

Development of HIV-1 Coreceptor Tropism Classifiers: An Approach to Improve X4 and R5X4 Viruses Prediction

José Fernando dos Anjos Rodrigues¹^a, Leticia Martins Raposo^{1,2}^b and Flavio Fonseca Nobre¹^c

¹*Programa de Engenharia Biomédica, Universidade Federal do Rio de Janeiro, Av. Horácio Macedo, 2030, Rio de Janeiro, Brazil*

²*Departamento de Métodos Quantitativos, Universidade Federal do Estado do Rio de Janeiro, Av. Pasteur, 458, Rio de Janeiro, Brazil*
{jfarod, raposo, flavio}@peb.ufrj.br

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Abstract: The pathway of human immunodeficiency virus (HIV) infection depends on the composition of a 35-amino acid variable region in its envelope, known as the V3 loop. Since this discovery, many tools have been developed to diagnose and predict viral tropism, from biochemical tests to various computational algorithms. To date, the biggest developmental difficulty is the correct prediction of X4 or R5X4-tropism virions. In this study, we evaluated some of these recommended criteria and proposed a random forest-based approach for better prediction of X4-capable (i.e., either X4-only, or R5X4-dual/mixed capability). All methods achieved a specificity higher than 87%, with geno2pheno 2.5% showing the best performance (98.2%). Nevertheless, the sensitivity (73.3%) was lower compared to the other approaches. The highest sensitivity was attained by our Complete Model with an undersampling strategy (90.1%). The accuracy of all approaches ranged from 87.4% to 93.0%. Complete Model with oversampling and Reduced Model with no balancing showed the highest MCC value (both with 0.796 score). Considering error rates and the number of explanatory variables, our main objective of increasing the ability to predict viral specimens with X4-tropism was achieved.

1 INTRODUCTION

The Human Immunodeficiency Virus (HIV) is the etiologic agent of the Acquired Immunodeficiency Syndrome (AIDS) (Barré-Sinoussi et al., 1983; Gallo et al., 1983). The virus is known to use the CD4 receptor to infect its host cell as well as a co-receptor, which might be a CCR5 or CXCR4 receptor (Clapham & McKnight, 2001).


The management of which coreceptor will be utilized by HIV in cell infection depends on the composition of a hyper-variable loop region within the gp120 protein receptor on the surface of HIV-1 virions called V3 loop. The chemical properties of amino acids can create an affinity for the chosen receptor. This affinity is also known as viral tropism (Schneider-Schaulies, 2000).


HIV tropism is split into three groups: R5 (specimens with CCR5-receptor tropism), X4 (with


CXCR4 tropism), and R5X4 (specimens whose tropism cannot be determined or have hybrid tropism) (Berger et al., 1998). Establishing HIV tropism is crucial to addressing anti-HIV treatment with more efficient and less harmful strategies. For instance, Maraviroc is a CCR5-specific inhibitor with mild side effects (Woollard & Kanmogne, 2015).

Based on this information, many tests have been developed to determine HIV tropism. The most accurate is Trofile®, a phenotypical biological method to identify the tropism of a patient's HIV (Whitcomb et al., 2007). Unfortunately, this test is expensive and very time-consuming for clinical analysis. Still, researchers rely on their findings to create HIV databases (Poveda et al., 2010).

Other procedures were developed, taking advantage of genomic sequencing technology and the increasing use of computational methods in healthcare. These procedures utilize advanced

^a <https://orcid.org/0000-0003-0287-4345>

^b <https://orcid.org/0000-0003-0613-5582>

^c <https://orcid.org/0000-0003-4261-8258>

statistical tools and classification algorithms. Some genotypic prediction servers are well known, such as `geno2pheno[coreceptor]` (Lengauer et al., 2007), `WebPSSM` (Jensen et al., 2003) and `T-CUP` (Heider et al., 2014). However, because of the lack of available data, these algorithms struggle to predict X4-capable group correctly. Since most of the sequences obtained from these viral samples are in the R5 group, services are better suited to predict these specimens, resulting in an overfitting issue (Dietterich, 1995).

In this study, we evaluated some of these established predictors and proposed a random forest-based approach to achieve better performing models.

2 MATERIALS AND METHODS

2.1 Data

For this study, we utilized 1622 amino acid sequences corresponding to the V3 region of HIV-1, subtype B. 1284 samples had R5-tropism and 338 had X4 or R5X4-tropism (both groups were merged as NR5-tropism). All sequence information, as well as viral tropism and subtype, were obtained from the Los Alamos National Laboratory database (<http://www.hiv.lanl.gov/>).

These sequences were converted from the single-letter amino acid code to numeric representation using the Engelman’s hydrophobicity scale through the `peptides` R package (Osorio, Rondón-Villarreal, & Torres, 2015). This scale was used because each amino acid has a distinct number to represent them (Engelman, Steitz, & Goldman, 1986).

2.2 Modelling

The sequences were divided into two groups at a ratio of 70:30, using the `caret` package (Kuhn, 2016). 1136 sequences (899 R5 and 237 NR5) were allocated to the training set and 486 sequences (385 R5 and 101 NR5) to the test group. The same test set was used to evaluate the models and all the other predictors involved in this study.

The random forest algorithm (Breiman, 2001) was employed to build the predictors using the `randomForest` R package (Liaw & Wiener, 2002). To verify if the unbalanced data could influence the model performance, we also developed models with oversampling and undersampling strategies. Oversampling randomly increases the number of records in the minority class, while undersampling

randomly discards the majority class samples in order to modify the class distribution.

We also tested if the removal of explanatory variables with low variance could affect the performance of the models. Hence, a training set with all 35 positions of the V3 sequence (henceforth Complete Model) was used, as well as a training set without positions with low variability. In this sense, we used the `nearZeroVar` function from `caret` R package to remove variables with low variance (henceforth Reduced Model). Seventeen variables were removed for the construction of the Reduced Model. The positions were: 1, 3, 4, 6, 7, 8, 9, 15, 16, 17, 23, 24, 28, 30, 31, 33 and 35. These positions showed at least 95% conservation among all the sequences used in this study.

Altogether, six random forest models were created to predict HIV-1 tropism.

2.3 Genotypic Predictors Comparison

We compared our approach with the following tools: `T-CUP 2.0`, `geno2pheno[coreceptor]` and `WebPSSM`. For `WebPSSM`, we used the scoring matrix `x4r5`, `T-CUP 2.0` was used with standard settings and, for `geno2pheno[coreceptor]`, we used false positive rate (FPR) cut-off at 2.5%, 5%, and 10%.

2.4 Performance Measures

For the assessment of performance of all tested algorithms, we calculated the sensitivity, specificity, accuracy and Matthews Correlation Coefficient (MCC). The MCC value ‘1’ points to the perfect prediction, whereas ‘0’ corresponds to a completely random prediction. The measures are defined as following:

$$Sensitivity (Se) = \frac{TP}{TP + FN} \times 100 \quad (1)$$

$$Specificity (Sp) = \frac{TN}{TN + FP} \times 100 \quad (2)$$

$$Accuracy (Acc) = \frac{TP + TN}{TP + FN + TN + FP} \times 100 \quad (3)$$

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FN)(TP + FP)(TN + FN)(TN + FP)}} \quad (4)$$

as TP stands for the count of true positives, TN true negatives, FP false positives and FN false negatives. The NR5 group was stated as the positive class.

The area under receiver operating characteristic curve (AUC) was also used to evaluate the random forest model performance. The `proc` R package was used (Robin et al., 2011). All analyses were

developed in R programming environment, version 3.6.0 (R Development Core Team, 2019).

3 RESULTS

To assess the overall performance of our classifiers, we calculated the AUC. Figure 1 shows the 95% confidence interval for AUC for each one of the six models. Both Complete and Reduced models exhibit very similar performance.

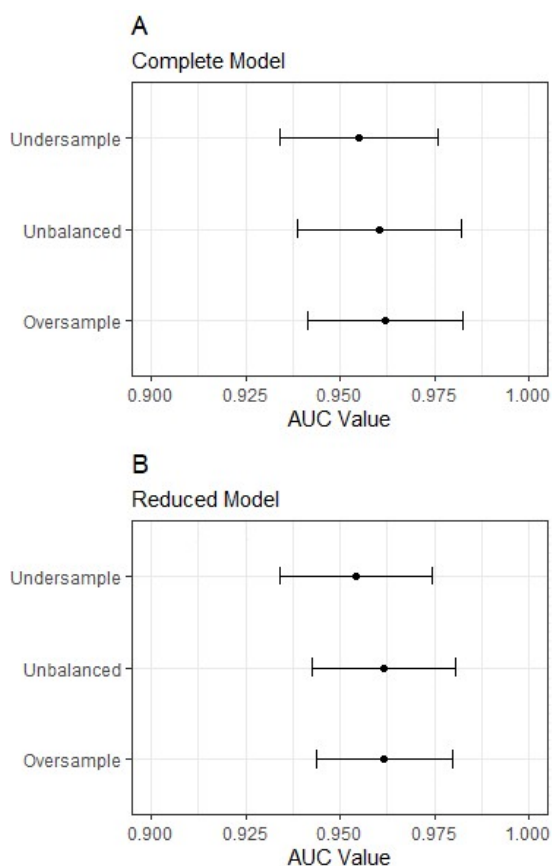


Figure 1: 95% confidence interval for AUC for both Complete (A) and Reduced (B) models.

The error rate along the construction of decision trees was also evaluated. In Figure 2, it is possible to observe that, from 200 trees, the error rates of the models stabilize. The models built with the undersampling approach presented higher fluctuations, while the oversampling model presented the lowest error rate, both for the Complete and Reduced models.

We additionally tested our proposed models and three other methods using an independent test set. Table 1 shows the performance results of the different

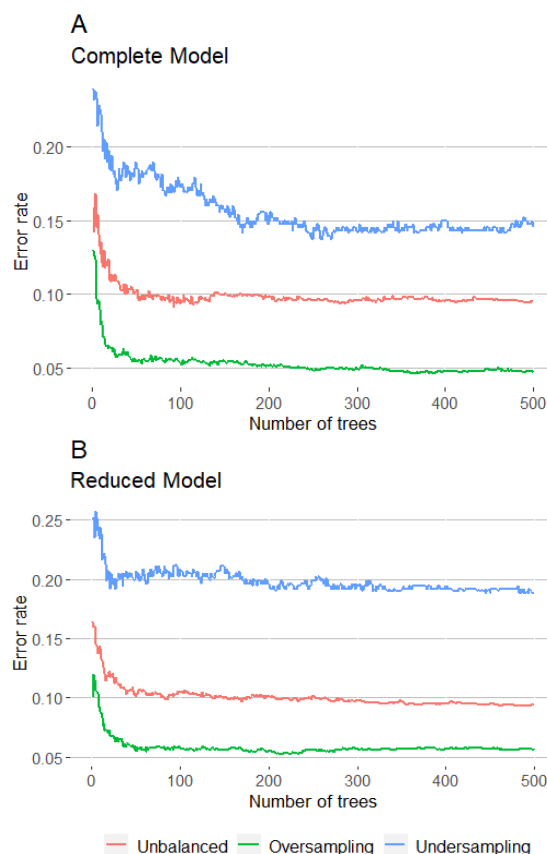


Figure 2: Error rate during the construction of forests for both Complete (A) and Reduced (B) models.

algorithms. All methods achieved a specificity higher than 87%, with *geno2pheno* 2.5% showing the best performance (98.2%). Nevertheless, the sensitivity (73.3%) was lower compared to the other approaches. Our Complete Model with an undersampling strategy (90.1%) attained the highest sensitivity. The accuracy of all approaches ranged from 87.4% to 93.0%. Complete Model with oversampling and Reduced model with no balancing showed the highest MCC value (both with 0.796 score).

By comparing the two approaches that use the random forest algorithms (our models and T-CUP 2.0) it is possible to observe that our classifiers (Complete with oversampling, Reduced with oversampling and Reduced with undersampling) presented a higher performance for the three evaluated measures.

4 DISCUSSION

In the current study, we developed random forest-based approaches for predicting HIV-1 coreceptor

Table 1: Performance comparison of different prediction methods. Highest values for each measure are marked in bold.

Model	Se	Sp	Acc	MCC
Comp Unb	90.1	91.4	91.2	0.759
Comp Over	84.2	94.0	92.0	0.796
Comp Under	88.1	92.5	91.6	0.709
Red Unb	88.1	92.7	91.8	0.796
Red Over	87.1	94.3	92.8	0.753
Red Under	84.2	93.8	91.8	0.722
g2p 10%	86.1	87.8	87.4	0.671
g2p 5%	79.2	93.8	90.7	0.721
g2p 2.5%	73.3	98.2	93.0	0.778
WebPSSM	68.3	93.5	88.3	0.635
T-CUP 2.0	82.2	93.2	90.9	0.733

usage. We used two strategies to enhance our model performance: methods for balancing training data and zero or near-zero variance predictors removal. In total, six approaches were evaluated.

The proposed models performed very similarly to each other. This information corroborates previous studies that showed the strength of the random forest algorithm, even with unbalanced training data (Dittman, Khoshgoftaar, & Napolitano, 2015). However, the error rate of the models suggests that the oversampling approach was more adequate for this type of problem.

T-CUP 2.0 uses random forest algorithm, like our model. However, the data preparation for our model showed influence in its performance. Perhaps, the choice of Engelman hydrophobicity scale, instead of Kyte-Doolittle scale (Kyte & Doolittle, 1982), used for T-CUP 2.0. Therefore, the evaluation of numerical conversion of amino acids should be considered as an important factor for the development of genotypic models.

Regarding the number of explanatory variables in the model, it was possible to observe that both approaches (Complete and Reduced models) had comparable performance, suggesting that there is no great difference between these models. However, on behalf of parsimony, it is preferable to have a model with minimal explanatory variables. Therefore, the Reduced Model is more suitable to our objective.

The charts also showed that the models barely change their error rate after 200-250 trees in the forest, except for the undersampled models. Thus, the model can perform optimally with a smaller number of trees, streamlining the process of prediction.

It is very significant that our model has achieved the highest sensitivity values. Although geno2pheno algorithm achieved the best performance in specificity and accuracy, our models showed best values of MCC, a robust parameter for evaluation of any prediction method. Our main goal in this study was to enhance the ability of algorithms to predict viral specimens with X4 tropism. The Complete Model with no balancing showed sensitivity and specificity above 90%, which suit our model into the European guidelines on the clinical management of HIV-1 tropism testing (Vandekerckhove et al., 2011). Therefore, our studies are very promising to achieve a new and more accurate genotypic predictor.

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