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| --- | --- | --- | --- |
| Description | Script | Input | output |
| Benchmark dataset generation | get.standard.answer.class1.py | 1.hla-genotyper.o.standard.class1  2.HLA-HD.o.standard.class1  3.HLA-VBSeq.o.standard.class1  4.OptiType.o.standard.class1  5.POLYSOLVER.o.standard.class1 6.SOAP-HLA.o.standard.class1  7.xHLA.o.standard.class1  8.Kourami.o.standard.class1 | result.t |
| Population and allelic frequency statistics | get\_top\_frequence.py; top20\_Population\_fre\_histogram.py | class1.result.json | data.txt; fig\_Accuracy\_histogram.pdf |
| Calculate the recall and accuracy of each tools | get\_accuracy.py | 1.hla-genotyper.o.standard.class1  2.HLA-HD.o.standard.class1  3.HLA-VBSeq.o.standard.class1  4.OptiType.o.standard.class1  5.POLYSOLVER.o.standard.class1  6.SOAP-HLA.o.standard.class1  7.xHLA.o.standard.class1  8.Kourami.o.standard.class1 | class1.accuracy.txt |
| Calculated the error rate of each tools on HLA class I | python get.WF.py | 1.hla-genotyper.o.standard.class1  2.HLA-HD.o.standard.class1  3.HLA-VBSeq.o.standard.class1  4.OptiType.o.standard.class1  5.POLYSOLVER.o.standard.class1  6.SOAP-HLA.o.standard.class1  7.xHLA.o.standard.class1  8.Kourami.o.standard.class1 | class1.right\_error.xls |
| Format the errors of each tools into matrix | get\_summary\_error\_rate\_of\_eight\_tools.py | 1.hla-genotyper.o.standard.class1.right\_error.xls  2.HLA-HD.o.standard.class1.right\_error.xls  3.HLA-VBSeq.o.standard.class1.right\_error.xls 4.OptiType.o.standard.class1.right\_error.xls 5.POLYSOLVER.o.standard.class1.right\_error.xls 6.SOAP-HLA.o.standard.class1.right\_error.xls 7.xHLA.o.standard.class1.right\_error.xls 8.Kourami.o.standard.class1.right\_error.xls | summary\_class1\_error\_rate\_of\_eight\_tools.xlsx |
| Get the ensemble results from top 3 tools | get\_simulation\_result\_by\_three\_software.py | 5.polysolver.o.standard.class1`  4.OptiType.o.standard.class1`  7.xHLA.o.standard.class1` | class1\_simulation\_result.txt |