# BioLaboro: A bioinformatics system for detecting molecular assay signature erosion and designing new assays in response to emerging and reemerging pathogens

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## Abstract

**Background:** Emerging and reemerging infectious diseases such as the novel Coronavirus disease, COVID-19 and Ebola pose a significant threat to global society and test the public health community's preparedness to rapidly respond to an outbreak with effective diagnostics and therapeutics. Recent advances in next generation sequencing technologies enable rapid generation of pathogen genome sequence data, within 24 hours of obtaining a sample in some instances. With these data, one can quickly evaluate the effectiveness of existing diagnostics and therapeutics using *in silico* approaches. The propensity of some viruses to rapidly accumulate mutations can lead to the failure of molecular detection assays creating the need for redesigned or newly designed assays.

**Results:** Here we describe a bioinformatics system named BioLaboro to identify signature regions in a given pathogen genome, design PCR assays targeting those regions, and then test the PCR assays *in silico* to determine their sensitivity and specificity. We demonstrate BioLaboro with two use cases: Bombali Ebolavirus (BOMV) and the novel Coronavirus 2019 (SARS-CoV-2). For the BOMV, we analyzed 30 currently available real-time reverse transcription-PCR assays against the three available complete genome sequences of BOMV. Only two met our *in silico* criteria for successful detection and neither had perfect matches to the primer/probe sequences. We designed five new primer sets against BOMV signatures and all had true positive hits to the three BOMV genomes and no false positive hits to any other sequence. Four assays are closely clustered in the nucleoprotein gene and one is located in the glycoprotein gene. Similarly, for the SARS-CoV-2, we designed five highly specific primer sets that hit all 145 whole genomes (available as of February 28, 2020) and none of the near neighbors.

**Conclusions:** Here we applied BioLaboro in two real-world use cases to demonstrate its capability; 1) to identify signature regions, 2) to assess the efficacy of existing PCR assays to detect pathogens as they evolve over time, and 3) to design new assays with perfect *in silico* detection accuracy, all within hours, for further development and deployment. BioLaboro is designed with a user-friendly graphical user interface for biologists with limited bioinformatics experience.

## Background

Emerging and reemerging infectious diseases have serious adverse impacts on society with respect to lives lost and annual economic losses [1-5], as being witnessed currently in the COVID-19 outbreak caused by a novel Coronavirus, SARS-CoV-2. As of March 9, 2020, there have been 113,584 confirmed cases of COVID-19 around the globe and 3,996 deaths [6-8]. Factors such as climate change, urbanization, zoonotic spillover, international travel, lack or breakdown of public health care systems, natural or man-made disasters, and pathogen evolution to name a few, contribute to infectious disease emergence and sustainment [2].

A unique challenge associated with emerging infectious diseases is rapidly identifying the etiological agent and developing or repurposing existing medical countermeasures (MCMs), including diagnostic assays, to curtail the spread of an outbreak. With respect to reemerging infectious diseases the challenge is to determine whether existing MCMs are effective or not, and in the latter case, develop or modify the MCMs in a timely manner. In some cases, the failure of existing MCMs can be accounted for by genetic drift and shift and the resulting altered genotypic and phenotypic profiles of the newly emergent pathogen. Ebolavirus is one such reemerging infectious disease agent that exhibits high degrees of genetic changes in every new outbreak.

Ebola virus disease (EVD) is one of the deadliest infectious diseases that continues to plague Central and Western Africa. It was discovered in 1976 when two consecutive outbreaks of fatal hemorrhagic fever occurred in different parts of Central Africa [9]. The first outbreak occurred in the Democratic Republic of the Congo (DRC, formerly Zaire) in a village near the Ebola River, which gave the virus its name [9]. Since 1976 more than 25 outbreaks have been recorded. The average case fatality ratio (CFR) for EVD is around 50% and varies from 25% to 90% in past outbreaks [9]. From 2014 to 2016, the world witnessed the worst-yet EVD outbreak, which originated in Western Africa. That outbreak started in a rural setting of southeastern Guinea, and quickly spread like a wildfire to urban areas and across borders to the neighboring countries of Liberia and Sierra Leone [10]. In the end, the outbreak infected 28,616 people and killed 11,310 of the victims (CFR of approximately 39.5%) [11]. In the current Democratic Republic of the Congo outbreak that began in August 2018, as of March 4, 2020, a total of 3,444 cases, total deaths 2,264 and 1,169 survivors have been reported [12].

Until recently, there was no approved vaccine or treatment for EVD although four experimental therapeutics, , (Regeneron's monoclonal antibody REGN-EB3, mAb-114 [Ridgeback Biotherapeutics], Remdesivir GS-5734 [Gilead] and ZMapp [MappBio Pharmaceutical] underwent clinical trials (the Pamoja Tulinde Maisha [PALM] study) during the current DRC outbreak [13]. On October 17, 2019, the Committee for Medicinal Products for Human Use granted a "conditional marketing authorization" for the Ebola Zaire vaccine ERVEBO by Merck Sharp and Dohme [14]. ERVEBO was reviewed under the European Medicines Agency's (EMA) accelerated assessment program. ERVEBO (v290) (Ebola Zaire Vaccine (rVSVΔG-ZEBOV-GP, live) is a genetically engineered, replication competent,

attenuated live vaccine that received approval from the U. S. Food and Drug Administration (FDA) on December 19, 2019 [15].

Ebolaviruses are one of three genera of filoviruses belonging to the Family *Filoviridae,* Cuevavirus and Marburgvirus being the other two. Filoviruses are non-segmented, negative-sense, single-stranded RNA viruses. Six species of Ebolaviruses have been described to date, Zaire (EBOV), Bundibugyo (BDBV), Sudan (SUDV), Taï Forest (TAFV), Reston (RESTV) and Bombali (BOMV). The prototypic viruses - EBOV, BDBV, SUDV and TAFV - have been associated with disease in humans [16, 17]. The RESTV causes disease in nonhuman primates and pigs [18, 19]. In a 2018 wildlife survey, BOMV RNA was recovered from insectivorous bats, but there are no known cases of human or animal disease caused by this species [20].

Research on EVD focuses on finding the virus' natural reservoirs and hosts from which spill over occurs, developing preventive measures such as vaccines to protect at-risk populations, and discovering therapies to improve treatment of infections. Biosurveillance data suggested that the reservoirs of ebolaviruses may be fruit and insect eating bats [21-24]. The new BOMV was identified in a biosurveillance project conducted in Sierra Leone to identify hosts of EBOV as well as any additional filoviruses that might be circulating in wildlife [20]. Oral and rectal swabs were collected from 535 animals (244 bats, 46 rodents, 240 dogs, 5 cats) from 20 locations in Sierra Leone in 2016. Of the 1,278 samples, five samples from three Little free-tailed bats and one Angolan free-tailed bat contained ebolavirus sequences. Two full genome sequences were assembled from two of the samples and they showed nucleotide identity of 55–59% and amino acid identity of 64–72% to other ebolaviruses [20]. Based on phylogenetic analyses of sequence data, it was determined that the genome was sufficiently distinct to represent the prototypic strain of a new species, Bombali Ebolavirus (BOMV) [20].

111 I*n vitro* studies of the BOMV demonstrated that a recombinant vesicular stomatitis virus
112 (rVSV) encoding the BOMV glycoprotein (GP) gene mediated virus entry into human host cells
113 [20]. Entry and infection of rVSV–BOMV GP was also completely dependent on Niemann-Pick
114 C1 (NPC1) protein, providing additional evidence that this is a universal receptor for filoviruses.
115 Although not conclusive, these data indicated the potential for BOMV to infect humans. Given
116 the high divergence from other Ebolaviruses, we examined whether existing real-time reverse-
117 transcription PCR (rRT-PCR) assays for Ebolaviruses would detect the new BOMV.

118 Potential determinants of Ebolavirus pathogenicity in humans were identified by
119 analyzing the differentially conserved amino acid positions called specificity determining
120 positions (SDPs) between human pathogenic ebolaviruses and the non-pathogenic Reston virus
121 [25]. Recently, this study was extended to include BOMV to assess its pathogenicity to humans
122 [26]. At SDPs, BOMV shared the majority of amino acids (63.25%) with the human pathogenic
123 Ebolaviruses. However, for two SDPs in viral protein 24 (VP24), which may be critical for the
124 lack of Reston virus human pathogenicity, the BOMV amino acids match those of Reston virus.
125 Thus, BOMV may not be pathogenic in humans [25, 26]. Nonetheless, rRT-PCR assays are
126 important for biosurveillance of BOMV and other potential new variants in the wild.

127 While our study on the BOMV use case for assay design was ongoing, the world
128 witnessed the emergence of a novel respiratory pneumonia disease (COVID-19) epidemic from
129 Wuhan city, Hubei province, China. In the aftermath of its rapid global spread and devastating
130 impact, on March 11, 2020, the WHO declared that COVID-19 can be characterized a pandemic
131 threat [27]. COVID-19 was determined to be caused by a severe acute respiratory syndrome
132 (SARS)-like corona virus (SARS-CoV-2) that quickly spread within Wuhan [28, 29] and crossed
133 borders to >104 countries/territories/areas as of March 09, 2020 [7, 8, 30].

Using next generation sequencing, the whole genome sequence (WGS) of SARS-CoV-2 are continuously being released and shared (306 complete genomes as of March 09, 2020) with the entire research community through Global Initiative on Sharing All Influenza Data (GISAID) [31]. The release of WGS allowed us to test the BioLaboro pipeline (described in this study) to evaluate currently used diagnostic assays and to rapidly design new assays.

In a previous study, we described a bioinformatics tool called PSET (PCR signature erosion tool) and used it to show *in silico*, confirmed with wet lab work, the effectiveness of existing Ebolavirus diagnostic assays against a large number of sequences available at that time [32]. The phrase "signature erosion" used here signifies potential false-positive or false-negative results in PCR assays due to mutations in the primers, probe, or amplicon target sequences (PCR signatures). Signature erosion could also mean failure of medical countermeasures; for example, a change in the genomic sequence resulting in an amino acid change that could potentially alter the efficacy of sequence-based therapeutics [33, 34].

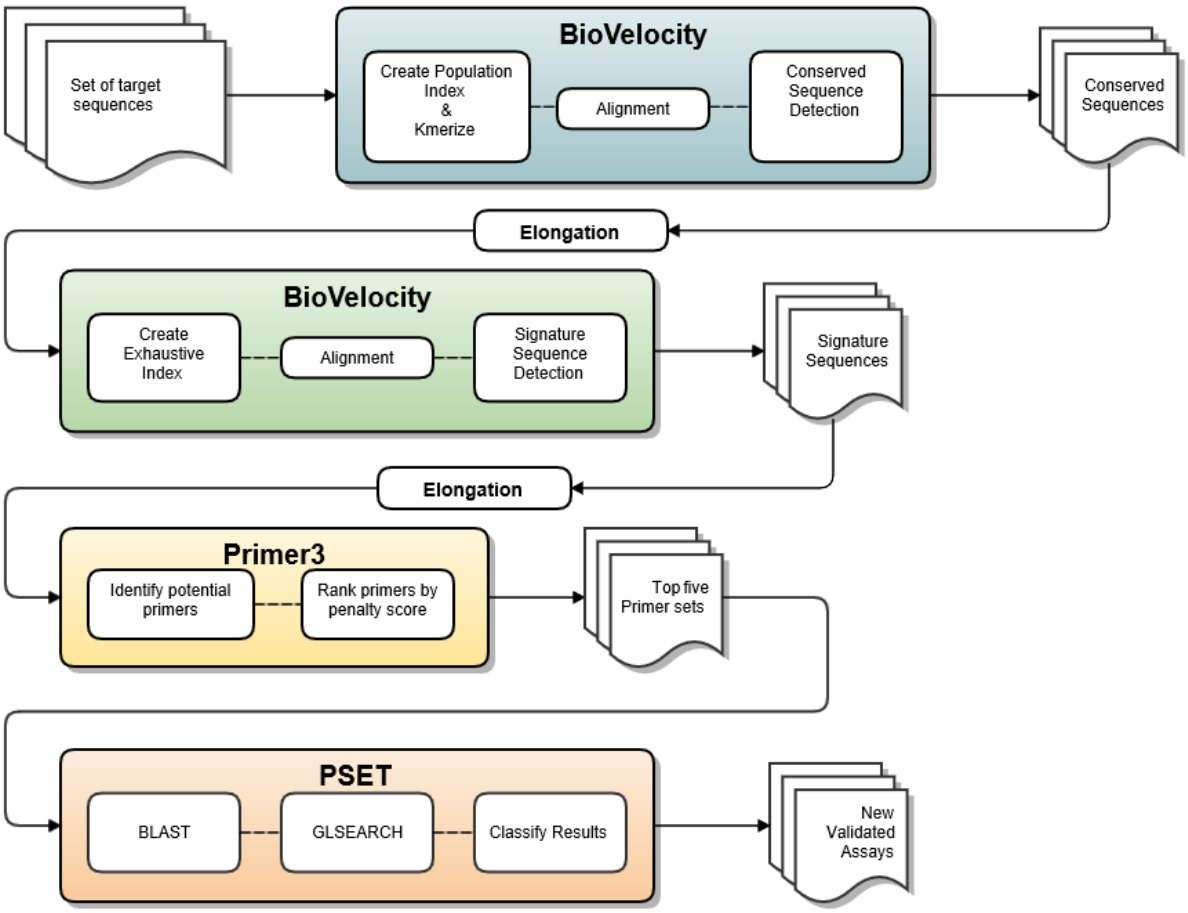
In this study, we describe an expanded bioinformatics pipeline called BioLaboro in which we have integrated several tools: BioVelocity®, Primer3 and PSET for end-to-end analysis of outbreak pathogen genome sequences to evaluate existing PCR assay efficacy against the new sequences, and to identify unique signature regions (BioVelocity), design PCR assays to these regions (Primer3), and test the new assays' efficacy (PSET) against current National Center for Biotechnology Information Basic Local Alignment Search Tool (BLAST) standard databases [35]. We have used the BOMV and SARS-CoV-2 sequences as proof of concept for BioLaboro to develop and evaluate new PCR assays *in silico.*

## Results

### BioLaboro architecture

BioLaboro is comprised of three algorithms - BioVelocity, Primer3, and PSET - which are built into a pipeline for *user-friendly* applications. The user has the option to launch one of four different job types: Signature Discovery, Score Assay Targets, Validate Assay, or New Assay Discovery. Each of the three algorithms can be run individually or together as a complete end-to-end pipeline (Figure 1). For the BOMV use case, in the first phase of the pipeline BioVelocity was used to analyze a set of genome sequences for unique regions that are both conserved and signature to the target sequences selected. This was achieved by splitting a chosen representative whole genome sequence into sliding 50 base pairs (bps) k-mers. Each k-mer was then scanned against all target sequences to determine conservation. Conserved k-mers were then elongated based on overlaps and formed into contigs. These contigs were then split into k-mers ≤ 250 bps and scanned against all non-target sequences to determine specificity. All passing sequences were then elongated based on overlaps and the signature contigs were passed to the next step in the pipeline. Primer3 was then used to evaluate the signature contigs to identify suitable primers and probes for assay development. Primer3 was run in parallel against all signatures and the output was ranked by penalty score in ascending order. The top five best primer sets were passed along to the final step in the pipeline, PSET. In this step the primer sets were run through a bioinformatics pipeline which aligned the sequences against large public sequence databases from NCBI using BLAST and GLSEARCH [36] to determine how well each assay correctly aligned to all target sequences while excluding off-target hits.

Figure 1. BioLaboro- New Assay Discovery pipeline.




179

180 **Performance assessment of currently available EBOV PCR assays on BOMV using PSET**

181 The phylogenetic classification criteria for filoviruses were reported to be 64–77%
182 similarity for species and 41–50% for genera, based on BLAST alignment results [37].
183 Compared to other ebolaviruses, the BOMV showed 55–59% nucleotide identity, 64–72% amino
184 acid identity [20]. Given the sequence diversity, we assessed if the current diagnostic assays
185 were effective against BOMV. We compared the current Ebola assay signatures against the three
186 available complete genome sequences of BOMV (NCBI Accession numbers: MF319185.1,
187 MF319186.1, and MK340750.1). Of the 30 Ebola assays examined (assay details in reference
188 [32]), only two met our *in silico* criteria for successful detection (90% identity over 90% of the
189 length for all primers and probe sequences in the amplicon). Of the two assays that did meet

190 detection criteria for BOMV, neither had perfect matches to the primer sequences. The primer set
191 match percentages (the average identity of all primers/probes) for all 30 Ebola assays against the
192 three BOMV complete genomes are shown in the heat map (Table 1). The two assays which pass
193 the *in silico* criteria are shown in green while the matches in red indicate failure or no alignment.
194 Table 1. Heat map of PSET results of Ebola assays against BOMV sequences

| Assay | MF319186.1 | MK340750.1 | MF319185.1 |
|---|---|---|---|
| EBO_GP | 94.21 | 94.21 | 94.21 |
| EBO1_2 | 72.50 | 75.00 | 72.50 |
| EBO3_4 | 74.34 | 74.34 | 74.34 |
| EBOGP | 78.41 | 76.75 | 78.41 |
| Ebola_Bundibugyo_MGB | None | None | None |
| Ebola_Bundibugyo_TM | None | None | None |
| Ebola_Ivory_Coast_MGB | None | None | None |
| Ebola_Ivory_Coast_TM | 72.22 | 69.44 | 70.83 |
| Ebola_Reston_MGB | None | None | None |
| Ebola_Reston_TM | None | None | None |
| Ebola_Sudan_MGB | 80.78 | 80.78 | 82.17 |
| Ebola_Sudan_TM | None | None | None |
| EboZNP | 75.66 | 76.01 | 75.66 |
| ENZ | 72.41 | 69.22 | 72.41 |
| Filo_AB | 73.48 | 73.48 | 73.48 |
| GAB_1 | 78.57 | 78.57 | 78.57 |
| KGH | None | None | None |
| Kulesh_MGB | 71.29 | None | 71.29 |
| Kulesh_TM | 74.74 | 74.74 | 74.74 |
| NGDS_Primary_amplicon | None | 61.39 | None |
| NGDS_Secondary_amplicon | 66.91 | None | 66.91 |
| pan_Ebola_Assay_MGB_EBOV | 76.74 | 76.74 | 76.74 |
| pan_Ebola_Assay_MGB_RESTV | 77.55 | 79.07 | 77.55 |
| pan_Ebola_Assay_MGB_SUDV | 70.63 | 72.30 | 70.63 |
| PanFiloL_1_2 | 85.55 | 85.55 | 85.55 |
| PanFiloL3_4 | 96.30 | 96.30 | 96.30 |
| Reston | 75.49 | 75.49 | 77.67 |
| Sudan | None | None | None |
| ZAI_NP | 80.59 | 80.59 | 80.59 |
| ZebovGP | None | None | None |

195

196 Table 1 Legend: The average primer set percent identity matches for thirty current Ebola assays
197 tested against the three BOMV genomes. Cells in green have an average primer identity over
198 90% which indicates likely primer binding while red cells have below 90% average identity or
199 no alignment at all, indicating likely primer binding failure.

200 Even the two assays that passed *in silico* criteria did not have perfect matches raising the
201 possibility that these assays may fail in wet lab testing due to mismatches against currently
202 available BOMV genomic sequences. Hence, as described below, we designed new assays using
203 the BioLaboro platform.

204 **Discovery of potential new BOMV assays using BioLaboro end-to-end pipeline**

205 Using BioLaboro we ran a New Assay Discovery job to discover new BOMV signatures
206 and determine their potential for accurate detection using PSET. In the first phase, BioVelocity
207 was used to search for conserved and signature regions within the selected genomes. We selected
208 the organism of interest by searching for "Bombali ebolavirus" from the database and selecting
209 the three available complete genomes. The MF319185.1 genome was used as the algorithmic
210 reference sequence as it is the same one that NCBI selected for the RefSeq database (Genbank
211 ID: NC_039345.1). The algorithmic reference sequence was first split into k-mers of 50 bps each
212 using a sliding window of 1 bp, which amounts to 18,994 k-mers to be evaluated with
213 BioVelocity's conserved sequence detection algorithm. BioVelocity found 27% (5,237) of these
214 k-mers to be conserved in all three of the BOMV genomes. The conserved k-mers were then
215 evaluated to determine overlapping segments and were combined into 120 conserved contigs.
216 These contigs were next evaluated with BioVelocity's signature sequence detection algorithm.
217 The contigs were split into signatures with a max size of 250 bps (longer contigs were split into
218 250 k-mers with a step size of 1). The conserved k-mer sequences were evaluated against

563,843 complete genomes and plasmids from the NCBI GenBank repository. There were 291 k-mers sequences found to be signatures to BOMV. The signatures were then evaluated to determine overlapping reads and combined back into 119 signature contigs. Metrics for the BioVelocity run in phase one are shown in Table 2.

Table 1. BioVelocity run statistics for BOMV.

| Type | Contigs | Total Bases | Average Length | Median Length | Genome Coverage |
|---|---|---|---|---|---|
| Conserved | 120 | 11,117 | 93 | 81 | 58.3% |
| Signature | 119 | 11,046 | 93 | 81 | 58.0% |

Table 2 Legend. Total number of conserved and signature contigs along with total bases, average sequence length, median sequence length, and percent coverage of the BOMV genome

In the second phase, Primer3 was used to identify potential primer pairs and probes for generating new PCR detection assays. For the BioLaboro pipeline, Primer3 is used to assess the suitability of a sequence to primer creation and generates viable primers which cover the identified signature regions. There were 151 primer sets created from the signatures run through Primer3 and assigned a penalty score to facilitate comparison of the results. The top five primer sets, by lowest penalty score (Table 3), were formatted and sent to the final step for validation using PSET.

Table 3. Primer3 identified PCR assays for BOMV.

| Identifier | Targets | Definition | Penalty Points |
|---|---|---|---|
| signatures.4 | 2010960 | [AGCTGGACCACTTAGGCCTA]GACACAAAAGAAAAGGAAATATTAATGAATTTCCATCAACGGAAAAATGAGATTAGTTTCCAGCAAACAAATGCAATGGTGTCCCTTCGCAAGGAGAGACTAGCAAAACTAACAGA(AGCTATTGCCGCTGCATCAGCC)CAAAGAGAGAGAGGCTACTACGACGATGACAATGAA[ATTCCGTTTCCAGGCCCAAT] | 0.083 |

| | | | |
|---|---|---|---|
| signatures.12 | 2010960 | [TGAAGCTGGAGAATGGGCTG]AGAATTGCTACAATCTAGAGATCAAGAAGCCTGATGGGAGTGAGT(GCTTACCGATGGCCCCAGAGG)GGAT[CCGTGGCTTCCCTAGATGTC] | 0.139 |
| signatures.5 | 2010960 | [AAGCAGCTGCAGCAATATGC]TGAAACACGTGAGCTGGACCACTTAGGCCTAGACACAAAAGAAAAGGAAATATTAATGAATTTCCATCAACGGAAAAATGAGATTAGTTTCCAGCAAACAAATGCAATGGTGTCCCTTCGCAAGGAGAGACTAGCAAAACTAACAGA(AGCTATTGCCGCTGCATCAGCC)CAAAGAGAGAGAGGCTACTACGACGATGACAATGAA[ATTCCGTTTCCAGGCCCAAT] | 0.143 |
| signatures.6 | 2010960 | [ATTCCGTTTCCAGGCCCAAT]CAATGACAATGATGACCAAGATCAGCATGTTGATG(ACCCAACAGATACCCAGGACACA)ACAATTCCAGACATTGTCG[TAGACCCAGACGATGGAGGG] | 0.147 |
| signatures.7 | 2010960 | [AGCTGGACCACTTAGGCCTA]GACACAAAAGAAAAGGAAATATTAATGAATTTCCATCAACGGAAAAATGAGATTAGTTTCCAGCAAACAAATGCAATGGTGTCCCTTCGCAAGGAGAGACTAGCAAAACTAACAGA(AGCTATTGCCGCTGCATCAGCC)CAAAGAGAGAGAGGCTACTACGACGATGACAATGAAATTCCGTTTCCAGGCCCAATCAATGACAATGATGACCAAGATCAGCATGTTGATGACCCAACAGATACCCAGGACACAACAATTCCAGACATTGTCG[TAGACCCAGACGATGGAGGG] | 0.148 |

Table 3 Legend. The five new assays identified by Primer3 ranked by lowest penalty score. The Identifier column is an automated ID generated from the pipeline, the Targets column is the Taxonomy ID for BOMV, the Definition column contains the amplicon sequence with the primers in brackets (orange) and the probe in parentheses (blue), and the Penalty Points column contains the score generated after taking into account primer design parameters.

The signature regions identified by BioVelocity and the five new assays selected by Primer3 were mapped to the BOMV genome (Figure 2). As shown, the four assays are clustered in the nucleoprotein (NP) gene and one is in the glycoprotein (GP) gene. The signature segments (blue) indicate that there are many potential assay regions throughout the genome.

Figure 2. Linear map of BOMV genome.

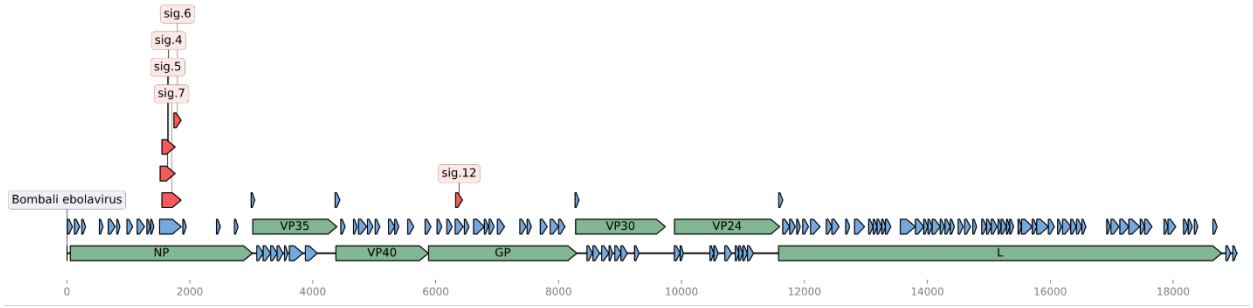



Figure 2 Legend: Linear map of the BOMV genome with annotations. The BOMV genes are colored in green, the signature segments are colored in blue, and the new assays are colored in red. The figure was created using the DNA Features Viewer Python library [38].

In the third phase, PSET was used to test the five newly designed assays identified by Primer3 *in silico* against publicly available sequences. PSET was used to analyze the primers and probes in the new assays using bioinformatics tools to identify potential false-positive and false-negative matches to NCBIs BLAST nucleotide sequence repositories (nt, gss, and env_nt) comprised of over 220 million sequences (as of last update in September 2019). BLAST+ was used to compare the assay amplicon sequences against these sequence repositories to identify matches. These matches were then used to create a custom library of sequences for GLSEARCH, a global-local sequence comparison tool in the FASTA suite of programs, which was used to search for the individual primers and probes. The resulting output was then processed and filtered based on pre-defined hit acceptance criteria. These criteria require that the assay components all hit to 90% identity over 90% of the component length, primer pairs were on opposite strands, and the total amplicon size was no greater than 1000 bps. The results were then validated by comparing the hits to the target NCBI Taxonomy identifier (ID), and true and false matches were reported. PSET results confirmed that the top five primer sets had true positive hits to all three BOMV genomes and no false positive hits to any other organism (Table 4).

Table 4. PSET results of BOMV assays

| Identifier | Targets | TP | TN | FP | FN |
|---|---|---|---|---|---|
| signatures.4 | 2010960 | 3 | 1647 | 0 | 0 |
| signatures.12 | 2010960 | 3 | 1678 | 0 | 0 |
| signatures.5 | 2010960 | 3 | 1678 | 0 | 0 |
| signatures.6 | 2010960 | 3 | 11 | 0 | 0 |
| signatures.7 | 2010960 | 3 | 1164 | 0 | 0 |

Table 4 Legend: True positive (TP: All assay components hit with >=90% identity over >=90% of the component length to the correct target), true negative (TN: Partial hit to assay amplicon but one or more assay components hit with <90% alignment to an incorrect target), false positive (FP: All assay components hit with >=90% identity over >=90% of the component length to an incorrect target), and false negative (FN: Partial hit to assay amplicon but one or more assay components hit with <90% alignment to the correct target) counts for each of the five new BOMV assays tested. The targets column is the NCBI Taxonomy ID of the target sequence, BOMV.

There are a high number of true negative (TN) results for 4 of 5 assays due to the similarity of the amplicon sequences with Zaire ebolavirus although these TNs are not expected to produce PCR positive results in wet lab experiments.

**Discovery of potential SARS-CoV-2 assays using BioLaboro end-to-end pipeline**

Using BioLaboro, we ran a New Assay Discovery job to discover SARS-CoV-2 signatures and determine their potential for true positive viral detection. In the first phase, BioVelocity was used to search for conserved and signature regions within the selected genomes. Ninety six complete SARS-CoV-2 whole genome sequences were downloaded from the GISAID and uploaded to BioLaboro as a custom database. These 96 genomes were used as our reference set and EPI_ISL_404253 (Genbank ID: MN988713.1) was used as the algorithmic reference

sequence. The algorithmic reference sequence was first split into k-mers of 50 bps each using a sliding window of 1 bp, which amounted to 29,833 k-mers to be evaluated with the conserved sequence detection algorithm. BioVelocity found 79% (23,542) of these k-mers to be conserved in all 96 of the SARS-CoV-2 genomes. The conserved k-mers were then evaluated to determine overlapping segments and were combined into 96 conserved contigs. These contigs were next evaluated with BioVelocity's signature sequence detection algorithm. The contigs were split into signatures with a max size of 250 bps (longer contigs were split into 250 k-mers with a step size of 1). The conserved k-mer sequences were evaluated against 563,941 complete genomes and plasmids from the NCBI GenBank repository. There were 11,152 sequences found to be signature to SARS-CoV-2. The signatures were then evaluated to determine overlapping reads and combined back into 91 signature contigs. Metrics for the BioVelocity run in phase one are shown in Table 5.

Table 5. BioVelocity run statistics for SARS-CoV-2.

| Type | Contigs | Total Bases | Average Length | Median Length | Genome Coverage |
|---|---|---|---|---|---|
| Conserved | 96 | 28,246 | 294 | 221 | 94.5% |
| Signature | 91 | 27,888 | 306 | 241 | 93.0% |

Table 5 Legend: Total number of conserved and signature segments along with total bases, average sequence length, median sequence length, and percent coverage of the SARS-CoV-2 genome.

In the second phase, Primer3 was used to identify potential primer pairs and probes for generating new PCR detection assays as described above for BOMV. There were 330 primer sets created from the signatures which were assigned a penalty score to facilitate comparison of the results. Primer sets were sorted by lowest penalty score and five potential assays were chosen

manually in order to distribute potential candidates across the genome. These assays were then formatted and sent to the final step for validation using PSET. Primer sets sent to PSET are shown in Table 6.

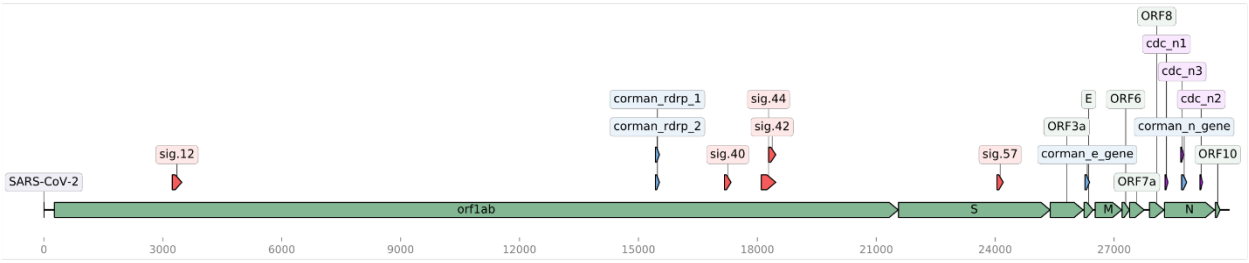
Table 6. Primer3 identified assays for SARS-CoV-2.

| Identifier | Targets | Definition | Penalty Points |
|---|---|---|---|
| signatures.12 | 2697049 | [ACGGCAGTGAGGACAATCAG]ACAACTACTATTCAAACAATTGTTGAGGTTCAACCTCAATTAGAGATGGAACTTACACCAGTTGTTCAGACTATTGAAGTGAATAGTTTTAGTGGTTATTTAAAACTTACTGACAATGTATACATTAAAAATGCAGACATTGTGGAAGAAGCTAAAAAGGTAAAA(CCAACAGTGGTTGTTAATGCAGCCA)ATGTTTACCTTAA[ACATGGAGGAGGTGTTGCAG] | 0.074 |
| signatures.40 | 2697049 | [GCCGCTGTTGATGCACTATG]TGAGAAGGCATTAAAATATTTGCCTATAGATAAATGTAGTAGAATTATACCTGC(ACGTGCTCGTGTAGAGTGTTTTGAT)AAATTCAAAGTGAATTCAACATTAGAACAGTATGTCTTTTGTACTGTAA[ATGCATTGCCTGAGACGACA] | 0.065 |
| signatures.42 | 2697049 | [TGTACGTGCATGGATTGGCT](TCGATGTCGAGGGGTGTCATGCT)ACTAGAGAAGCTGTTGGTACCAATTTACCTTTACAGCTAGGTTTTTCTACAGGTGTTAACCTAGTTGCTGTACCTACAGGTTATGTTGATACACCTAATAATACAGATTTTTCCAGAGT[TAGTGCTAAACCACCGCCTG] | 0.072 |
| signatures.44 | 2697049 | [CAGGCACCTACACACCTCAG]TGTTGACACTAAATTCAAAACTGAAGGTTTATGTGTTGACATACCTGGCATACCTAAGGACATGACCTATAGAAGACTCATCTCTATGATGGGTTTTAAAATGAATTATCAAGTTAATGGTTACCCTAACATGTTTATCACCCGCGAAGAAGCTATAAGACATGTACGTGCATGGAT(TGGCTTCGATGTCGAGGGGTGT)CATGCTACTAGAGAAGCTGTTGGTACCAATTTACCTTTACAGCTAGGTTTTTCTACAGGTGTTAACCTAGTTGCTGTACCTACAGGTTATGTTGATACACCTAATAATACAGATTTTTCCAGAGT[TAGTGCTAAACCACCGCCTG] | 0.074 |
| signatures.57 | 2697049 | [TGCAGATGCTGGCTTCATCA]AACAATATGGTGATTGCCTTGGTGATATTGCTGCTAGAGACCTCATTTGTGCACAAAAGTTTA(ACGGCCTTACTGTTTTGCCACCT)TTGCTCACAGATGAAATGATTGCTCAATACACTT[CTGCACTGTTAGCGGGTACA] | 0.073 |

Table 6 Legend: The five new assays identified by Primer3 ranked by lowest penalty score. The Identifier column is an automated ID generated from the pipeline, the Targets column is the Taxonomy ID for SARS-CoV-2, the Definition column contains the amplicon sequence with the primers in brackets (orange) and the probe in parentheses (blue), and the Penalty Points column contains the score generated after taking into account primer design parameters.

316 The five new assays were mapped to the SARS-CoV-2 genome presented below (Figure 3). This
317 figure shows that four assays are in the ORF1ab and one is located in the spike (S) gene. By
318 comparison, the CDC and Corman group assays are clustered primarily at the 3' end of the
319 genome in the envelope (E) and nucleocapsid phosphoprotein (N) genes.

320 Figure 3. Linear map of SARS-CoV-2.

321 


322 Figure 3 Legend. A linear map of the SARS-CoV-2 genome with annotations. The genes and
323 open reading frames (ORFs) are colored in green and the new assays are colored in red, Corman
324 assays (blue), CDC assays (purple), and assays discovered in this study (red). The figure was
325 created using the DNA Features Viewer Python library [36].

326 In the third phase, PSET was used to test the five newly designed assays identified by
327 Primer3 *in silico* against publicly available sequences as described above for BOMV signatures.
328 The results were then validated by comparing the hits to the target NCBI Taxonomy identifier
329 (ID), and true and false matches were reported. PSET confirmed that the top five primer sets had
330 true positive hits to all 145 (SARS-CoV-2) genomes (as of February 28, 2020) and no false
331 positive hits to any other organism. An additional table lists the identifiers and metadata for these
332 145 complete genome sequences generated from human samples and not from other sources such
333 as bat or pangolin [see Additional Table 2]. Results are shown alongside assays from CDC and
334 Corman et al. [39, 40] (Table 7).

335 Table 7. PSET results of SARS-CoV-2 PCR assays.

| Identifier | Targets | TP | TN | FP | FN |
|---|---|---|---|---|---|
| signatures.12 | 2697049 | 145 | 2 | 0 | 0 |
| signatures.40 | 2697049 | 145 | 316 | 0 | 0 |
| signatures.42 | 2697049 | 145 | 275 | 0 | 0 |
| signatures.44 | 2697049 | 145 | 277 | 0 | 0 |
| signatures.57 | 2697049 | 145 | 359 | 0 | 0 |
| cdc_n1 | 2697049 | 145 | 284 | 0 | 0 |
| cdc_n2 | 2697049 | 145 | 282 | 0 | 0 |
| cdc_n3 | 2697049 | 145 | 14 | 273 | 0 |
| corman_e_gene | 2697049 | 144 | 4 | 283 | 1 |
| corman_n_gene_ | 2697049 | 145 | 22 | 266 | 0 |
| corman_rdrp_1 | 2697049 | 145 | 2957 | 420 | 0 |
| corman_rdrp_2 | 2697049 | 145 | 2853 | 52 | 0 |

336

337 Table 7 Legend: True positive (TP: All assay components hit with >=90% identity over >=90%
338 of the component length to the correct target), true negative (TN: Partial hit to assay amplicon
339 but one or more assay components hit with <90% alignment to an incorrect target), false positive
340 (FP: All assay components hit with >=90% identity over >=90% of the component length to an
341 incorrect target), and false negative (FN: Partial hit to assay amplicon but one or more assay
342 components hit with <90% alignment to the correct target) counts for each of the five new
343 SARS-CoV-2 assays tested. The targets column is the NCBI Taxonomy ID of the target
344 sequence, SARS-CoV-2.

345 There are a high number of true negative (TN) results for 4 of 5 assays due to the
346 similarity of the amplicon sequences with SARS coronavirus near neighbors. The FP results
347 from some Corman and CDC assays are due to near neighbor hits since these assays are pan
348 assays. The one FN identified for corman_e_gene is to sequence EPI_ISL_410486 (Additional
349 Table 2) which contains a large stretch of Ns over the majority of the amplicon sequence (80%)
350 which is likely due to missing sequences.

We also tested the SARS-CoV-2 assays using PSET on near neighbor sequences that were generated during this outbreak, such as the bat and pangolin sequences. As expected the analyses showed a range of TP from pan assays, FN results due to sequence divergence (Table 8).

Table 8. PSET results of SARS-CoV-2 PCR assays against bat and pangolin SARS-CoV sequences.

| Identifier | Targets | TP | TN | FP | FN |
|---|---|---|---|---|---|
| signatures.12 | 2697049 | 0 | 0 | 0 | 8 |
| signatures.40 | 2697049 | 1 | 0 | 0 | 7 |
| signatures.42 | 2697049 | 3 | 0 | 0 | 5 |
| signatures.44 | 2697049 | 2 | 0 | 0 | 6 |
| signatures.57 | 2697049 | 1 | 0 | 0 | 7 |
| cdc_n1 | 2697049 | 3 | 0 | 0 | 5 |
| cdc_n2 | 2697049 | 1 | 0 | 0 | 7 |
| cdc_n3 | 2697049 | 1 | 0 | 0 | 7 |
| corman_e_gene | 2697049 | 8 | 0 | 0 | 0 |
| corman_n_gene_ | 2697049 | 2 | 0 | 0 | 6 |
| corman_rdrp_1 | 2697049 | 8 | 0 | 0 | 0 |
| corman_rdrp_2 | 2697049 | 3 | 0 | 0 | 6 |

Table 8 Legend: TP, TN, FP and FN definitions are similar to Table 7.

## Discussion

Since its discovery in 2016, BOMV RNA has been detected in oral and rectal swabs as well as internal organs of *Mops condylurus* and *Chaerephon pumilus* bats in Sierra Leone, Kenya and Guinea [20, 41, 42]. These data add to the body of evidence suggesting that bats are a reservoir for filoviruses. However, these did not conclusively link the presence of viral RNA in bats to human infections with filoviruses. The discovery of BOMV in bats residing near and in human dwellings and residential areas further highlights the gaps in knowledge about ebolavirus

366 diversity and ecology. Given these gaps and the human and economic impacts of ebolavirus
367 disease, there is an ongoing need for ebolavirus biosurveillance and further characterization of
368 BOMV. Availability of efficient viral RNA detection assays is critical for bio surveillance of
369 these reservoirs.

370 Based on *in silico* analyses, we determined that current EBOV assays could potentially
371 fail to detect BOMV sequences, and thus there is a need for BOMV specific assays. Using
372 BioLaboro we rapidly designed and evaluated new, more specific assays. An advantage of
373 BioVelocity is that the end user obtains results quickly with high confidence that the output of
374 conserved and unique signature regions are accurate and not based on heuristics and
375 probabilities. Additionally, Primer3 allows an end user to determine which signatures yield the
376 best primers and probes, based on an objective penalty scoring system. PSET tests the PCR
377 assays *in silico* against the latest versions of public sequence repositories, including newly added
378 strain genomes, to validate that the primers and probes match only to their intended targets.
379 BioLaboro's easy-to-use Graphical User Interface (GUI) provides full functionality for
380 submitting a new job, viewing the current job queue, checking results from previously completed
381 jobs, and exploring the system database management and settings. The dedicated large RAM
382 system easily supports multiple users with discrete logins and rapid operations. Moreover, the
383 user-friendly GUI allows scientists without command-line experience to design and evaluate an
384 assay for immediate wet lab testing.

385 Due to the relative novelty of BOMV there are currently only three complete genomes
386 available from NCBI. As more samples are identified and sequenced the genetic diversity will
387 likely increase. During the 2014 - 2016 Western African EBOV outbreak, rapid accumulation of
388 inter- and intra-host genetic variations were observed [43]. Since many of the nucleotide

389 mutations altered protein sequences, it became apparent that the changes should be monitored for
390 impacts on diagnostics, vaccines, and therapies critical to outbreak response. In an earlier study
391 conducted to decipher the impact of the then-available diagnostics, we determined that many of
392 the real-time reverse transcription PCR (rRT-PCR) assays that were in use during that outbreak
393 identified regions outside of those that BioVelocity selected as unique to EBOV, SUDV, and
394 RESTV [32]. In another study, signature erosion of diagnostic assays was identified during the
395 2018 outbreak in North Kivu and Ituri Provinces of the Democratic Republic of the Congo [44].
396 Using the *in silico* methods described here, only two of the 30 EBOV rRT-PCR assays evaluated
397 against BOMV target sequences met our criteria for successful detection and neither showed
398 perfect matches. For ongoing biosurveillance, we recommend wet lab testing and validation of
399 the rRT-PCR assays described here to ensure detection of BOMV.

400 We also tested the BioLaboro pipeline with available SARS-CoV-2 viral genomes and
401 rRT-PCR assays. We identified five signature sequences distributed across the genome and in
402 different regions than those of the CDC or German group [39, 40]. There are seven assays
403 currently in use (3 CDC and 4 German) for SARS-CoV-2 diagnostics and they all produced true
404 positive results against the human-derived sample sequences without any signs of signature
405 erosion. A few whole genome sequences that showed false negative results were from
406 environmental samples (Bat and Pangolin origin) indicating that the diagnostic assays are
407 specific for human isolates. The assays that produced true positive results were pan assays. The
408 lack of signature erosion is in agreement with the whole genome sequence data analyzed thus far
409 (February 28, 2020). A simple pipeline consisting of Multiple Sequence Alignment using Fast
410 Fourier Transform (MAFFT), snp-sites, and R we calculated 228 single nucleotide
411 polymorphisms (SNPs) (159 unique) across 145 genomes [45-47]. Each of the 145 WGS

412 contains less than 10 SNPs with the exception of one having 25. None of the variations impact
413 the diagnostic assay signatures. However, real-time monitoring of these assays against WGS as
414 they become available, will enable rapid identification of signature erosion if it occurs and
415 generation of new assays as needed. The newly designed assays we have described here need to
416 be validated in wet lab testing and with appropriate clinical matrices to determine their
417 performance. However, we have demonstrated that the BioLaboro pipeline can be used
418 effectively and rapidly to validate available assays and to design new assays using genome
419 sequences of newly emerging pathogens.

420 **Conclusions**

421 By periodically re-running BioLaboro on emerging and reemerging pathogen sequences
422 as they become available, over time the relative diversity can be monitored, and assays can be
423 updated to remain current with regards to available data. By tracking assay performance
424 measures over time, one can evaluate the efficacy of MCMs on a routine basis. These analyses
425 would ensure that the most accurate MCMs are available when an outbreak response is
426 necessary. In this study we demonstrate the value of real-time genomic sequencing and MCM
427 evaluation to provide actionable information before and during a public health emergency.
428 Combined with an active biosurveillance of zoonotic reservoirs and generation of sequence data
429 to understand the genetic diversity of these pathogens, BioLaboro is broadly applicable for
430 providing effective diagnostics and medical countermeasures during a crisis involving future
431 threats.

432

433

## Methods

### BioLaboro System Description

BioLaboro is an application for rapidly designing *de novo* assays and validating existing PCR detection assays. It is composed of three tools: BioVelocity, Primer3, and PSET which are built into a pipeline for user-friendly new assay discovery via an interactive graphic user interface.

**BioVelocity** is a bioinformatics tool based on an innovative algorithm and approach to genomic reference indices [32]. Using a fast and accurate hashing algorithm, BioVelocity can quickly align reads to a large set of references. BioVelocity takes advantage of large RAM systems (hardware specification described in Additional Table 1) and creates a k-mer index of all selected reference sequences (e.g. GenBank) by identifying all possible base pair sequences of various k-mer lengths. This index is used to determine all possible matches between query sequences and references, simultaneously. The advantage of this approach is that it allows for rapid identification of sequences conserved within or omitted from a set of target references. Thus, the used has high confidence in the conserved and signature (unique) designations because they are not based on heuristics and probabilities.

**Primer3** [48] is a tool for designing primers and probes for real-time PCR reactions. It considers a range of criteria such as oligonucleotide melting temperature, size, GC content, and primer-dimer possibilities. Potential new primer sets are identified within the signature regions using Primer3 analysis. For the BioLaboro pipeline, Primer3 has been configured to analyze 22 parameters influencing suitability of a sequence to primer creation and construct viable primers which cover identified signature regions. These primers are scored with a penalty scoring

system to attempt to determine the fitness of the resulting primers thus allowing an end user to assess which signatures yield the best primers when the signatures themselves may be of similar size.

**PSET** is configured to test PCR assays *in silico* against the latest versions of public sequence repositories to determine if the primers and probes still match only to their intended targets. An elaborate description of PSET is provided in ref [32]. As NCBI's database and other public databases are updated periodically, newly added genomic sequences can reveal where primers and probes may no longer be functional or where PCR assays may detect previously un-sequenced near neighbors. Using this information, an assay provider can be better aware of potential false hits and design new primers when false hits become an issue. PSET is used to test currently deployed assays as well as new assays designed using BioLaboro's capabilities.

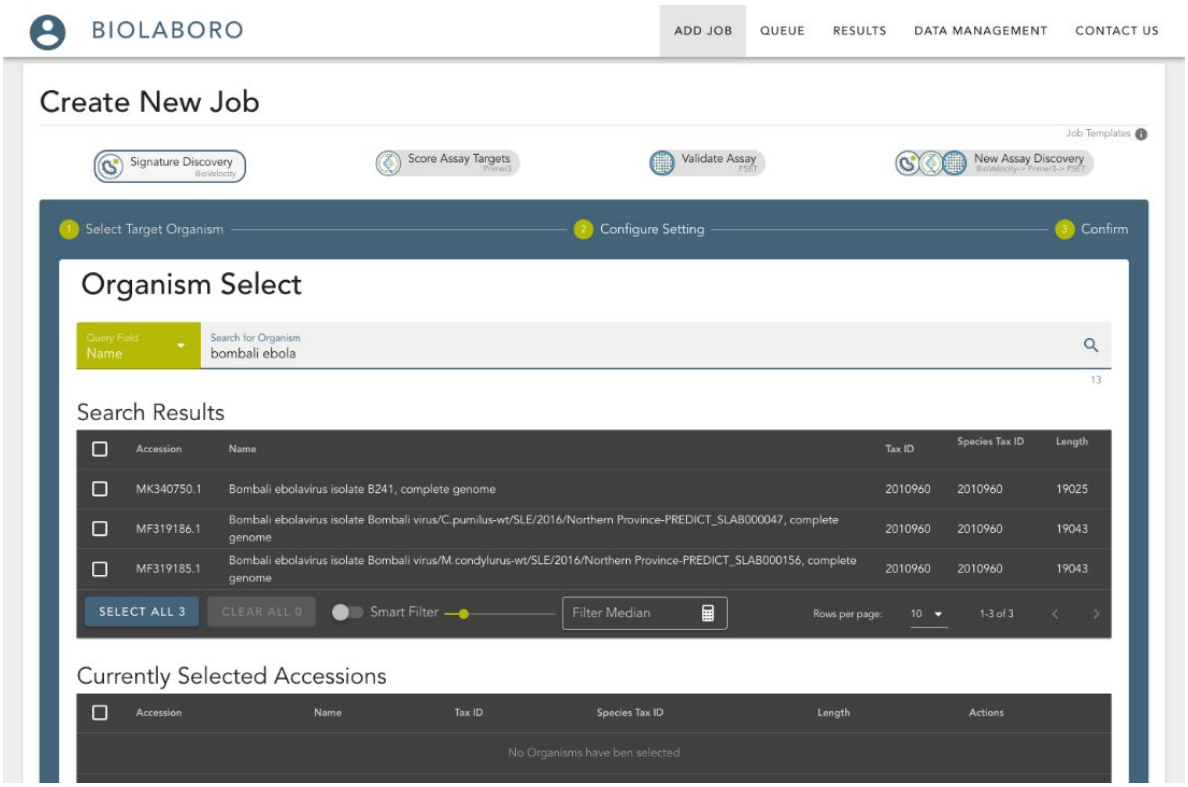
The BioLaboro application is composed of a fully functional GUI front-end that allows users to submit jobs to the back-end bioinformatics pipeline hosted on a dedicated large RAM system. The system has multi-user capability with discrete logins and a single job queue. The landing screen, shown in Figure 4, gives the user options for submitting a new job, viewing the current job queue, checking results from previously completed jobs, and exploring the system database management and settings.

Figure 4. The landing page of BioLaboro.


474

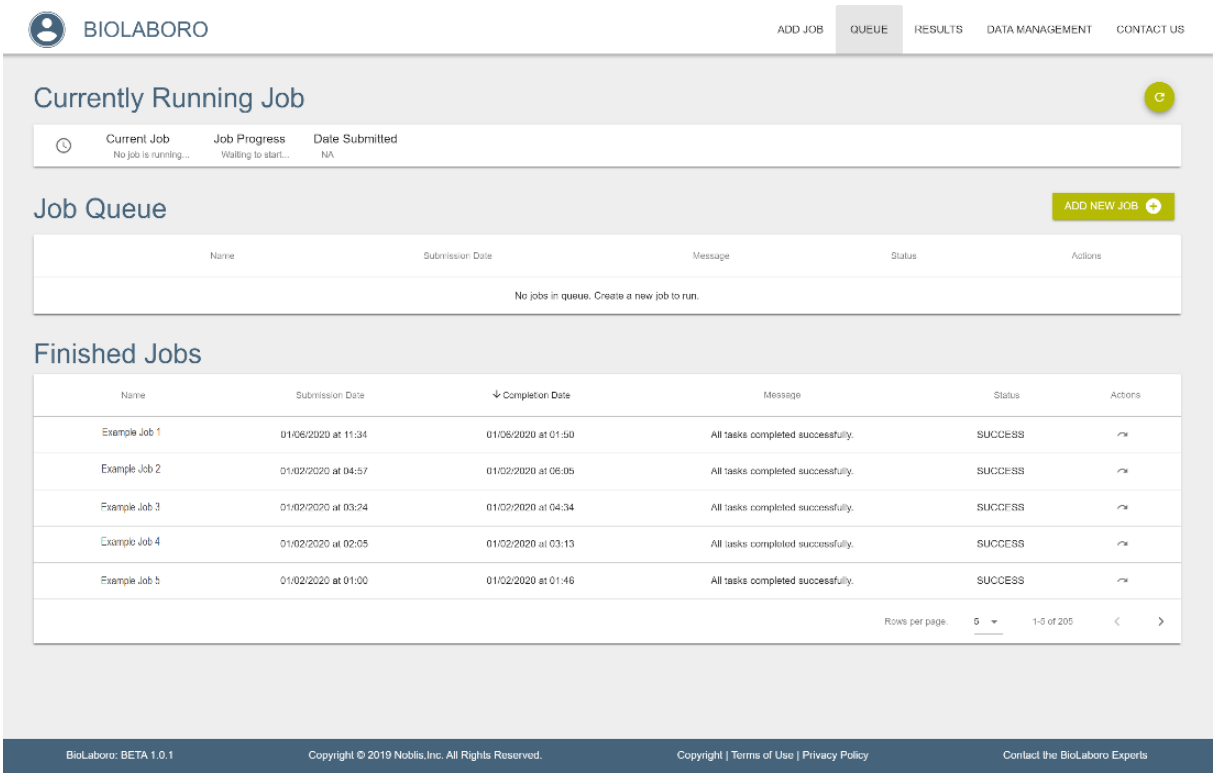
475 The BioLaboro application allows job submissions through a simplified user interface
476 designed for scientists with minimal or no command-line experience. The user can search for
477 sequences of interest using the built-in Organism Select tool, Figure 5, which allows for
478 searching on free text, NCBI Accession number, or NCBI Taxonomy ID. The results can then be
479 filtered using a "smart filter" which will only include sequences within +/- 10% of the calculated
480 median genome length of the results. This tool is useful for automatically excluding plasmids or
481 sequence fragments which can negatively impact signature identification. Alternatively, custom
482 sequence size filters can also be used if the user wants to target specific plasmids or
483 chromosomes. Once all sequences are selected and added the user can optionally choose a
484 specific sequence to serve as the algorithmic reference.

485 Figure 5. The Job Submission page for the BioVelocity component of BioLaboro showing the
486 BOMV sequences.




BioLaboro employs a queuing system to manage job submissions due to the high computational requirements of the BioVelocity algorithm. The queue page identifies the currently running job, the ordered list of queued jobs, and a list of previously finished jobs with timestamps and completion status, Figure 6. Each finished job can be re-launched from this dialog in the future with previously used parameters while utilizing the newest available datasets.

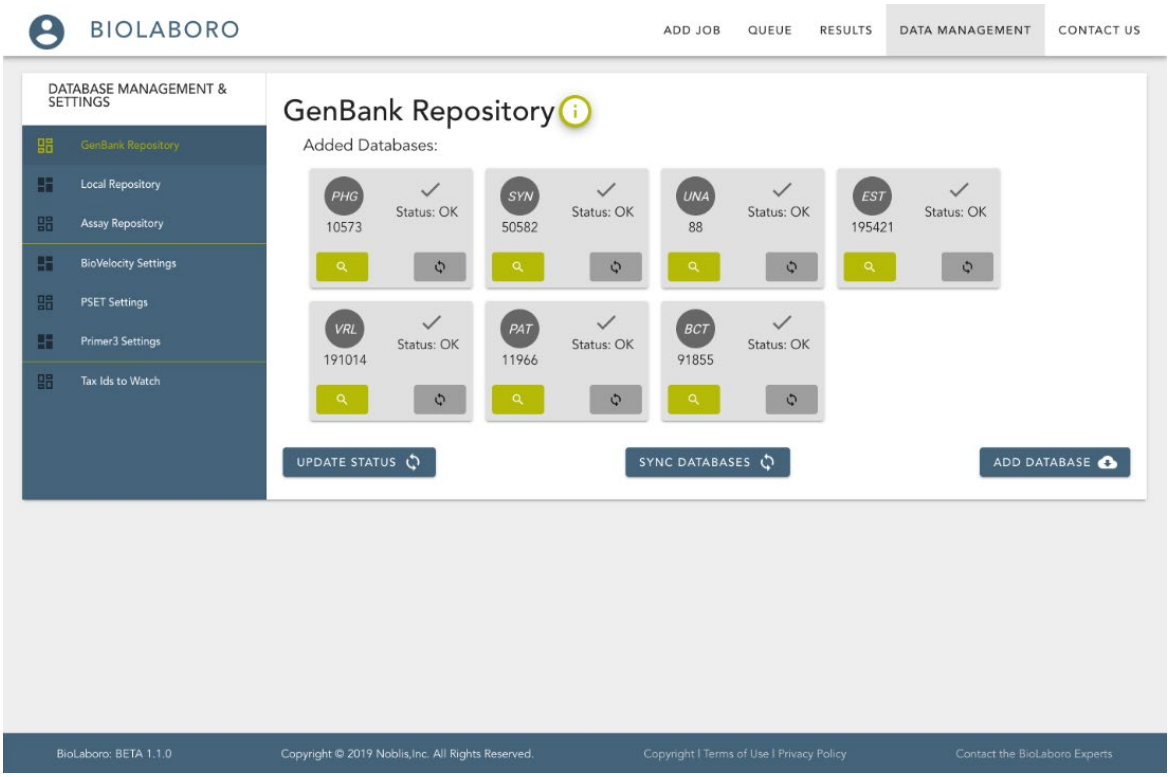
Figure 6. The BioLaboro job queue.




The queue includes three sections: 1) The currently running job is identified with information on the current sub-process, 2) The job queue is shown, which can be re-arranged as needed, and 3) The finished jobs section shows completed jobs with timestamp metadata and an option to re-run the same job with identical parameters.

The Database Management and Settings Page contains many options for maintaining system data and pipeline settings. BioLaboro's simple user interface design allows the user to manage the genomic reference databases from within the GUI. The GenBank Repository page, Figure 7, lists the databases loaded on the system along with the number of sequences each contains. These databases are used for selecting sequences for signature creation and can be updated on-demand by submitting a sync job to the queue. Other GenBank databases or custom sequence databases can also be added and maintained through this entry point.

Figure 7. The BioLaboro GenBank Repository located in the Database Management and Settings page.




PCR detection assays are also maintained in the system and can be viewed and searched for in the Assay Repository. The system maintains a history of past assay runs so that the user can track performance of assays over time, as well as re-run assays when new sequences of interest are available. Lastly the Database and Management Settings page maintains the default settings for each of the three system tools which can be permanently set here, or specifically tailored for each job at run-time. Results for completed runs are available from the Results page which allows the user to view raw data or system generated reports as well as download them to local copies.

## Supplementary Information

Additional Table 1. Large RAM System Hardware Specifications.

| Component | Value |
|---|---|
| Architecture | ppc64le |
| RAM | 1 terabyte |
| CPUs | 160 |
| Threads per core | 8 |
| Cores per socket | 5 |
| Sockets | 4 |
| Local Storage | 15 terabytes |

519 Additional Table 2. (gisaid_sequences.xlsx) List of whole genome sequences downloaded from
520 GISAID and used in this study. The "Signature Creation" column indicates which sequences
521 were used to generate the signatures, and the "Validation" column indicates which sequences
522 were used to validate the signatures with PSET.

523 **Abbreviations**

524 bp: base pair (bps, plural base pairs)

525 BDBV: Bundibugyo ebolavirus

526 BLAST: Basic Local Alignment Search Tool

527 BOMV: Bombali ebolavirus

528 CFR: Case Fatality Ratio

529 COVID-19: Coronavirus Disease 2019

530 DNA: deoxyribonucleic acid

531 DRC: Democratic Republic of the Congo

532 EBOV: Zaire ebolavirus

533 EMA: European Medicines Agency

534 EVD: Ebola Virus Disease

535 FDA: Food and Drug Administration

FN: False Negative

FP: False Positive

GC: guanine cytosine

GP: glycoprotein

GUI: Graphic User interface

ID: identifier

mAb: monoclonal antibody

MAFFT: Multiple Sequence Alignment using Fast Fourier Transform

MCM: medical countermeasure

N: nucleocapsid phosphoprotein

N/A: Not available

NCBI: National Center for Biotechnology Information

NIAID: National Institute of Allergy and Infectious Diseases

NP: nucleoprotein

NPC1: Niemann-Pick C1

ORF: Open Reading Frame

PALM: Pamoja Tulinde Maisha study

PCR: polymerase chain reaction

PSET: PCR signature erosion tool

RAM: random access memory

RESTV: Reston ebolavirus

RNA: ribonucleic acid

rRT-PCR: real-time reverse-transcription polymerase chain reaction

rVSV: recombinant vesicular stomatitis virus

SARS: severe acute respiratory syndrome

SNP: single nucleotide protein

SUDV: Sudan ebolavirus

TAFV: Taï Forest ebolavirus

564 TN: True Negative

565 TP: True Positive

566 WGS: Whole Genome Sequence

567 WHO: World Health Organization

568 **Declarations**

569 **Ethics approval and consent to participate:** Not applicable

570 **Consent for publication**: Not applicable

571 **Availability of data and materials:**

572 Weekly updates of SARS-CoV assay performance using PSET are posted at Viological.org.

573 (http://virological.org/t/preliminary-in-silico-assessment-of-the-specificity-of-published-

574 molecular-assays-and-design-of-new-assays-using-the-available-whole-genome-sequences-of-

575 2019-ncov/343/16).

576 The datasets analyzed during the current study are available in the following:

577 Three available complete genome sequences of BOMV NCBI Accession numbers: MF319185.1

578 https://www.ncbi.nlm.nih.gov/nuccore/MF319185.1/, MF319186.1

579 https://www.ncbi.nlm.nih.gov/nuccore/MF319186.1, MK340750.1

580 https://www.ncbi.nlm.nih.gov/nuccore/MK340750.1

581 Complete genome sequences of SARS-CoV-2: We gratefully acknowledge the authors,

582 originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database on

583 which this research is based. https://www.gisaid.org/

584 NCBI Taxonomy database: https://www.ncbi.nlm.nih.gov/taxonomy

585 EMBL-EBI FASTA GLSEARCH: https://www.ebi.ac.uk/Tools/sss/fasta/nucleotide.html

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**Authors' contributions**: MH, DN, SM, SS conceptualized the study. MH, DN, SM, ND, MI, ST developed BioLaboro. MH, DN, SM, SS analyzed the data. BG provided study resources. MH, DN, SM, MI, TB, KJ, SS wrote and edited the manuscript.

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