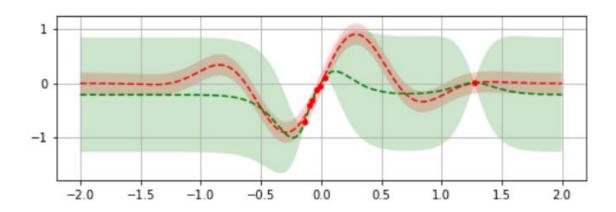




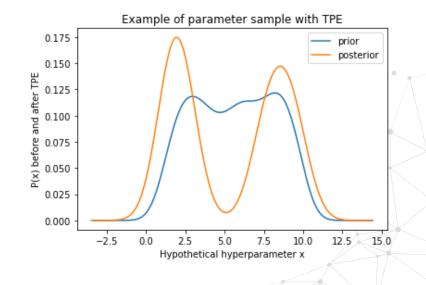
TPE
Why tree
structured?

GP vs TPE

- Surrogate model for f(x) P(y|x)
- f(x) takes a value given all hyperparameters



- Surrogate model for P(x | y)
- 1 probability per hyperparameters
 - Hyperparameter spaces can be nested





Why Tree-structured?

Because TPE estimates a distribution for each hyperparameter, it will only estimate distributions for parameters when they "exist".

```
space = hp.choice('classifier_type', [
    'type': 'svm',
    'C': hp.lognormal('svm_C', 0, 1),
    'kernel': hp.choice('svm_kernel', [
        {'ktype': 'linear'},
        {'ktype': 'RBF', 'width': hp.lognormal('svm rbf width',
0, 1)
        ]),
    'type': 'dtree',
    'criterion': hp.choice('dtree criterion', ['gini',
'entropy']),
    'max_depth': hp.choice('dtree_max_depth',
        [None, hp.qlognormal('dtree_max_depth_int', 3, 1, 1)]),
    'min samples split':
hp.qlognormal('dtree_min_samples_split', 2, 1, 1),
```

Node 1

Parameters only make sense inside each Node

Node 2

Why Tree-structured?

Because TPE estimates a distribution for each hyperparameter, it will only estimate distributions for parameters when they "exist".

```
space = hp.choice('classifier_type', [
    'type': 'svm',
    'C': hp.lognormal('svm_C', 0, 1),
    'kernel': hp.choice('svm_kernel', [
        {'ktype': 'linear'},
                                                Sub - Node 1
                                                                                            Node 1
        {'ktype': 'RBF', 'width': hp.lognormal('svm_rbf_width',
                                                                        Sub - Node 2
0, 1)
        ]),
                                                                                          Parameters only make
                                                                                          sense inside each Node
    'type': 'dtree',
    'criterion': hp.choice('dtree criterion', ['gini',
'entropy']),
                                                                                            Node 2
    'max_depth': hp.choice('dtree_max_depth',
        [None, hp.qlognormal('dtree_max_depth_int', 3, 1, 1)]),
    'min samples split':
hp.qlognormal('dtree_min_samples_split', 2, 1, 1),
```



THANK YOU

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