```
In [1]: import torch
        import torch geometric
        import networkx as nx
        import matplotlib.pyplot as plt
        from torch geometric.datasets import Planetoid
        from torch geometric.nn import GCNConv
        from torch geometric.transforms import NormalizeFeatures
        from sklearn.manifold import TSNE
        from sklearn.metrics import accuracy score
        dataset = Planetoid(root='/tmp/Cora', name='Cora', transform=NormalizeFeatures())
        data = dataset[0]
       Downloading https://github.com/kimiyoung/planetoid/raw/master/data/ind.cora.x
       Downloading https://github.com/kimiyoung/planetoid/raw/master/data/ind.cora.tx
       Downloading https://github.com/kimiyoung/planetoid/raw/master/data/ind.cora.allx
       Downloading https://github.com/kimiyoung/planetoid/raw/master/data/ind.cora.y
       Downloading https://github.com/kimiyoung/planetoid/raw/master/data/ind.cora.ty
       Downloading https://github.com/kimiyoung/planetoid/raw/master/data/ind.cora.ally
       Downloading https://github.com/kimiyoung/planetoid/raw/master/data/ind.cora.graph
       Downloading https://github.com/kimiyoung/planetoid/raw/master/data/ind.cora.test.index
       Processing...
       Done!
In [4]: import torch.nn.functional as F
```

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```
In [5]: class GCN(torch.nn.Module):
            def init (self):
                super(GCN, self).__init__()
                self.conv1 = GCNConv(dataset.num features, 16)
                self.conv2 = GCNConv(16, dataset.num_classes)
            def forward(self, data):
                x, edge_index = data.x, data.edge_index
                x = self.conv1(x, edge_index)
                x = torch.relu(x)
                x = F.dropout(x, p=0.5, training=self.training)
                x = self.conv2(x, edge_index)
                return torch.log_softmax(x, dim=1)
In [6]: device = torch.device('cpu')
        model = GCN().to(device)
        data = data.to(device)
        optimizer = torch.optim.Adam(model.parameters(), lr=0.01, weight decay=5e-4)
        criterion = torch.nn.CrossEntropyLoss()
        def train():
            model.train()
            optimizer.zero_grad()
            out = model(data)
            loss = criterion(out[data.train mask], data.y[data.train mask])
            loss backward()
            optimizer.step()
        def test():
            model.eval()
            out = model(data)
            pred = out.argmax(dim=1)
            correct = pred[data.test mask] == data.y[data.test mask]
            acc = int(correct.sum()) / int(data.test mask.sum())
            return acc, pred
        for epoch in range(200):
            train()
        acc, pred = test()
        print(f'Accuracy: {acc:.4f}')
```

code

Accuracy: 0.8190

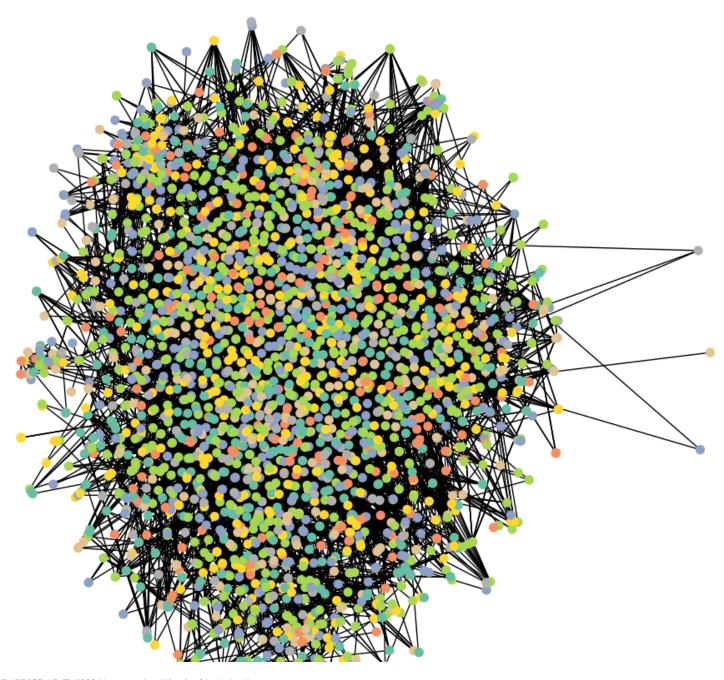
```
In [8]: pred

Out[8]: tensor([3, 4, 4, ..., 1, 3, 3])

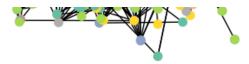
In [7]: def plot_graph(pred):
        G = nx.Graph()
        edge_index = data.edge_index.cpu().numpy()
        for i in range(edge_index.shape[1]):
            G.add_edge(edge_index[0, i], edge_index[1, i])

        pos = TSNE(n_components=2).fit_transform(data.x.cpu().numpy())
        plt.figure(figsize=(10, 10))
        nx.draw(G, pos=pos, node_color=pred.cpu().numpy(), cmap=plt.get_cmap("Set2"), node_size=50)
        plt.show()

        plot_graph(pred)
```



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code

```
In [9]: from torch_geometric.datasets import TUDataset
         from torch geometric.loader import DataLoader
         from torch_geometric.nn import global_mean_pool
         imdb_dataset = TUDataset(root='/tmp/IMDB-BINARY', name='IMDB-BINARY')
         enzyme dataset = TUDataset(root='/tmp/ENZYMES', name='ENZYMES')
        Downloading https://www.chrsmrrs.com/graphkerneldatasets/IMDB-BINARY.zip
        Processing...
        Done!
        Downloading https://www.chrsmrrs.com/graphkerneldatasets/ENZYMES.zip
        Processing...
        Done!
In [15]: def preprocess dataset(dataset):
             for data in dataset:
                 if data.x is None:
                     data.x = torch.ones((data.num_nodes, 1), device=data.edge_index.device)
             return dataset
         imdb dataset = preprocess dataset(imdb dataset)
         enzyme_dataset = preprocess_dataset(enzyme_dataset)
In [20]: imdb dataset
Out[20]: IMDB-BINARY(1000)
In [25]: class GCNGraph(torch.nn.Module):
             def __init__(self, num_node_features, num_classes):
                 super(GCNGraph, self). init ()
                 self.conv1 = GCNConv(num node features, 64)
                 self.conv2 = GCNConv(64, 64)
                 self.fc = torch.nn.Linear(64, num classes)
```

```
def forward(self, data):
    if data.x is None:
        data.x = torch.ones((data.num_nodes, 1), device=data.edge_index.device)

    x, edge_index, batch = data.x, data.edge_index, data.batch
    x = self.conv1(x, edge_index)
    x = torch.relu(x)
    x = self.conv2(x, edge_index)
    x = global_mean_pool(x, batch) # Aggregate graph-level features
    x = F.dropout(x, p=0.5, training=self.training)
    x = self.fc(x)
    return torch.log_softmax(x, dim=1)
```

```
In [24]: def train_graph_model(dataset, epochs=100):
             device = torch.device('cuda' if torch.cuda.is_available() else 'cpu')
             num_node_features = dataset.num_features if dataset.num_features > 0 else 1
             loader = DataLoader(dataset, batch size=32, shuffle=True)
             model = GCNGraph(num_node_features, dataset.num_classes).to(device)
             optimizer = torch.optim.Adam(model.parameters(), lr=0.01)
             criterion = torch.nn.CrossEntropyLoss()
             for epoch in range(epochs):
                 model.train()
                 for batch in loader:
                     batch = batch.to(device)
                     optimizer.zero grad()
                     out = model(batch)
                     loss = criterion(out, batch.y)
                     loss backward()
                     optimizer.step()
             model.eval()
             correct = 0
             for batch in loader:
                 batch = batch.to(device)
                 out = model(batch)
                 pred = out.argmax(dim=1)
                 correct += int((pred == batch.y).sum())
```

```
accuracy = correct / len(dataset)
  return accuracy

imdb_acc = train_graph_model(imdb_dataset)
enzyme_acc = train_graph_model(enzyme_dataset)

print(f'IMDB-BINARY Accuracy: {imdb_acc:.4f}')
print(f'ENZYMES Accuracy: {enzyme_acc:.4f}')
```

IMDB-BINARY Accuracy: 0.5900
ENZYMES Accuracy: 0.2917

Interesting about reading

I found the fast approximation of convolutions on graphs interesting. How they got from equation 3 to equation 7/8. Going from direct spectral graph convolution to approximating them using Chebyshev's polynomials allowed for faster computation and having local convolution filters instead of graph wide filters.

Difficulty Understanding

I had difficulty understanding and visualizing some of the math, especially when it comes to why the approximations are valid, or even its necessary to go over direct spectra graph convolutions when the eigenvectors in the actual layers are lost as you doing spatial instead of spectral

In []: