ORES Metrics Documentation

Disclaimer: No guarantee for the correctness of information / explanations / sources is given.

1 Crucial metrics: damaging-model

Examined metrics Quickview:

Metric	**Quick Definition**	**Value**
accuracy	Portion of correctly predicted data	$\frac{\texttt{TP+TN}}{\texttt{Total}}$
counts	Number of **F**&**T**-labels and predictions	
f1	Harmonic mean of recall and precision	$2 * \frac{\texttt{rec*prec}}{\texttt{rec+prec}}$
filter_rate	Portion of observations predicted to be negative	$1 - \texttt{match\_rate} = \frac{\texttt{TN+FN}}{\texttt{Total}}$
fpr	Probability of a false alarm	$\frac{\texttt{FP}}{\texttt{FP+TN}}$
match_rate	Portion of observations predicted to be positive	$\frac{\texttt{TP+FP}}{\texttt{Total}}$
pr_auc	Measure of classification performance	
precision	Ability to find only relevant cases	$\frac{\texttt{TP}}{\texttt{TP+FP}}$
rates	Proportion of **F**&**T**-labels to the total	
recall	Ability to find **all** relevant cases	$\frac{\texttt{TP}}{\texttt{TP+FN}}$
roc_auc	Measure of classification performance	
!f1	Negated f1	$2 * \frac{\texttt{!rec*!prec}}{\texttt{!rec+!prec}}$
!precision	Negated precision	$\frac{\texttt{TN}}{\texttt{TN+FN}}$
!recall	Negated recall	$\frac{\texttt{TN}}{\texttt{TN+FP}}$

For each metric (if possible) there will be:

1. The formula based on the **confusion matrix**

2. A definition

3. An intuitive explanation referring to the example introduced below

4. Its meaning based on the **loan threshold** representation by Google (Link)

5. Additional information (if necessary)

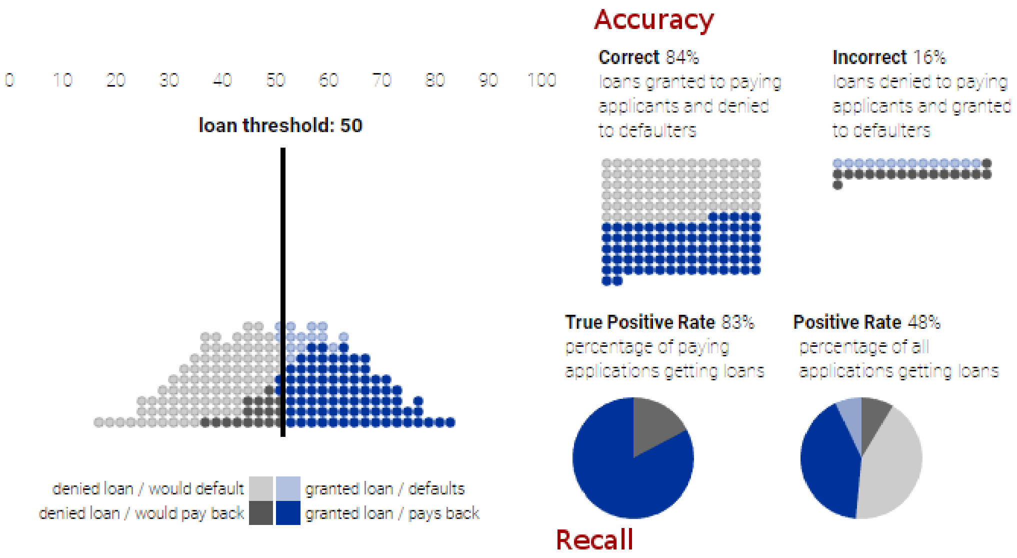
Explanations: References

- Confusion Matrix

		Actual	
		Positive	Negative
Predicted	Positive	**True Positive**	**False Positive**
	Negative	**False Negative**	**True Negative**

Abbreviations: **TP**, **FP**, **FN** and **TN**.

- Loan Threshold

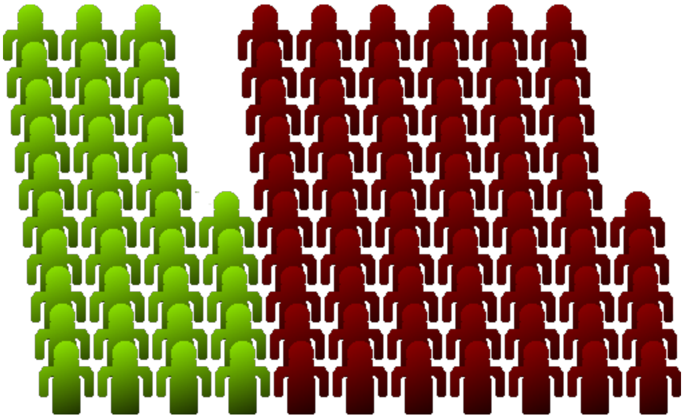


The example scenario

To ease the understanding, let's stick to the following scenario and refer to it for each metric:

- 100 people represent our total population
- 35% of our population is infected with disease X

  That leaves us with the following **labels**: **35** **positives** and **65** **negatives** (being tested for disease X;)



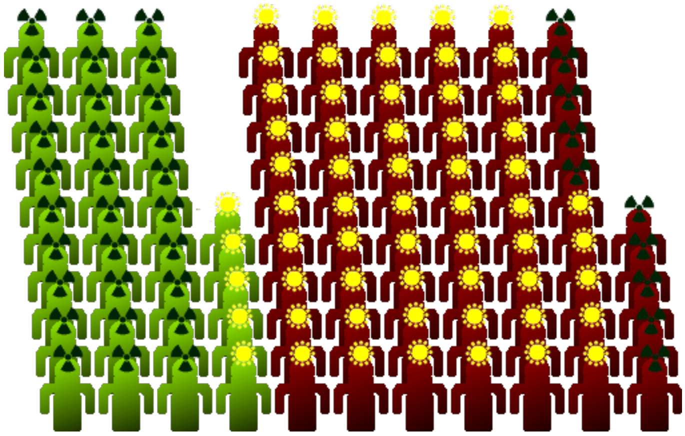
- A classifier is now supposed to classify every person of our population (based on their visible symptoms for example). This is the **prediction**:
  - If our algorithm says a person is infected, that person will be classified as a **positive**, and marked with radioactive symbol:

    ☢

  - If the prediction results in a **negative**, the person will be marked with a sun symbol:

    ☀

- The classifier may predict that:
  - out of the 35 infected people, **30** are infected (those 30 are what we call **true positives**) and **5** are not (those 5 are **false negatives**)
  - out of the 65 non infected people, **10** are infected (**false positives**) and **55** are not (**true negatives**)



true positive: infected and correctly predicted (**30**)

false negative: infected and incorrectly predicted (**5**)

true negative: not infected and correctly predicted (**55**)

false positive: not infected and incorrectly predicted (**10**)

Let's get started.

1.1 recall

1. $\frac{\texttt{TP}}{\texttt{TP+FN}}$

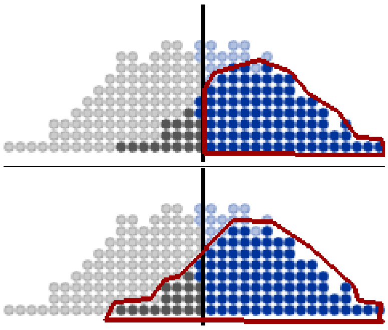
2. Recall (≡ true positive rate ≡ "sensitivity") is the ability of a model to find **all** relevant cases within the dataset.

3. Now, in our example scenario, the relevant cases are the infected people. We absolutely want to identify those: 🧍. The ability of the model to identify those depends on how many will be **correctly** predicted to be infected: ☢.

   In other words, we are looking for the ratio of correctly predicted to be infected people to all infected people.

   That leads to $\frac{\sum ☢}{\sum 🧍}$, with 🧍 $=$ ☢ $+$ ☀, which is equivalent to the formula in **1.**, if you replace the symbols with their confusion matrix counterpart according to the legend in **The example scenario**.

   In terms of numbers for our example that would be $\frac{30}{30+5} \approx 0.86$

4. 

1.2 precision

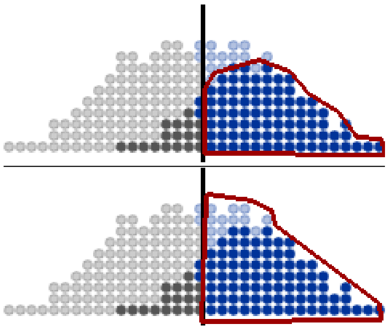
1. $\frac{\texttt{TP}}{\texttt{TP+FP}}$

2. Ability of the model to find **only** relevant cases within the dataset

3. Again, we take a look at the relevant cases, the infected people: 🧍. This time around though, we are **not** interested in the ratio of correctly predicted to be infected people to **all** infected people. Instead we want to know how good the model is at only predicting those to be infected,

that actually are. Therefore, we want the ratio of all 🟩 to all those predicted to be infected: 🟩 + 🟥

$$= \frac{\sum \text{🟩}}{\sum \text{🟩} + \sum \text{🟥}} = \frac{30}{30+10} = 0.75$$

4. 

1.3 f1

1. -

2. f1-Score, the harmonic mean of recall and precision, a metric from **0** (worst) to **1** (best), used to evaluate the accuracy of a model by taking into account recall and precision: $= 2 * \frac{\texttt{precision}*\texttt{recall}}{\texttt{precision}+\texttt{recall}}$

3. For our example model, that would result in $= 2 * \frac{0.75*\frac{30}{35}}{0.75+\frac{30}{35}} = 0.8$

4. -

5. <u>Additional information</u>: Compared to the simple average (of recall and precision), the harmonic mean punishes extreme values (e.g. precision 1.0 and recall 0.0 → average = 0.5, but f1 = 0). Also note that, even though the f1-score can theoretically take values up to 1.0, the hightest f1-score achieved by the damaging model for enwiki is 0.461.

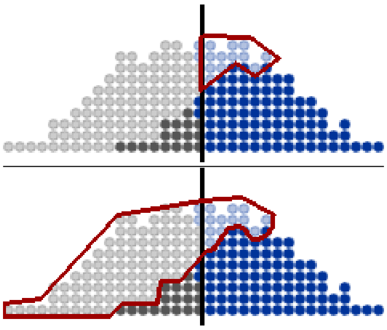
1.4 fpr

1. $\frac{\texttt{FP}}{\texttt{FP}+\texttt{TN}}$

2. The false positive rate is the probability of a false alarm.

3. In our example, a false alarm would obviously be labeling someone as infected, who isn't: 🧍. Now we just have to ask ourselves what portion of those, that, if they **were** incorrectly predicted as infected (because they **are not** infected: 🧍), **are** incorrectly predicted as infected? Hence, we are looking for the ratio of 🧍 to all non infected people: 🧍 + 🧍.

   $$= \frac{\sum 🧍}{\sum 🧍 + \sum 🧍} = \frac{10}{10+55} \approx 0.15$$

4. 

1.5 roc_auc

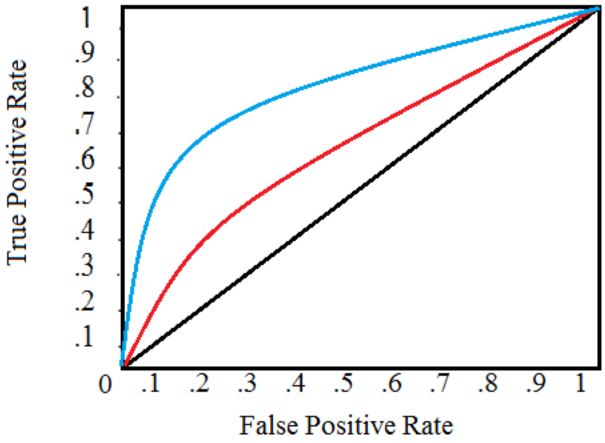
1. -

2. The **area under** the **curve** of the **ROC**-curve, a measure between 0.5 (worthless) and 1.0 (perfect: getting no FPs), is the probability of ranking a random positive higher than a random negative and serves as a measure of classification performance.

3. In our example, we haven't used the notion of threshold yet. For classifying people as infected or not, the classifier will evaluate multiple criteria and calculate the probability that a patient is infected. Many binary classifiers have the threshold at 0.5, meaning that, if the probability of a true outcome is higher than 50%, it is classified as a positive; or in our case as an infected patient. Depending on the situation however, it can be useful to move that threshold.

   The receiver operating characteristic (ROC) curve is used to visualize the performance of a classifier

The ROC curve plots the TPR versus FPR as a function of the model's threshold for classifying a positive.



Increasing the threshold → moving up a curve (≡ model) to the top right corner, where all data is predicted as positive (threshold = 1.0) and vice versa

Our best case is a curve hugging the top left corner, because that means a low **fpr** and high **tpr**, which, again, means a lot of positives and few negatives on the right of the thresholds, looking at class curves like the **Loan Threshold** one.

Assuming that we have had a threshold of 0.5 all along to get the previous results, one point on our ROC curve would be: $(0.15, 0.86) = (\texttt{fpr}, \texttt{tpr})$.

We would now have to change the thresholds, look at the (probably) changed resulting data (new numbers in terms of positives and negatives, as well as **TP**, **FN**, **TN** and **FP**) and then plot every resulting $(\texttt{fpr}, \texttt{tpr})$-point in order to plot the full ROC curve.

We would most certainly like to quantify this visualized performance of our binary classifier, which is why we calculate the area under the curve (**auc**) of the ROC curve.

4. -

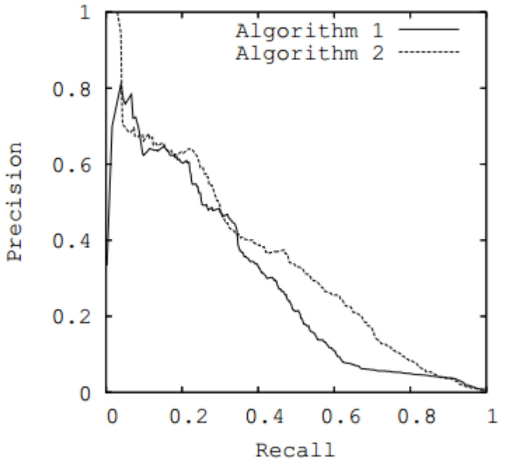
5. Additional information: We can think of AUC as representing the probability that a classifier will rank a randomly chosen positive observation higher than a randomly chosen negative observation. That's why **roc_auc** is a useful metric even for datasets with highly unbalanced classes. (Source)

1.6 pr_auc

1. -

2. Similarly to the **roc_auc**, the area under the precision recall curve **pr_auc** evaluates a classifiers performance. The main difference, however, is that the **pr_auc** does not make use of **true negatives**. It is therefore favourable to use **pr_auc** over **roc_auc** if true negatives are unimportant to the general problem or if there are a lot more negatives than positives.

   The PR-curve plots the Precision versus the Recall:

   Instead of the top left corner for the ROC-curve, here, we want our curve to reach the top right corner for our classifier to be perfect.

   The following scenario provides a good example (Source 1 and Source 2) of a case where PR is superior to ROC:

   - Out of 1 million documents, we want to find the 100 relevant ones.
   - The task is accomplished by two different algorithms:
     (a) 100 retrieved documents, 90 relevant
     (b) 2000 retrieved documents, 90 relevant
   - Algorithm (a) is obviously preferable.
   - We know that ROC- and PR-curves both plot coordinates with `tpr` = `recall` as one dimension. Now the question is: how do they differ in the other dimension, when plotting both algorithms?

- In all cases $\texttt{tpr} = \texttt{recall} = 0.9$. We also have:
  (a) $\texttt{TN} = 999890$ and $\texttt{FP} = 10$
  (b) $\texttt{TN} = 997990$ and $\texttt{FP} = 1910$
- ROC:
  (a) $\texttt{fpr} = \frac{\texttt{FP}}{\texttt{FP+TN}} = \frac{10}{10+999890} = 0.00001$
  (b) $\texttt{fpr} = \frac{1910}{1910+997990} = 0.00191$

  Having retrieved many more documents, and therefore having many more **false positives**, algorithm (b) has a higher **fpr** than algorithm (a).

  The **fpr** also takes into account the vast amount of **true negatives** though, which is why the difference between the two **fpr**s is still quite small: 0.0019.
- PR:
  (a) $\texttt{precision} = \frac{\texttt{TP}}{\texttt{TP+FP}} = \frac{90}{90+10} = 0.9$
  (b) $\texttt{precision} = \frac{90}{90+1910} = 0.045$

  Not accounting for **true negatives**, the **precision** is not affected by the relative imbalance.

  We are presented a remarkable difference of 0.855.
- To close on this topic, not the following (by Randy C): "Obviously, those are just single points in ROC and PR space, but if these differences persist across various scoring thresholds, using ROC AUC, we'd see a very small difference between the two algorithms, whereas PR AUC would show quite a large difference."

3. Similarly to the **roc_auc**, the point on the PR curve of our example for the standard threshold of 0.5 would be: $(\texttt{precision}, \texttt{recall}) = (0.75.0.86)$.

4. -

1.7 accuracy

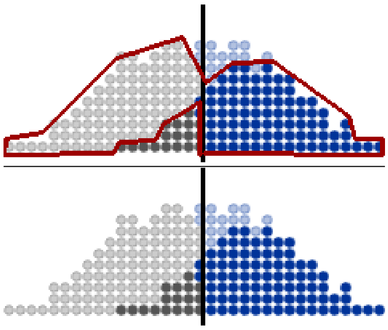
1. $\frac{\texttt{TP+TN}}{\texttt{Total}}$

2. Accuracy measures the portion of correctly predicted data

3. In our example scenario, this is equal to asking ourselves *out of all patients, what's the portion of correctly predicted cases?* The correctly

predicted cases are infected patients, predicted to be infected (🟩), and non infected patients, predicted not to be infected (🟥). This wanted proportion results in:

$$=\frac{\sum\text{🟩}+\sum\text{🟥}}{\sum\text{🟩}+\sum\text{🟥}}=\frac{30+55}{35+65}=0.85$$

4. 

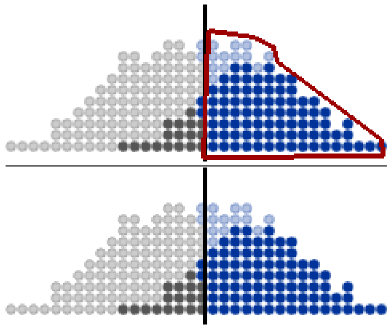
1.8 match_rate

1. $\frac{\texttt{TP+FP}}{\texttt{Total}}$

2. The match rate is the proportion of observations matched/not-matched, meaning the ratio of observations predicted to be positive to the total of observations.

3. Concerning our example, this would be equal to wanting to know what portion of the population was predicted to be infected. Those groups are: 🟩 and 🟥.

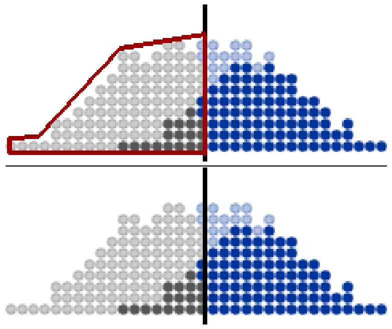
$$=\frac{\sum\text{🟩}+\sum\text{🟥}}{\sum\text{🟩}+\sum\text{🟥}}=\frac{30+10}{35+65}=0.4$$

4. 

1.9 filter_rate

1. $1 - \texttt{match\_rate} = \frac{\texttt{TN+FN}}{\texttt{Total}}$
2. The filter rate is the proportion of observations filtered/not-filtered, meaning the ratio of observations predicted to be negative to the total of observations. This is the complement of the match rate.
3. In our example scenario, this would be equal to wanting to know what portion of the population was predicted not to be infected.

$$= \frac{\sum \text{🟥} + \sum \text{🟩}}{\sum \text{🟩} + \sum \text{🟥}} = \frac{55+5}{35+65} = 0.6 = 1 - \texttt{match\_rate}$$

4. 

1.10 counts

1.
   - **labels**:
     - false: $\texttt{TN} + \texttt{FP}$
     - true: $\texttt{TP} + \texttt{FN}$
   - **n**: `Total`
   - **predictions**:
     - false:

        * false: `TN`
        * true: `FP`
    - true:
        * false: `FN`
        * true: `TP`

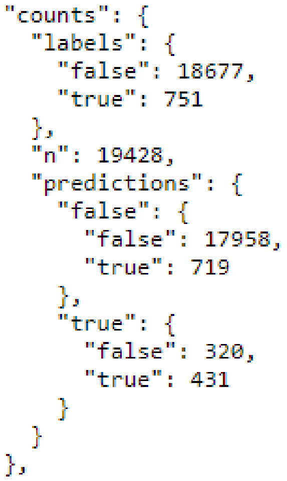
2. - **labels**: The number of edits (*manually*) labeled as *false* and *true*: these values represent the **actual** positives and negatives.
   - **n**: The sample size; total number of edits taken into account
   - **predictions**: edits ...
     - false: ... actually being false ...
       * false: ... and predicted to be false
       * true: ... but predicted to be true
     - true: ... actually being true ...
       * false: ... but predicted to be false
       * true: ... and predicted to be true

3. Concerning our example:
   - **labels**:
     - false (non infected people): + $= 55 + 10 = 65$
     - true (infected people): + $= 30 + 5 = 35$
   - **n** (Total): 100
   - **predictions**:
     - false (non infected people ...)
       * false (... and predicted not to be infected): $= 55$
       * true (... but predicted to be infected): $= 10$
     - true (infected people ...)
       * false (... predicted not to be infected): $= 5$
       * true (... predicted to be infected): $= 30$

4. -

5. <u>Additional information</u>:

When calling the enwiki damaging model for example (Link), you will get the following output for counts:



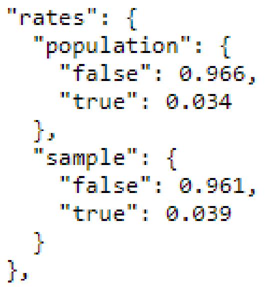
```
"counts": {
  "labels": {
    "false": 18677,
    "true": 751
  },
  "n": 19428,
  "predictions": {
    "false": {
      "false": 17958,
      "true": 719
    },
    "true": {
      "false": 320,
      "true": 431
    }
  }
},
```

⇒ e.g. out of 18677 edits that were labeled as *false*, 719 were false positives

1.11 rates

1. - false: $\frac{\texttt{counts\_labels\_false}}{\texttt{counts\_n}}$
   - true: $\frac{\texttt{counts\_labels\_true}}{\texttt{counts\_n}}$
2. The rates simply give us the proportion of edits labeled as false or true to the total number of edits taken into account.
3. For the example scenario:
   - false (proportion of infected people to the total number of people tested): $\frac{\sum \text{🟥}}{100} = \frac{65}{100} = 0.65$
   - true (proportion of infected people to the total number of people tested): $\frac{\sum \text{🟩}}{100} = \frac{35}{100} = 0.35$
4. -
5. <u>Additional information</u>:

   Calling the API the same way as for **counts** (Link), we get:



```
"rates": {
  "population": {
    "false": 0.966,
    "true": 0.034
  },
  "sample": {
    "false": 0.961,
    "true": 0.039
  }
},
```

The number of edits taken into account for **sample** equals the **n** from **counts** = 19428.

Now we see that, also looking at the output under **counts**, *rates_sample_false*: $0.961 = \frac{18677}{19428}$.

Note that we are shown results for "population" and "sample". There is a significant number of bot edits and edits that don't need reviewing (admins, autopatrolled users). The **sample** of edits does not contain any of those.

1.12 !<metric>

- Any <metric> with an exclamation mark is the same metric for the negative class
- e.g. recall $= \frac{\texttt{TP}}{\texttt{TP}+\texttt{FN}} \Rightarrow$ **!**recall $= \frac{\texttt{TN}}{\texttt{TN}+\texttt{FP}}$
- Example usage: find all items that are not "E" class (itemquality model) → look at **!**recall for "E" class.

1.12.1 Existing !<metric>s

- !f1
- !precision
- !recall