

Internship

Automated HIV-1 Genotyping

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Outline

Outline

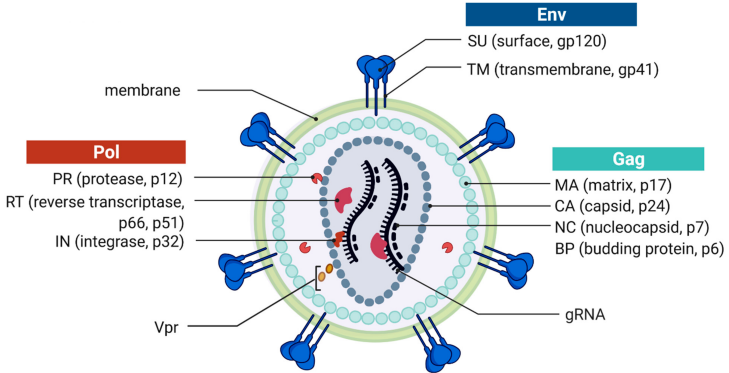
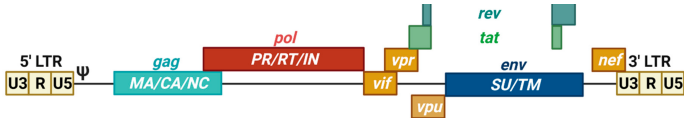
Introduction

Analysis

Conclusions

Introduction

INTRO: HIV-1 [1]



Subtyping is performed by using a combination of the following tools.

Online Subtyping Tools

- STANFORD (sierrapy)
<https://hivdb.stanford.edu/hivdb/by-sequences/>
- COMET (https requests)
<https://comet.lih.lu/>
- REGA (manual)
<https://www.genomedetective.com/app/typingtool/hiv>

HIV-1 Groups

Human immunodeficiency virus (HIV) displays an extraordinary genetic diversity with four distinct groups:

- M (major)
- O (outlier)
- N (non M/O)
- P (putative)

HIV-1 Subtypes

Within the major M Group are 9 different subtypes, at least 98 circulating recombinant forms (CRFs), and multiple unique recombinant forms (URF).

- A (A1, A2, A3, A4, A5, A6)
- B
- C
- D
- F (F1, F2)
- G
- H
- J
- K

<http://www.hiv.lanl.gov/content/sequence/HIV/CRFs/CRFs.html>

Analysis

SUBTYPING (Toolwise)

ID	PR, RT
1	A
2	B
...	...
n	F

ID	IN
1	A
2	B
...	...
n	F

ID	ENV
1	A
2	B
...	...
n	F

SUBTYPING (Fragmentwise)

ID	REGA	STANFORD	COMET
1	B	B	B
2	G	CRF02_AG	G (check for 02_AG)
...
n	CRF11_cpx	A + J	CRF11_cpx

Customer's preferences

```
$ nextflow ../Scripts/subtyping_pipeline.nf --outdir ../Results --run MS95
N E X T F L O W ~ version 22.04.4
Launching `../Scripts/subtyping_pipeline.nf` [furious_hodgkin] DSL2 - revision: 333a2ff10d
executor > local (23)
[cf/8c3339] process > mark_fasta (3) [100%] 3 of 3 ✓
[81/ccdddc] process > stanford (1) [100%] 3 of 3 ✓
[28/907f6f] process > json_to_csv (3) [100%] 3 of 3 ✓
[84/234416] process > rega_to_csv (1) [100%] 3 of 3 ✓
[6c/14640d] process > comet (2) [100%] 3 of 3 ✓
[14/7da948] process > prrt_joint (1) [100%] 1 of 1 ✓
[cf/83225a] process > env_joint (1) [100%] 1 of 1 ✓
[2f/847e9f] process > int_joint (1) [100%] 1 of 1 ✓
[15/761046] process > tags_to_csv (3) [100%] 3 of 3 ✓
[66/8de6bb] process > decision_to_csv (1) [100%] 1 of 1 ✓
[b5/161910] process > full_joint [100%] 1 of 1 ✓
[- ] process > report -
[- ] process > phylo_fasta -
```

- Inability to specify product but product type.

- Number of reviews is of great benefit to sales volume

TOOLS



- sierrapy, miller, mafft, iqtree



- DSL2



- sys, re, collections, requests
pandas, time, wrap, json, bio




- GitHub



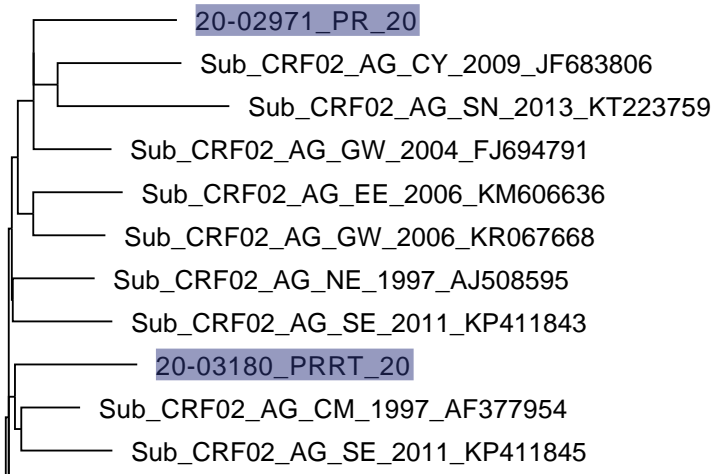
 <https://github.com/vera-rykalina/rki>

Acquisition

- Complementary profile of both companies (Electronidex is more focused on high end products and Blackwell on lower end).
- Blackwell could expand its customer database (9800 new clients)
- Low frequent products of Electronidex could be easily sold by Blackwell
- Due to financial difficulties Electronidex is a bargain
- Inability to directly collate Electronidex's and Blackwell's (5 product match only)



```
├─ AllSeqsC020
│   ├── MS95_Seqs_ENV_C020_V5.xlsx
│   ├── MS95_Seqs_INT_C020_V5.xlsx
│   └── MS95_Seqs_PRRT_C020_V5.xlsx
├─ InputFasta
│   ├── MS95_ENV_20.fasta
│   ├── MS95_INT_20.fasta
│   └── MS95_PRRT_20.fasta
├─ ManualREGA
│   ├── manual_rega_MS95_ENV_20M.csv
│   ├── manual_rega_MS95_INT_20M.csv
│   └── manual_rega_MS95_PRRT_20M.csv
└─ Scripts
    ├── comet_rest.py
    ├── decision.py
    ├── fasta_to_phylo.py
    ├── full_join.py
    ├── nexflow.config
    ├── rega_parser.py
    ├── repeat_marking.py
    ├── report.py
    ├── stanford_parser.py
    ├── subtyping_pipeline.nf
    └── tag_parser.py
```



Conclusions

Conclusions

- Need to increase amount of data
- Data quality investment (Demographic & Historical)
- New marketing strategies based on clients preferences
- Campaigns to induce customers to write reviews
- Development of Recommender System
- More transaction data to make a decision concerning acquisition

Thank you!

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Questions?

References



Yasemin van Heuvel et al. "Infectious RNA: Human Immunodeficiency Virus (HIV) Biology, Therapeutic Intervention, and the Quest for a Vaccine". In: *Toxins* 14.2 (2022). ISSN: 2072-6651. DOI: 10.3390/toxins14020138. URL: <https://www.mdpi.com/2072-6651/14/2/138>.