Usage

Using our privacy preserving precision medicine software is easy. Simply follow the steps below.
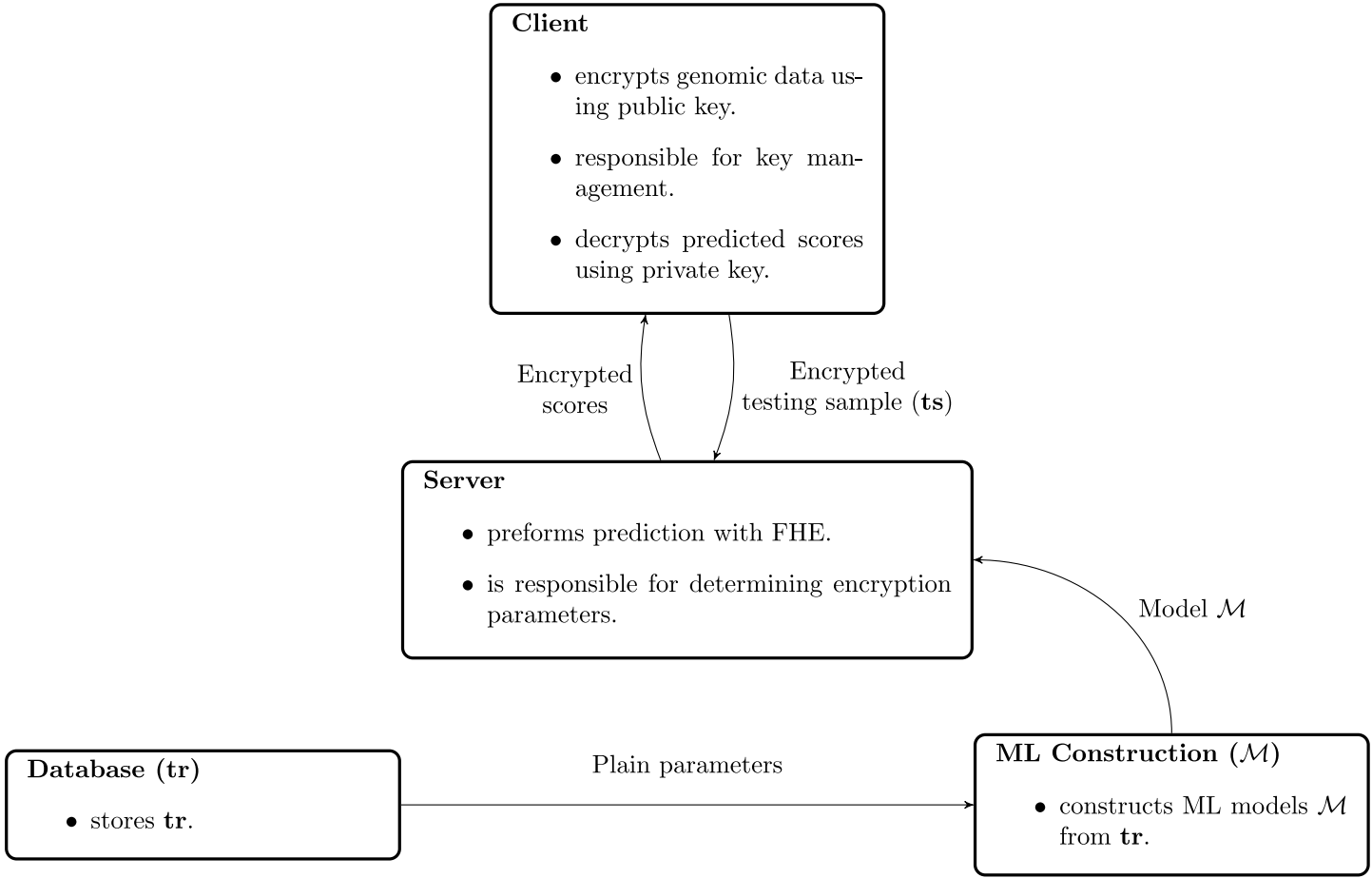
1. Download the client application from our downloads page
2. Create a CSV containing your test samples, with no column headers, where the ith row corresponds to the ith sample and the jth column corresponds to the jth feature, and place it in the same directory as the client applicaiton
3. Open a command line and run the client application by typing the name of the applicaiton, "MLE", and pressing enter
4. Follow the prompts that appear. Results will be saved in a file called Results.csv where the ith row corresponds to the ith sample and the kth column corresponds to the kth class

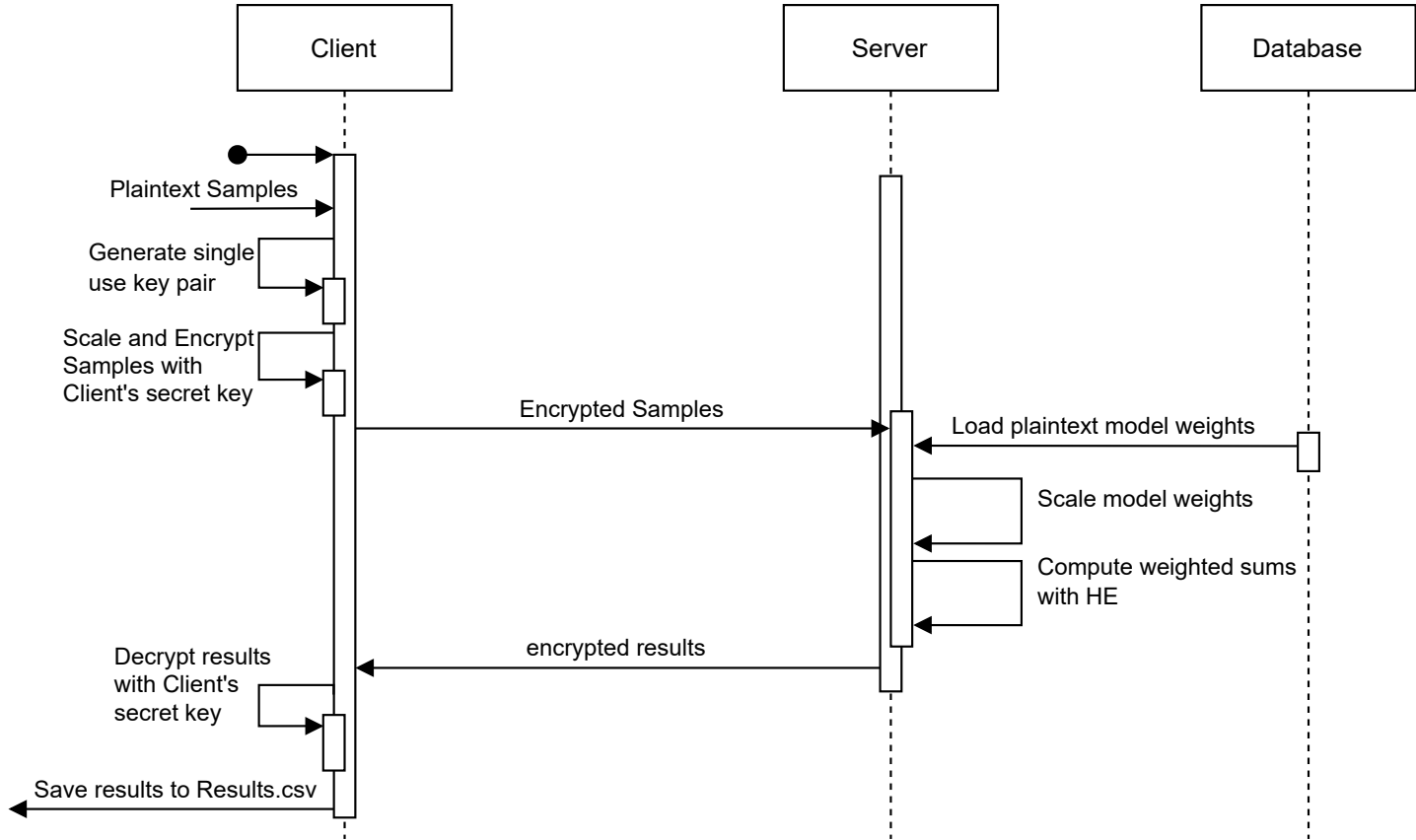The features used for the privacy preserving genomic analysis model are those used in Penson et al.

The classes with their corresponding index are:

0. Bladder Cancer
1. Breast Cancer
2. Cholangiocarcinoma
3. Colorectal Cancer
4. Endometrial Cancer
5. Esophagogastric Cancer
6. Gastrointestinal Stromal Tumor
7. Germ Cell Tumor
8. Glioma
9. Head and Neck Cancer
10. Melanoma

11. Mesothelioma
12. Neuroblastoma
13. Non Small Cell Lung Cancer
14. Ovarian Cancer
15. Pancreatic Cancer
16. Pancreatic Neuroendocrine Tumor
17. Prostate Cancer
18. Renal Cell Cancer
19. Small Cell Lung Cancer
20. Thyroid Cancer
21. Uveal Melanoma

Architecture:

In the current prototype, the client and server have a single interaction. The Client sends the encrpyted test samples along with the public key to the server, and the server returns the encrypted weighted sums, which are decrpyted on the server side using the client's private key. A new key pair is automatically generated for each interaction and disposed of after a single use. Therefore, the server never has access to the private key or the plain text sample data, only the encrypted sample data and the encrypted weighted sums. Below is a sequence diagram further illustrating this interaction

References:

Penson A, Camacho N, Zheng Y, et al. Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. JAMA Oncol. 2020;6(1):84–91. doi:10.1001/jamaoncol.2019.3985

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