**hiBRCApCR, predicting pCR for breast cancer subtypes**

**Basic information**

Version: 1.0.0  
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**Running environment**

The software hiBRCApCR version 1.0.0 was tested on the computer with Windows 10 operating system with 32GB memory. The programming environment was Python version 3.7.4rc1 (X86_64).

The software hiBRCApCR version 1.0.0 relied on the following Python packages to run:  
- numpy (version 1.11.1)  
- sympy (version 1.0)  
- xgboost (version 0.90)  
- scipy (version 0.18.1)  
- scikit-learn (from sklearn) (version 0.17.1)

**Command line syntax**

```
python hiBRCApCR-r1 <Subtype> <Size1> <Size2> <Size3>
```

- `<Subtype>`: one of the four subtypes of breast cancers, i.e., TN, HER2, LBP and LBN  
- `<Size1>`, `<Size2>` and `<Size3>` were the tumor sizes of the first three neoadjuvant chemotherapies in cm^2 (centimeter squared)

The prediction result 1 suggested that this patient may achieve pCR=1 after a total series of at least 6 neoadjuvant chemotherapies. Otherwise, this patient will have pCR=0 after the totally six or more treatments.