

Progress update

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DBSSE

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- W-L implementation
- Go through MMD code

- Not much to optimize there.

Weisfeiler-Lehmann kernel

- Computing $\phi(G)$ needs to be done explicitly and can be done independently (and in parallel) prior to computing $K_{WL} = \phi(G)^T \phi(G')$
- How to compute $\phi(G)$? `networkx` has a function called `weisfeiler_lehman_subgraph_hashes`.
- Since we don't care about the order in the resulting $K_{WL} = \phi(G)^T \phi(G')$, we can list each product that needs to be done and execute them in parallel as well.

Weisfeiler-Lehmann kernel

What does the implementation look like?

```
def set_weisfeiler_lehman_hashes(  
    self, graph_type: str, n_iter: int  
) -> None:  
    hashes = dict(  
        Counter(  
            flatten_lists(  
                list(  
                    nx.weisfeiler_lehman_subgraph_hashes(  
                        self.graphs[graph_type],  
                        node_attr="residue",  
                        iterations=n_iter,  
                    ).values()  
                )  
            )  
        )  
    )  
    self.descriptors[graph_type]["weisfeiler-lehman-hist"] = hashes
```

Figure 1: Setting the hash histogram for each protein

Weisfeiler-Lehmann kernel

What does the implementation look like?

```
def compute_prehashed_kernel_matrix(
    self, X: Iterable, Y: Union[Iterable, None]
) -> Iterable:
    def parallel_dot_product(lst: Iterable) -> Iterable:
        res = list()
        for x in lst:
            res.append(dot_product(x))
        return res

    def dot_product(dict1: dict, dict2: dict) -> int:
        running_sum = 0
        # 0 * x = 0 so we only need to iterate over common keys
        for key in set(dict1.keys()).intersection(dict2.keys()):
            running_sum += dict1[key] * dict2[key]
        return running_sum

    if Y == None:
        Y = X

    # It's faster to process n_jobs lists than to have one list and
    # dispatch one item at a time.
    iters = list(chunks(list(itertools.product(X, Y)), self.n_jobs))

    return flatten_lists(
        distribute_function(
            parallel_dot_product,
            iters,
            "Dot product of elements in matrix",
            n_jobs=self.n_jobs,
        )
    )
```

Figure 2: Computing the dot product of the feature maps in parallel.

Weisfeiler-Lehmann kernel

How does it perform?

```
(proteingnnmetrics)
~/Documents/Git/msc_thesis/exploring/kernel_exploration on main 11:16:39
$ python kernel_matrix_computations.py
python kernel_matrix_computations.py
Data path: /Users/philiphartout/Documents/Git/msc_thesis/data
Loading proteins from /Users/philiphartout/Documents/Git/msc_thesis/data/.cache/sample_human_proteome_alpha_fold
### Grakel Implementation ###
Function Name      :compute_naive_kernel
Time               :24.521407292 seconds
Function Name      :compute_naive_kernel
Current memory usage:0.419422MB
Peak              :202.385493MB
### Custom Implementation *without* precomputed W-L hashes ###
Computing Weisfeiler-Lehman Hashes: 100%|
Dot product of elements in matrix: 100%| 100/100 [00:05<00:00, 17.78it/s]
Function Name      :compute_hashes_then_kernel
Time               :7.004050707999998 seconds
Function Name      :compute_hashes_then_kernel
Current memory usage:434.53531MB
Peak              :478.530507MB
### Custom Implementation *with* precomputed W-L hashes ###
Dot product of elements in matrix: 100%| 6/6 [00:01<00:00, 4.44it/s]
Function Name      :compute_kernel_using_precomputed_hashes
Time               :1.3574982499999999 seconds
Function Name      :compute_kernel_using_precomputed_hashes
Current memory usage:0.300306MB
Peak              :44.184051MB
```

Figure 3: Performance and memory footprint of grakel vs. custom. Both are done with 10 iterations of the W-L hashing step.

MMD implementations are different, why is the estimate more useful?

```
def mmd(X, Y, kernel, estimate_variance=False):
    """Calculate MMD between two sets of samples, using a kernel.
    """
    X = np.asarray(X)
    Y = np.asarray(Y)

    # Following the original notation of the paper
    m = X.shape[0]
    n = Y.shape[0]

    K_XX = kernel(X, X)
    K_YY = kernel(Y, Y)
    K_XY = kernel(X, Y)

    # We could also skip diagonal elements in the calculation above but
    # this is more computationally efficient.
    np.fill_diagonal(K_XX, 0)
    np.fill_diagonal(K_YY, 0)

    k_XX = np.sum(K_XX)
    k_YY = np.sum(K_YY)
    k_XY = np.sum(K_XY)

    mmd = 1 / (m * (m - 1)) * k_XX \
        + 1 / (n * (n - 1)) * k_YY \
        - 2 / (m * n) * k_XY

    if estimate_variance:
        var = mmd_variance_estimate(K_XX, K_YY, K_XY)
        return mmd, var

    return mmd
```

Figure 4: MMD estimate, from ICLR graphgeneval

```
class MaximumMeanDiscrepancy(DistanceFunction):
    """Implements maximum mean discrepancy"""

    def __init__(self, kernel: Kernel):
        self.kernel = kernel

    def evaluate(self, X: Any, Y: Any) -> float:
        Xt = check_dist(X)
        Yt = check_dist(Y)

        # Following the original notation of the paper
        m = len(Xt)
        n = len(Yt)

        K_XX = self.kernel.transform(Xt)
        K_YY = self.kernel.transform(Yt)
        K_XY = self.kernel.transform(Xt, Yt)

        # We could also skip diagonal elements in the calculation above but
        # this is more computationally efficient.

        k_XX = np.sum(K_XX)
        k_YY = np.sum(K_YY)
        k_XY = np.sum(K_XY)

        mmd = 1 / (m ** 2) * k_XX + 1 / (n ** 2) * k_YY - 2 / (m * n) * k_XY

        return math.sqrt(mmd)
```

Figure 5: MMD computation, from proteinggnmetrics

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