

From DNA to
actionable result.
Right now



HYRAX
BIOSCIENCES



Exatype: automated SARS-CoV-2 variant typing directly from NGS sequence data

The identification of SARS-CoV-2 variants that exhibit increased transmissibility and may impact vaccine efficacy has accelerated the need for global genomic surveillance of SARS-CoV-2.

While DNA sequencing provides the most comprehensive approach for characterising variants, the analysis and interpretation of sequence data at scale remains a challenge.

Hyrax Biosciences' Exatype platform provides fast, automated SARS-CoV-2 lineage/clade typing.

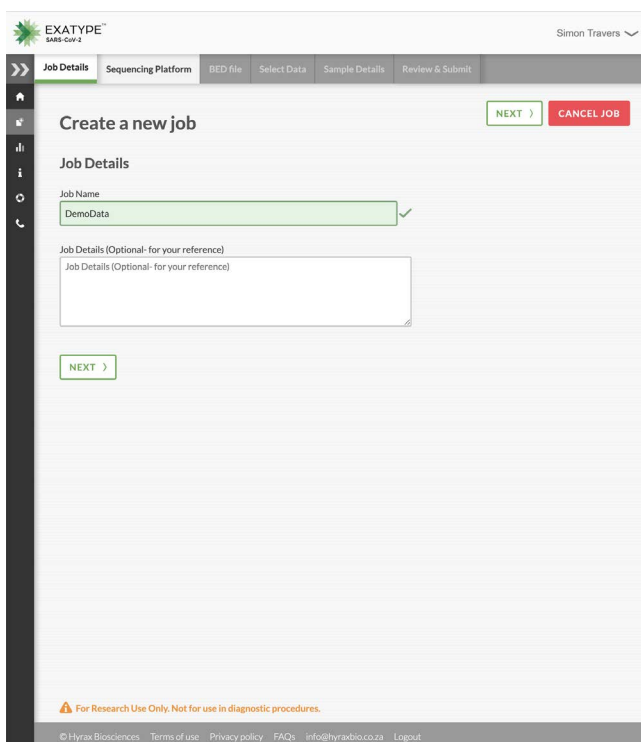
Exatype features:

- Reports detected variants using both Pangolin lineages and Nextstrain clades nomenclature
- Analyses data from a range of sequencing platforms and can process data generated from any amplification protocol/assay
- Requires no expert training and no software needs to be installed
- Easily scaled with **parallel** processing in the cloud or through direct **integration** with sequencers and/or LIMS
- Is secure and complies with all necessary HIPAA requirements
- Uses algorithms with proven superior accuracy in read mapping and variant calling in viral data



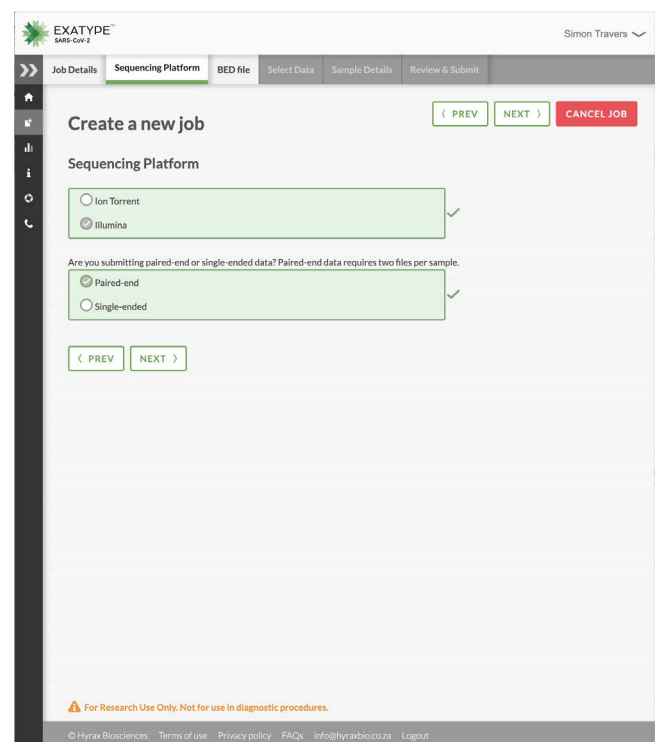
Once you've set up an account, analysing your data is simple:

1. Name your job:



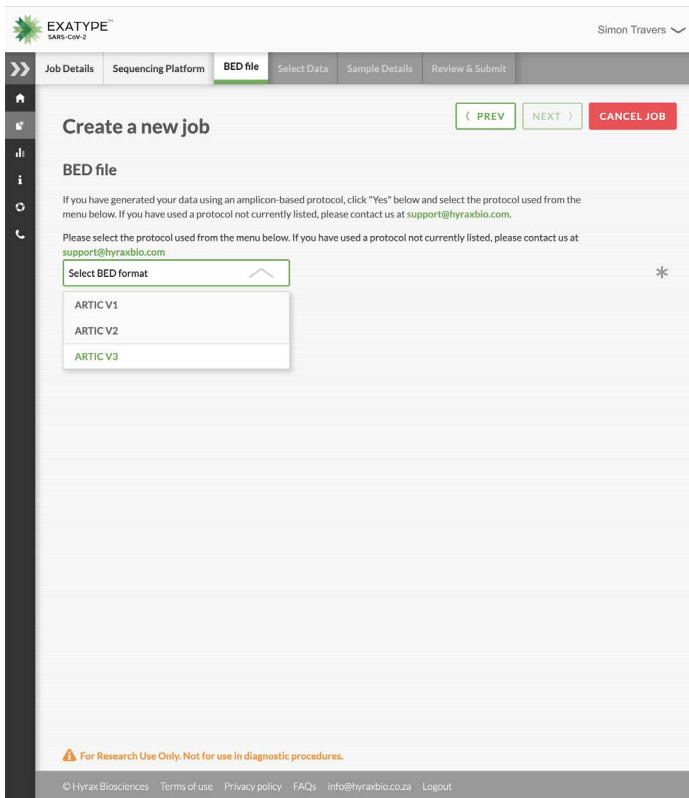
The screenshot shows the 'Create a new job' form in the 'Job Details' step. The 'Job Name' field contains 'DemoData' and has a green checkmark. Below it is a text area for 'Job Details (Optional- for your reference)'. A 'NEXT >' button is at the bottom right of the form. The top navigation bar includes 'Job Details', 'Sequencing Platform', 'BED file', 'Select Data', 'Sample Details', and 'Review & Submit'. The user's name 'Simon Travers' is in the top right corner.

2. Select the sequencing platform:

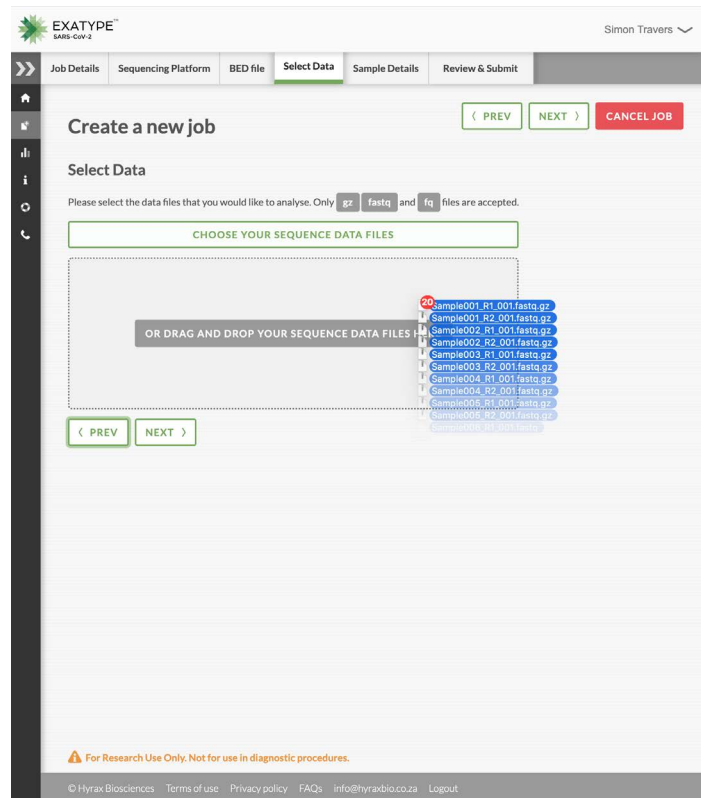


The screenshot shows the 'Create a new job' form in the 'Sequencing Platform' step. The 'Sequencing Platform' field has 'Illumina' selected with a radio button and a green checkmark. Below it, the question 'Are you submitting paired-end or single-ended data?' has 'Paired-end' selected with a radio button and a green checkmark. A 'PREV <' button is on the left and a 'NEXT >' button is on the right. The top navigation bar is the same as in the previous step.

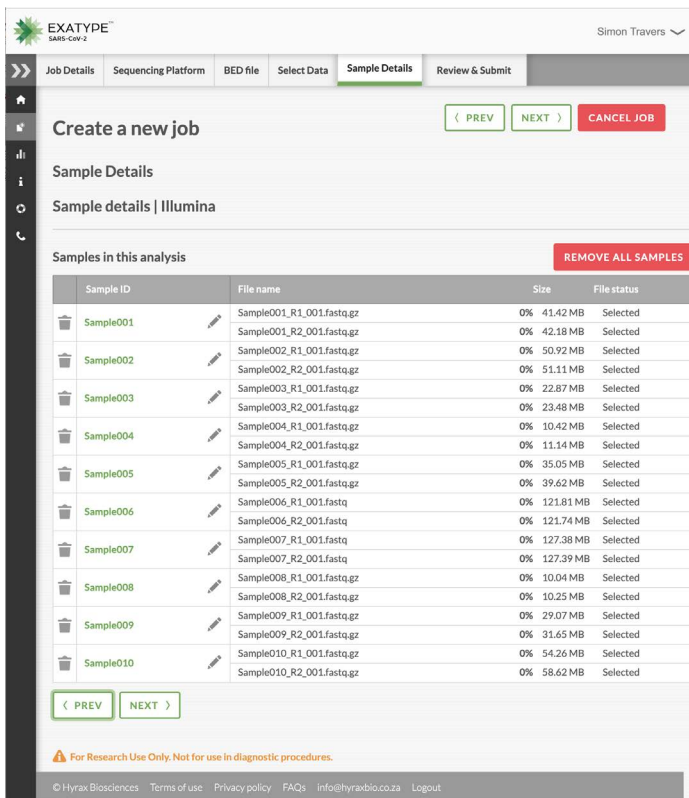
3. Select the assay used to generate the data:



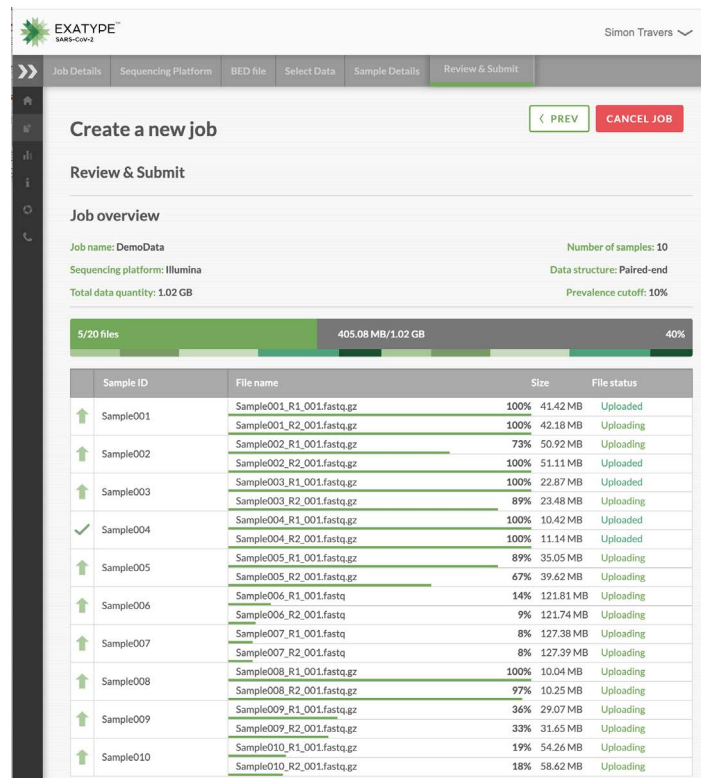
4. Drag and drop your fastq files into the browser:



5. Exatype automatically groups files for paired-end data and extracts sample names (you can edit these manually if you wish):



6. That's it! Click upload and walk away. You will receive an email once your analysis is complete:



Outputs

1. Explore per-sample results through the front-end:

SAMPLE NAME 🔍

RESULTS

Completed samples

Sample001

Sample002

Sample003

Sample004

Sample005

Sample006

Sample007

Sample008

Sample009

Sample010

Sample011

Sample012

Sample013

Sample014

Sample name: Sample010 Sample ID: 064bd93d-31eb-4134-b10b-226d855d6735

Sequencing platform: Illumina Sample status: Completed

Sample coverage plot

Read coverage of SARS-CoV-2 for sample Sample010

Lineage/Clade Typing

| Pangolin (2.1.10) ¹ | Nextstrain clade (0.12.0) ² | Nextstrain AA substitutions (0.12.0) ² | Nextstrain AA deletions (0.12.0) ² |
|--------------------------------|--|--|---|
| B.1.351 | ✓ 20H/501Y.V2 | ORF1a: T265I, K1655N, H2799Y, S2900L, K3353R, M3655I ORF1b: P314L S: D80A, L242H, R246I, K417N, E484K, N501Y, D614G, A701V ORF3a: Q57H, S171L E: P71L ORF6: D30N N: T205I | S: A243-, L244-, H245- |

[📄 DOWNLOAD AS CSV](#)

¹<https://github.com/cov-lineages/pangolin>
²<https://clades.nextstrain.org/>

File downloads

2. Exatype uses both Pangolin lineages (cov-lineages.org) and Nextstrain clades (nextstrain.org) and outputs a table showing calls from each approach. It includes amino acid substitutions and deletions observed in each sample.

| Sample | Pangolin (2.1.10) ¹ | Nextstrain clade (0.12.0) ² | Nextstrain AA substitutions (0.12.0) ² | Nextstrain AA deletions (0.12.0) ² |
|-----------|--------------------------------|--|--|--|
| Sample003 | B.1.338 | ✓ 20C | ORF1a: T265I, A2129V ORF1b: P314L S: D614G ORF3a: Q57H | None detected |
| Sample005 | B.1 | ⚠️ 20C | ORF1a: T265I, I1206K ORF1b: P314L, S2430R S: D614G ORF3a: Q57H | ORF1a: P1207-, K1208-, E1209-, E1210-, V1211-, K1212- |
| Sample011 | P.1 | ✓ 20J/501Y.V3 | ORF1a: S1188L, K1795Q, S2947N, A3523V ORF1b: P314L, E1264D S: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, D614G, H655Y, T1027I, V1176F ORF3a: S253P F8: E92K | ORF1a: S3675-, G3676-, F3677- |

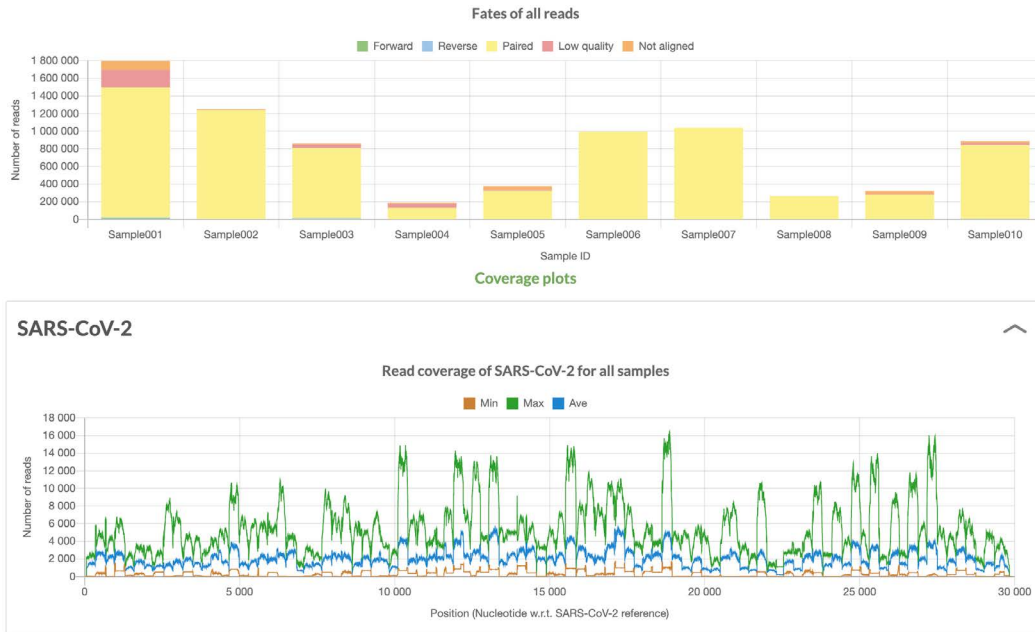
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²<https://clades.nextstrain.org/>

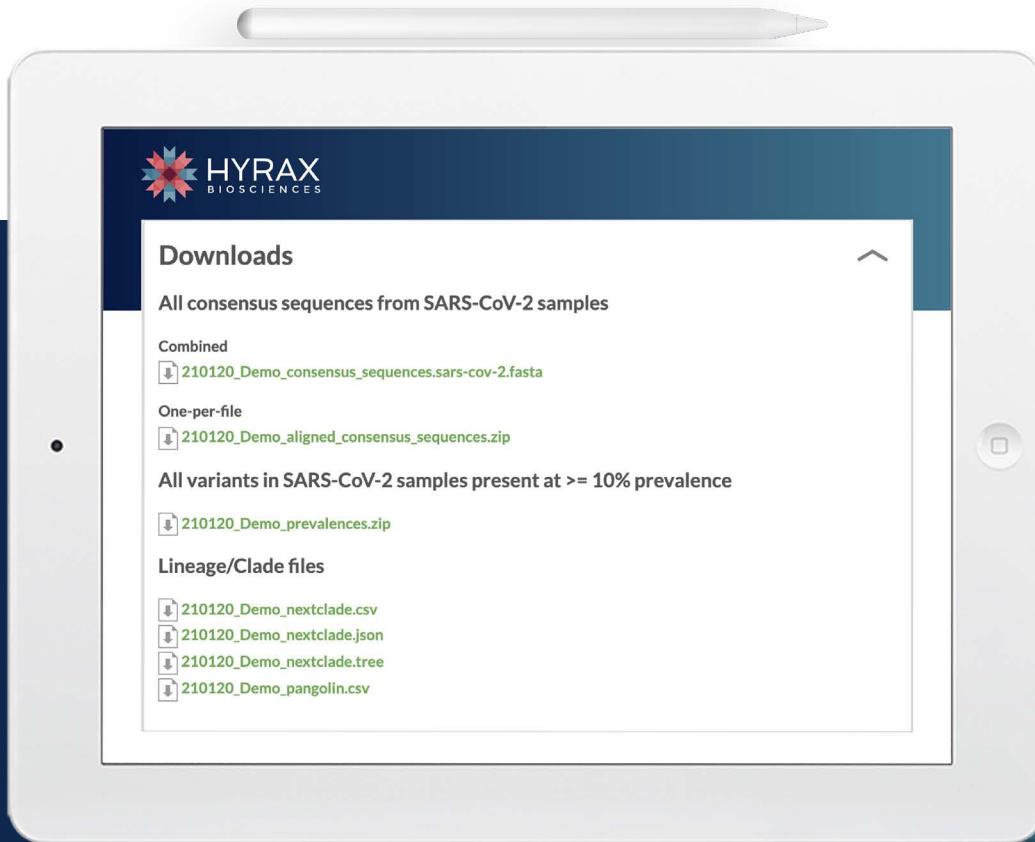
Sample011

- ✓ Missing data: Good
- ✓ Mixed sites: Good
- ✓ Private mutations: Good
- ✓ SNP clusters: Good

3. QC plots provide a valuable oversight of data quality:



4. A wide range of outputs in standardised formatting are available for download for further analysis or for publication of outputs to public repositories e.g. consensus sequences can be uploaded to GISAID:



How to get in touch

Visit sars-cov-2.exatype.com to sign up for a free account and upload your first sample.

Contact us at info@hyraxbio.com to discuss how we can provide companion software for your needs.