_ppt\_content.py  fill\_ppt\_with\_content.py |

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| **Class : get\_web\_content.py**  **[Module to scrape web content]** |
| Methods:  \_init\_(exac\_url, ncbi\_url,  uniport\_url)  .exac\_tab\_vals()  .entrez\_gene\_summary()  .uniprot\_gene\_summary() |
| Called program:  NA |