```
In [1]: # Configure matplotlib.
        %matplotlib inline
In [2]: # Import our package.
        import sys, importlib
        sys.path.append("/home/ubuntu/cell counting")
        from src import dataset, visualization, preprocess, metric
        from src.model import model
        from src.model import neural net
        from src.model.segment counting.convnet1 import convnet1
        /home/ubuntu/anaconda3/envs/tensorflow_p36/lib/python3.6/importlib/_bootstrap.py
        :219: RuntimeWarning: compiletime version 3.5 of module 'tensorflow.python.frame
        work.fast tensor util' does not match runtime version 3.6
          return f(*args, **kwds)
In [ ]: # (if changes are made) Re-import our package.
        for module in (dataset, visualization, preprocess, metric, model, neural net, conv
        net1):
            importlib.reload(module)
In [3]: # Load the microbia segments dataset.
        def image path getter(example metadata):
            return "/home/ubuntu/cell counting/data/microbia segments/raw/" + example meta
        data["Segment Relative Path"]
        def mask path getter(example metadata):
            return "/home/ubuntu/cell counting/data/microbia segments/raw/" + example meta
        data["Binary Segment Relative Path"]
        def label getter(example metadata):
            return example metadata["data"]["segment type"]["data"]
        microbia segments = dataset.Dataset(1000)
        microbia segments.load images masks labels from json(
            "/home/ubuntu/cell counting/data/microbia segments/raw/enumeration segments.js
        on", image path getter,
            mask path getter, label getter, (128, 128))
```

```
In [4]: # Plot a few batches.
           for batch in range(3):
               inputs, outputs = microbia segments.get batch(8)
               visualization.show image grid(inputs, 1, 8, 2.5, 16, "Batch #{0} Images".forma
                     ["cell count: {0}".format(count + 1 if count != 7 else "<OUTLIER>") for co
          unt in outputs])
                                                      Batch #0 Images
             cell count: 1
                          cell count: 1
                                       cell count: 2
                                                                 cell count: 3
                                                                              cell count: 2
                                                                                           cell count: 1
                                                                                                       cell count: 1
                                                      Batch #1 Images
                                       cell count: 1
                                                                 cell count: 3
                                                                              cell count: 1
                                                                                          cell count: 1
             cell count: 2
                          cell count: 1
                                                    cell count: 1
                                                      Batch #2 Images
                                                                cell count: 4
             cell count: 4
                          cell count: 3
                                       cell count: 1
                                                    cell count: 1
                                                                              cell count: 1
                                                                                          cell count: 2
                                                                                                       cell count: 2
In [5]:
          # Make the labels one-hot.
          def to one hot(examples):
               inputs, outputs = examples
               outputs = preprocess.one hot encode(outputs, 7)
               return inputs, outputs
          microbia segments.map batch(to one hot)
In [6]: # Split the dataset.
          train, test = microbia segments.split(0.1)
In [7]: # Create the net.
          import tensorflow as tf
          net = convnet1.ConvNet1("saves/17-12-05-AM-08-14", 120)
          INFO:tensorflow:Using config: {'_model_dir': 'saves/17-12-05-AM-08-14', '_tf_ran dom_seed': None, '_save_summary_steps': 100, '_save_checkpoints_steps': None, '_save_checkpoints_secs': 120, '_session_config': None, '_keep_checkpoint_max': 2,
          '_keep_checkpoint_every_n_hours': 10000, '_log_step_count_steps': 100, '_service
          ': None, '_cluster_spec': <tensorflow.python.training.server_lib.ClusterSpec obj
          ect at 0x7f83b688dc88>, '_task_type': 'worker', '_task_id': 0, '_master': '', '_
```

is_chief': True, '_num_ps_replicas': 0, '_num_worker_replicas': 1}

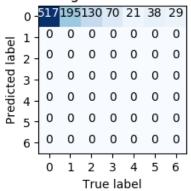
```
In [9]: # Create some metrics.
         train_data = train.get_batch(1000)
         test data = test.get batch(1000)
         def loss fn(labels, predictions):
             with tf.Session() as sess:
                 predictions = tf.add(predictions, tf.constant(1e-4))
                 loss = tf.losses.softmax cross entropy(labels, predictions)
                 loss = sess.run(loss)
             return loss
         metrics = {
             "train_conf_mtx": metric.ConfusionMatrixMetric(train_data, 7),
             "test conf mtx": metric.ConfusionMatrixMetric(test data, 7),
             "train_nx_conf_mtx": metric.NonexclusiveConfusionMatrixMetric(train_data, 7),
             "test_nx_conf_mtx": metric.NonexclusiveConfusionMatrixMetric(test_data, 7),
             "train_loss": metric.LossMetric(train_data, loss_fn),
             "test loss": metric.LossMetric(test_data, loss_fn),
             "train_off_by_counts": metric.OffByCountMetric(train_data, 7),
             "test_off_by_counts": metric.OffByCountMetric(test_data, 7)
         }
In [10]: # Make a function for plotting the metrics.
         def plot metrics():
             train_conf_mtx = metrics["train_conf_mtx"].get_results()[1][-1]
             visualization.plot confusion matrix(train conf mtx, "Training Confusion Matrix
         ", 2.5, 2.5)
             test conf mtx = metrics["test conf mtx"].qet results()[1][-1]
             visualization.plot_confusion_matrix(test_conf_mtx, "Test Confusion Matrix", 2.
         5, 2.5)
             train nx conf mtx = metrics["train nx conf mtx"].get results()[1][-1]
             visualization.plot confusion matrix(train nx conf mtx, "Nonexclusive Training
         Confusion Matrix", 2.5, 2.5)
             test nx conf mtx = metrics["test nx conf mtx"].get results()[1][-1]
             visualization.plot confusion matrix(test nx conf mtx, "Nonexclusive Test Confu
         sion Matrix", 2.5, 2.5)
             xs, ys = metrics["train loss"].get results()
             visualization.plot line(xs, ys, "Training Loss", "training iterations", "cross
         -entropy loss", 2.5, 12)
             xs, ys = metrics["test loss"].get results()
             visualization.plot_line(xs, ys, "Test Loss", "training iterations", "cross-ent
         ropy loss", 2.5, 12)
             xs, sets of ys = metrics["train off by counts"].get results()
             visualization.plot_lines(xs, sets_of_ys, "Training Off-By Counts", "training i
         terations", "count of examples",
                                      ["off by \{0\}".format(x) for x in range(-7, 7 + 1)], 2.
         5, 12)
             xs, sets of ys = metrics["test off by counts"].get results()
             visualization.plot_lines(xs, sets_of_ys, "Test Off-By Counts", "training itera
         tions", "count of examples",
```

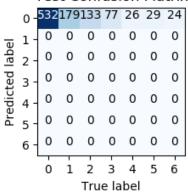
5, 12)

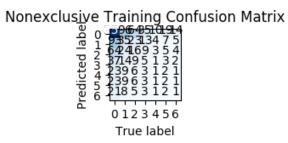
["off by $\{0\}$ ".format(x) for x in range(-7, 7 + 1)], 2.

```
In [11]: # Alternately train and evaluate the net for 30 minutes.
for _ in range(30//3):
    net.train(train, 3*60)
    net.evaluate(metrics)
    plot_metrics()
```

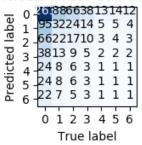


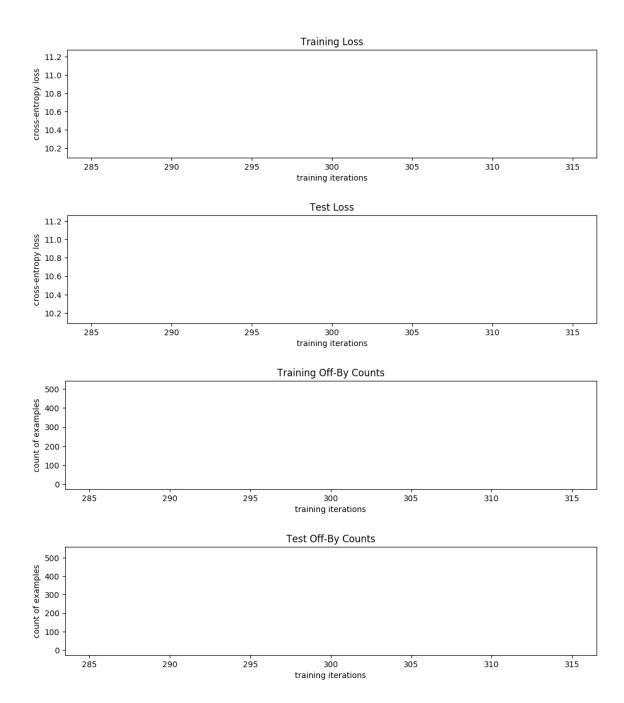




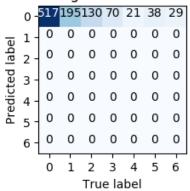


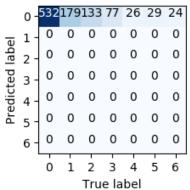
Nonexclusive Test Confusion Matrix

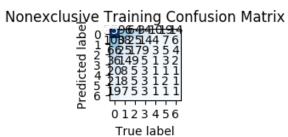




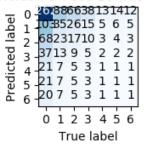


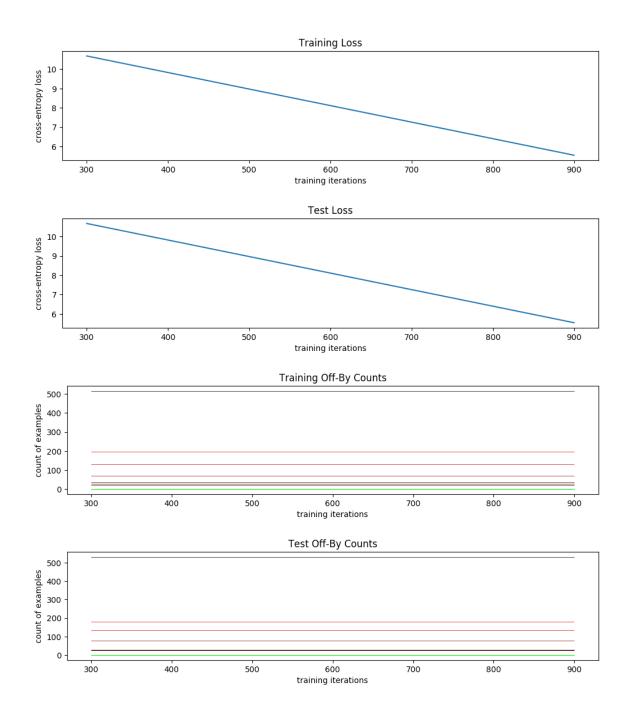




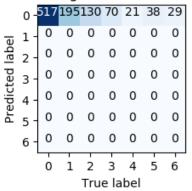


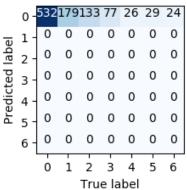
Nonexclusive Test Confusion Matrix

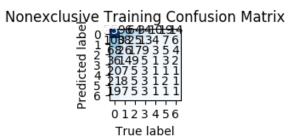




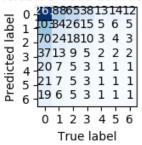


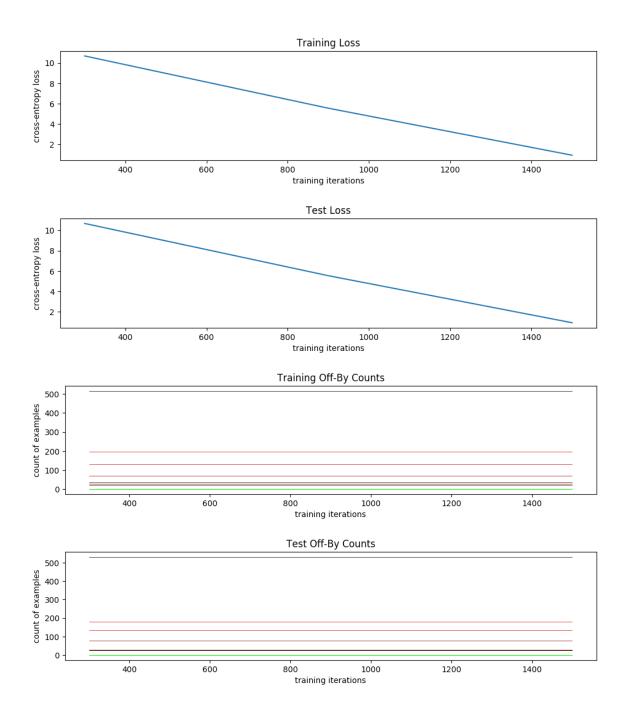




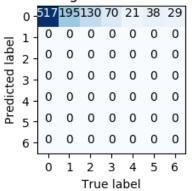


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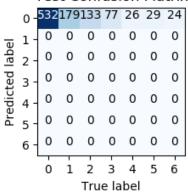


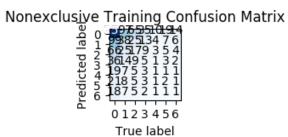




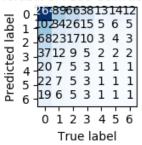


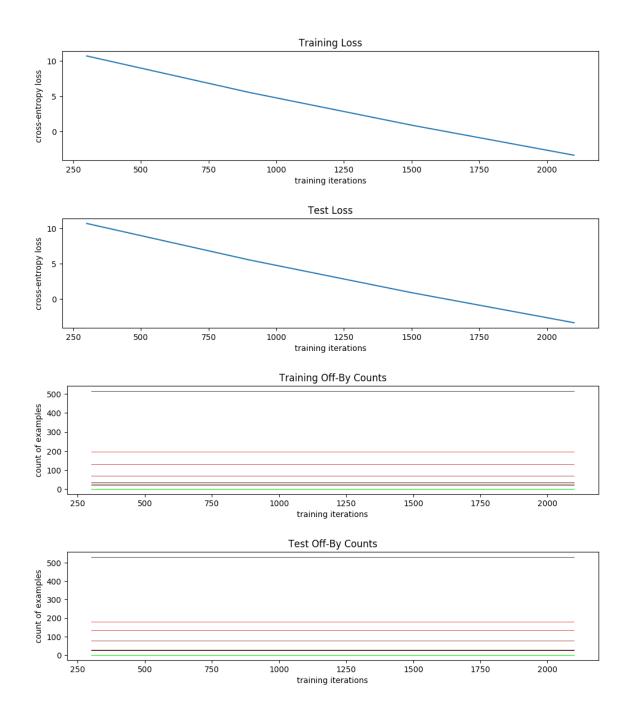
Test Confusion Matrix



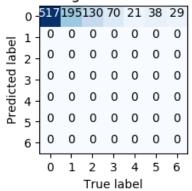


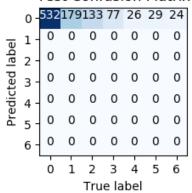
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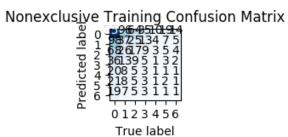




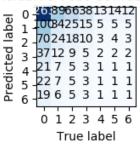


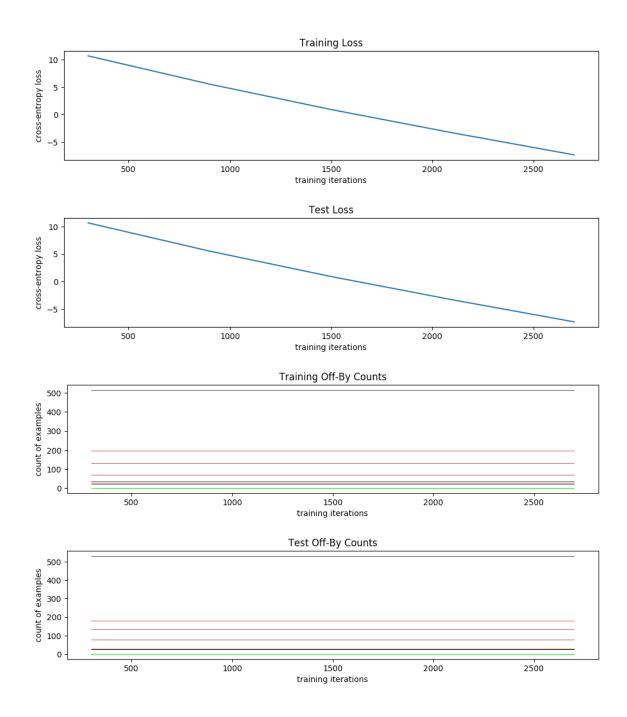




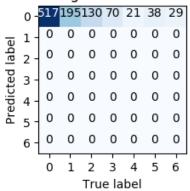


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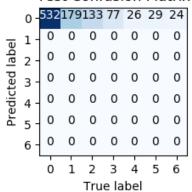


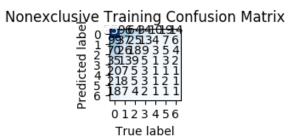




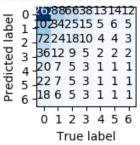


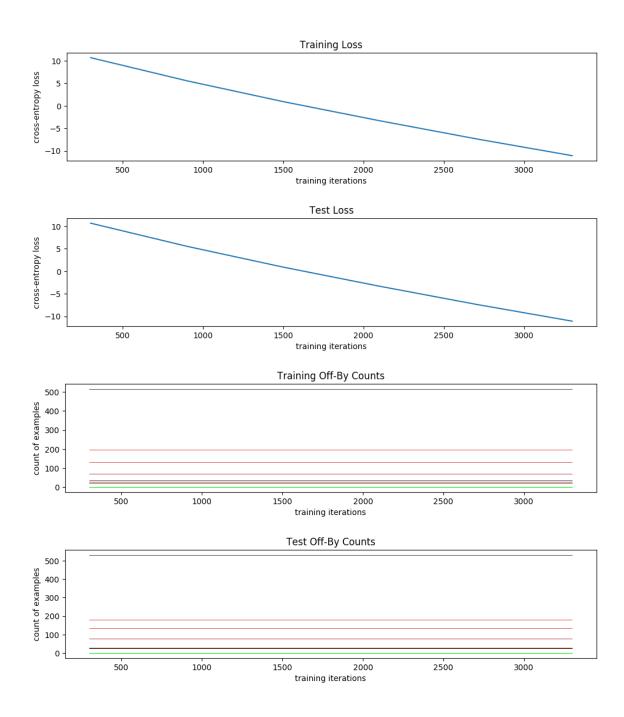
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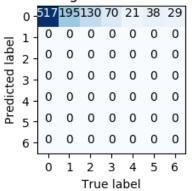


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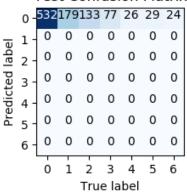


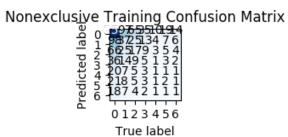




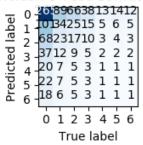


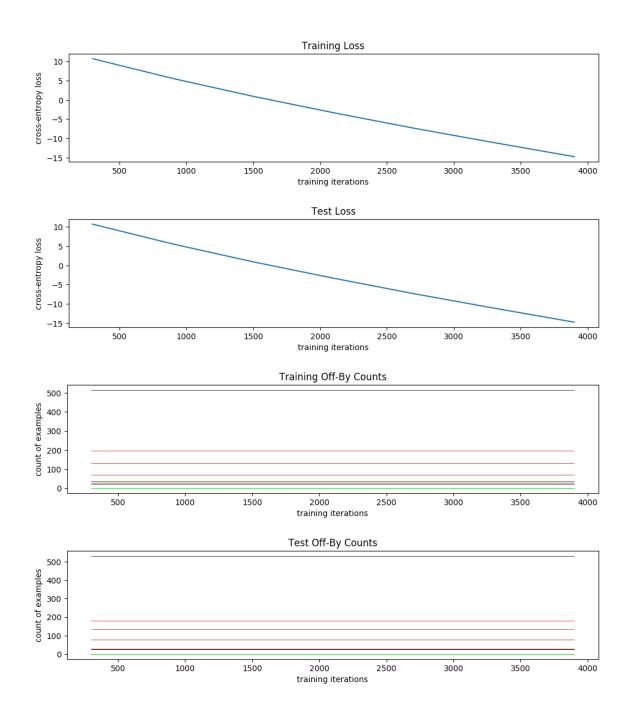
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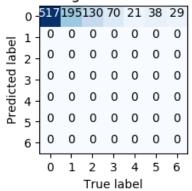


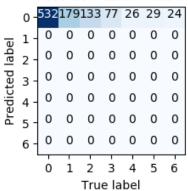
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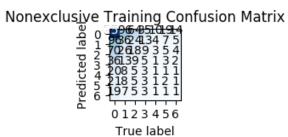




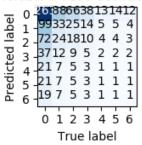


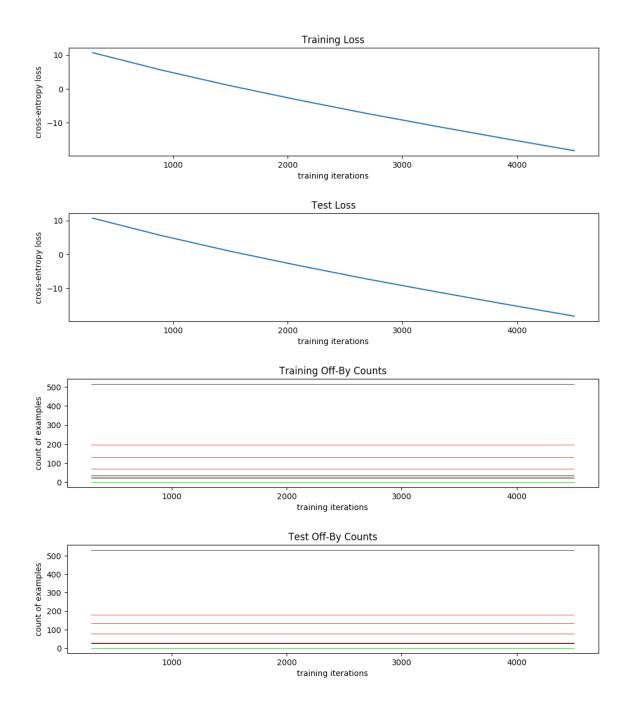




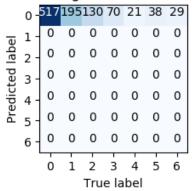


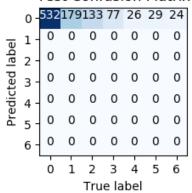
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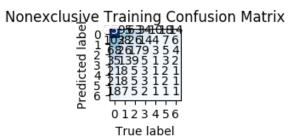




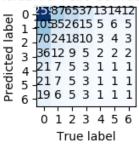


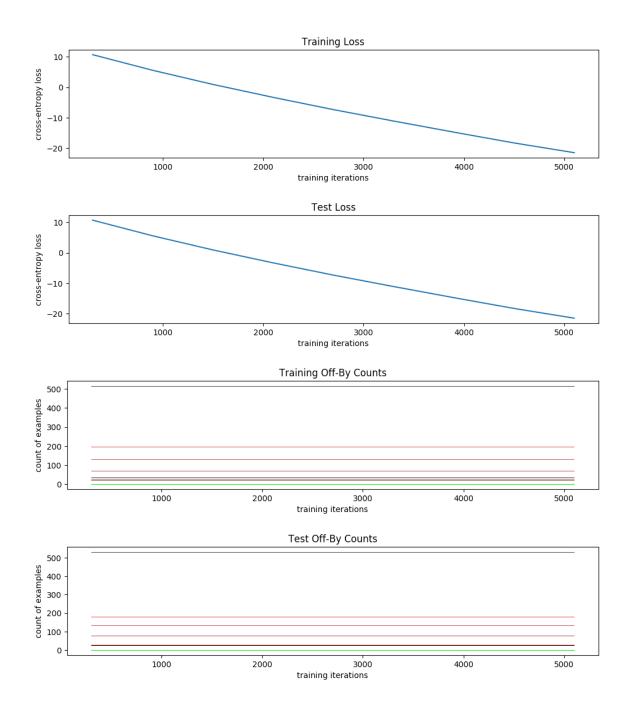




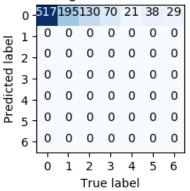


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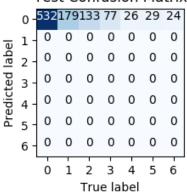


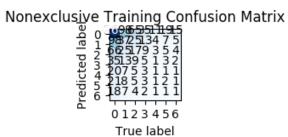




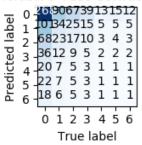


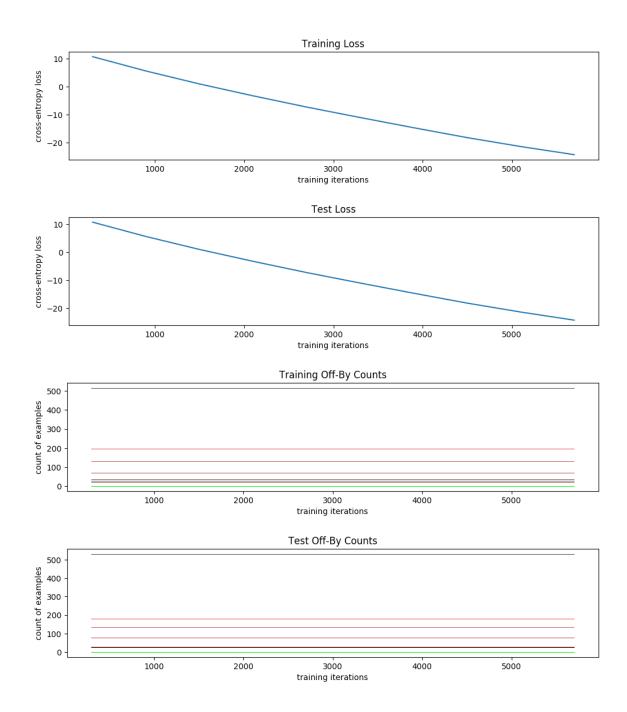
Test Confusion Matrix





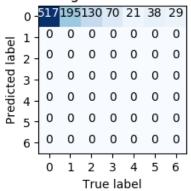
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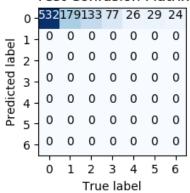


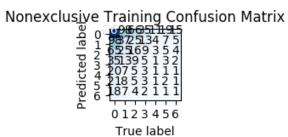


```
In [12]: # Alternately train and evaluate the net for 30 minutes.
for _ in range(30//3):
    net.train(train, 3*60)
    net.evaluate(metrics)
    plot_metrics()
```

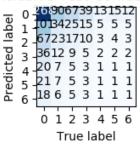


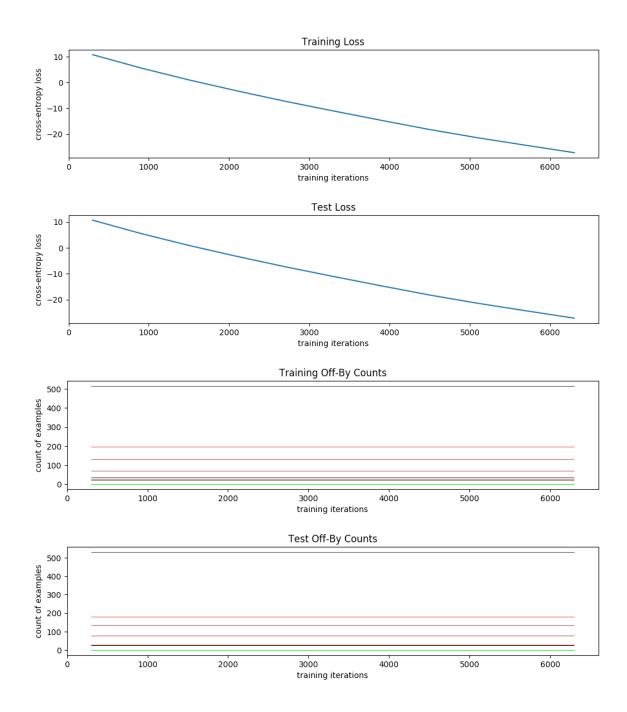




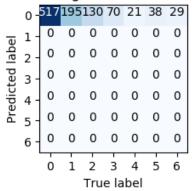


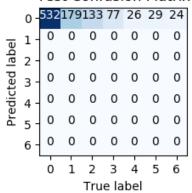
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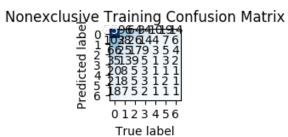




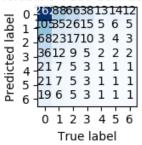


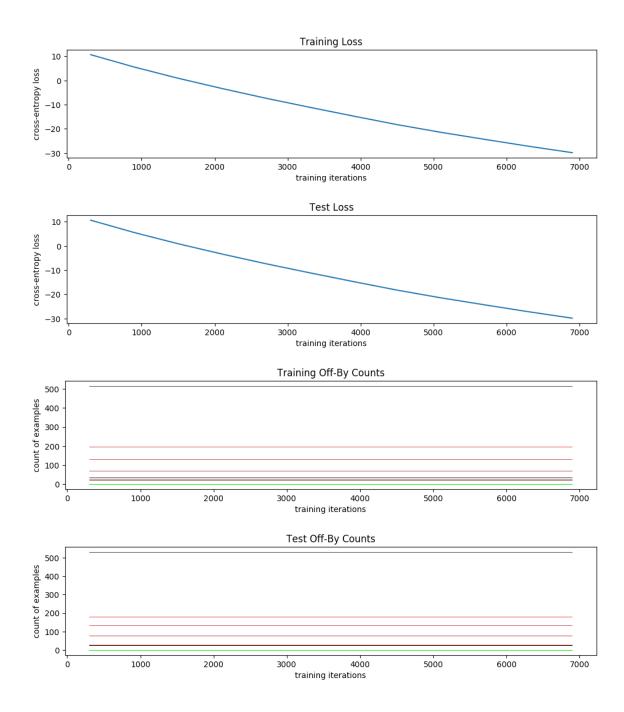




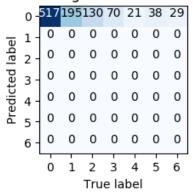


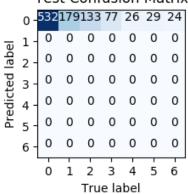
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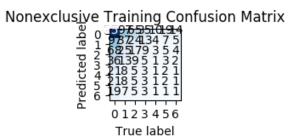




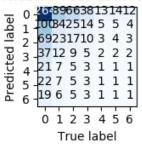


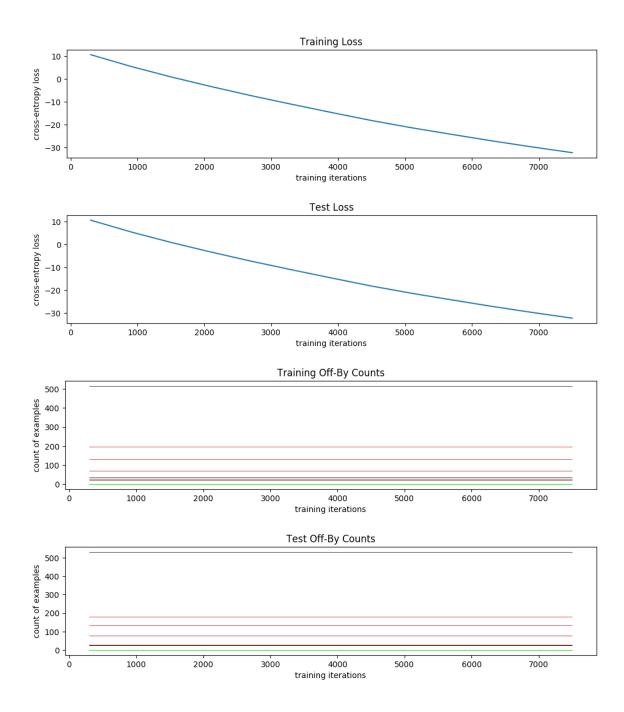




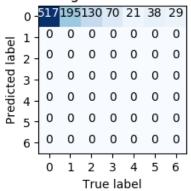


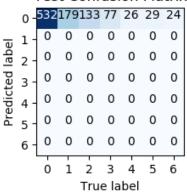
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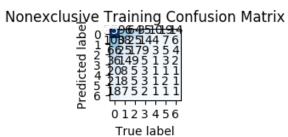




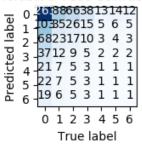


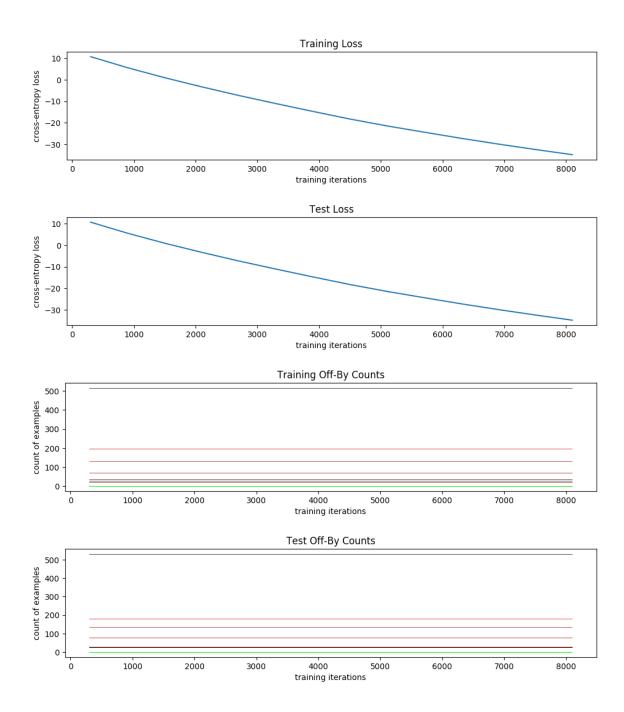




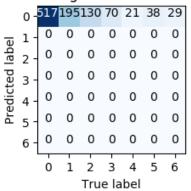


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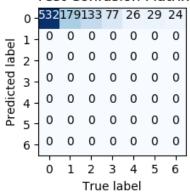


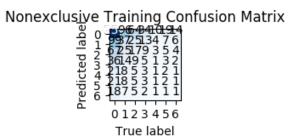




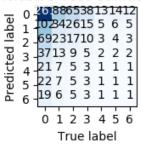


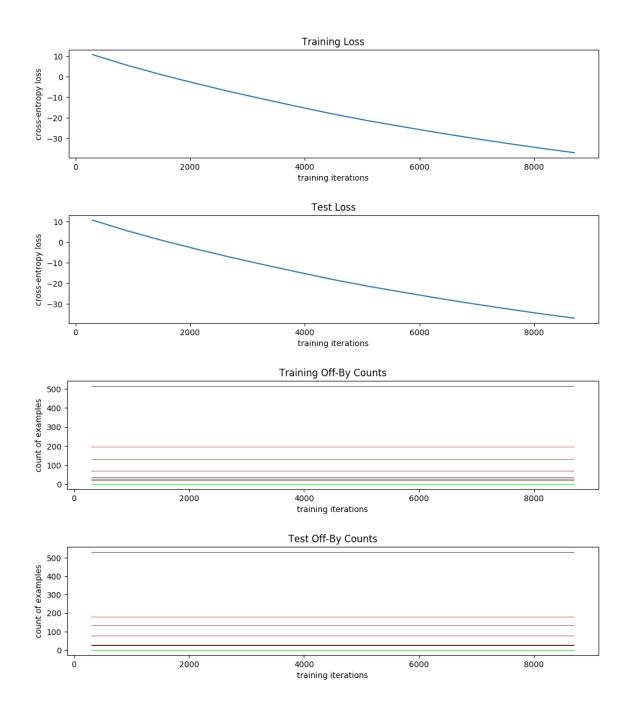
Test Confusion Matrix



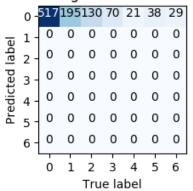


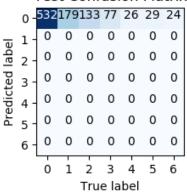
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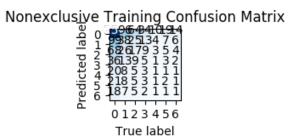




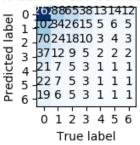


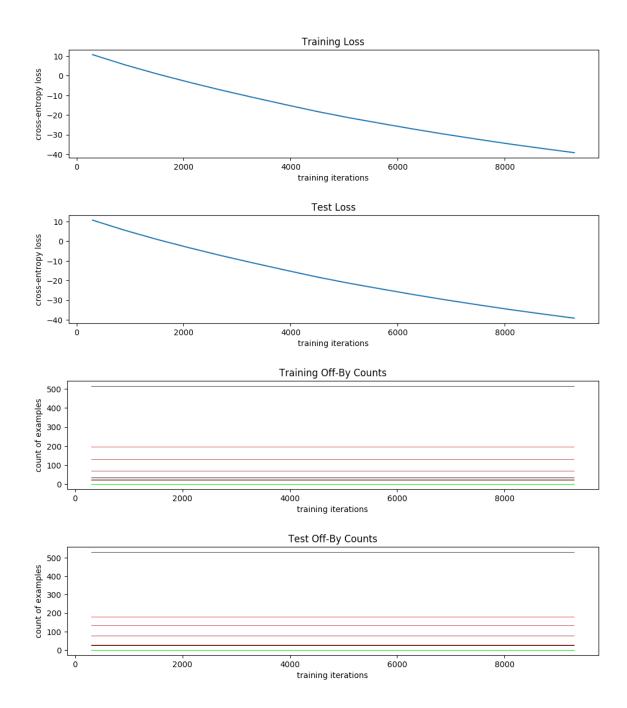




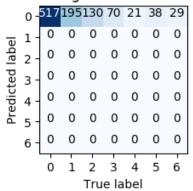


Nonexclusive Test Confusion Matrix

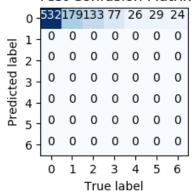


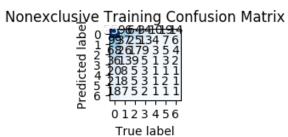


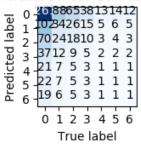


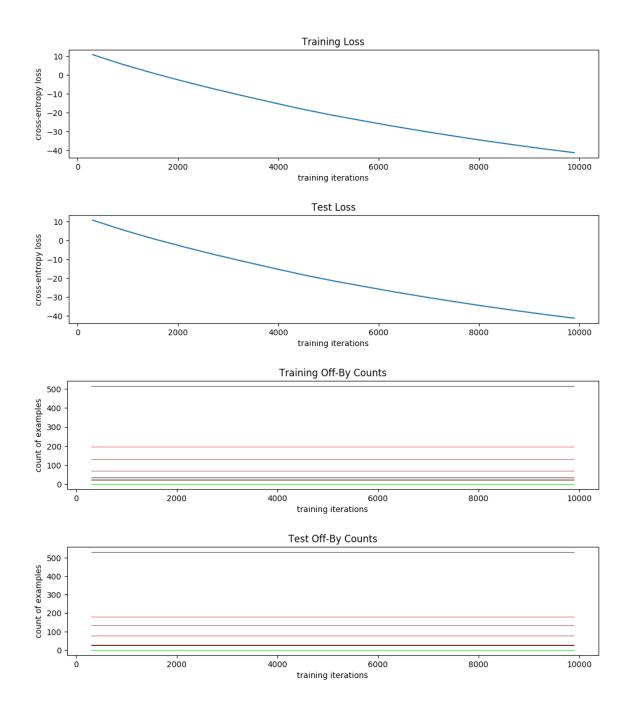


Test Confusion Matrix

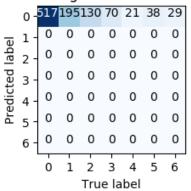




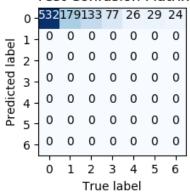


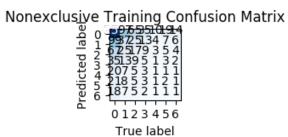


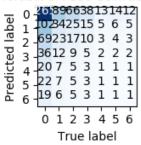


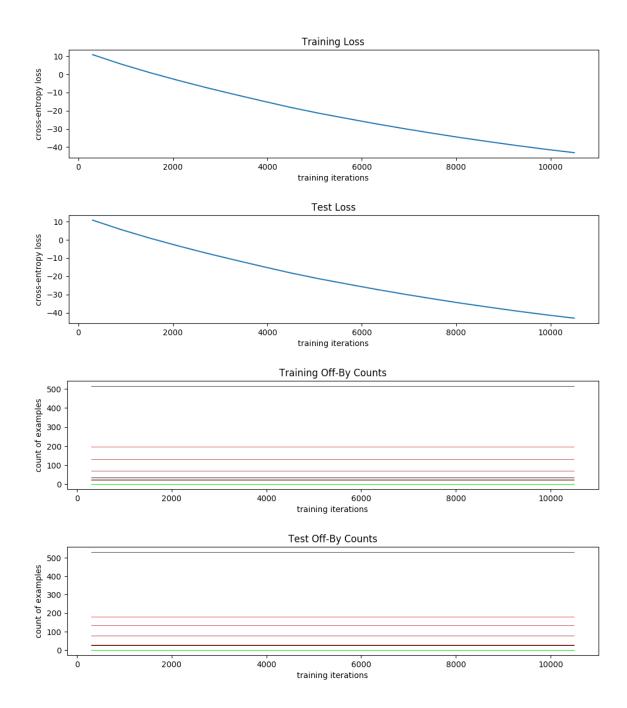


Test Confusion Matrix

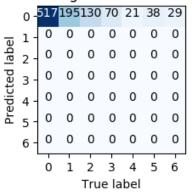




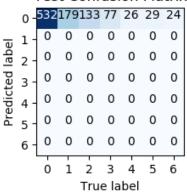


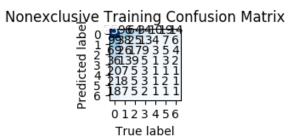


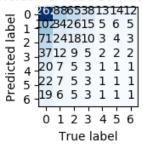


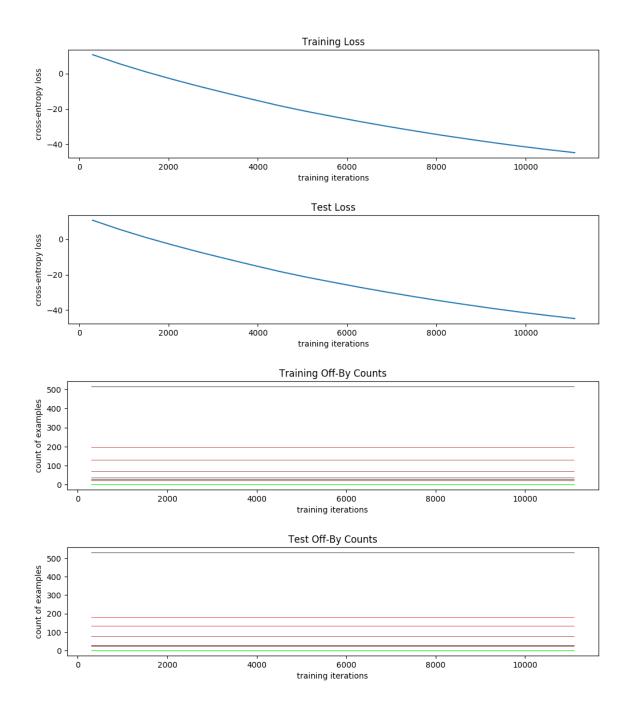


Test Confusion Matrix

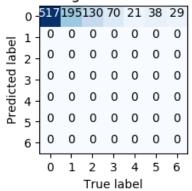


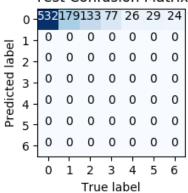


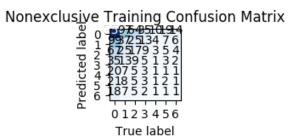




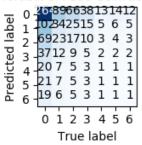


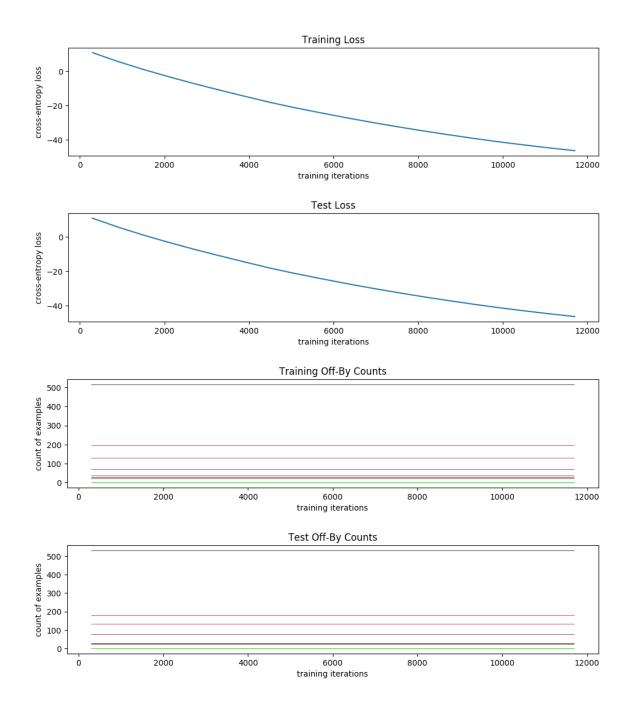






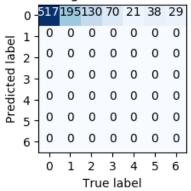
Nonexclusive Test Confusion Matrix

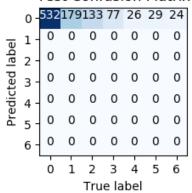


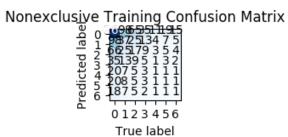


```
In [13]: # Alternately train and evaluate the net for 30 minutes.
for _ in range(30//3):
    net.train(train, 3*60)
    net.evaluate(metrics)
    plot_metrics()
```

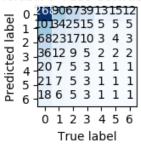


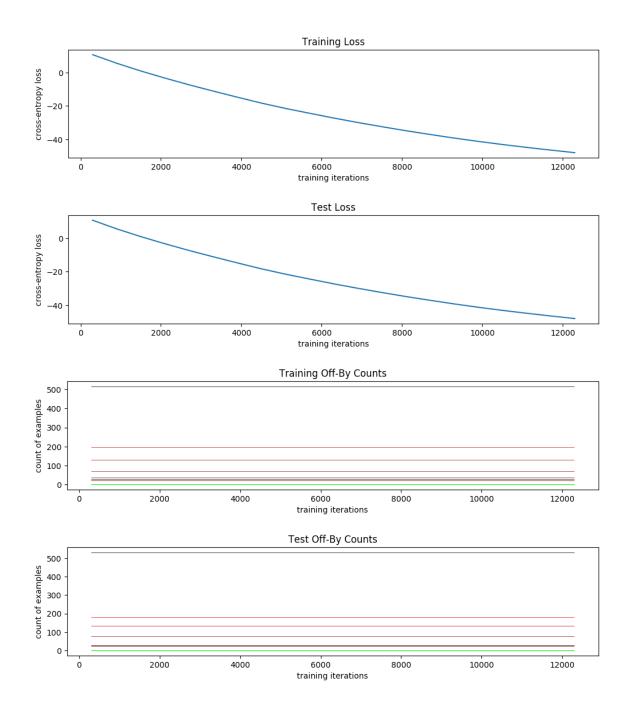




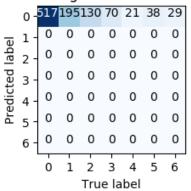


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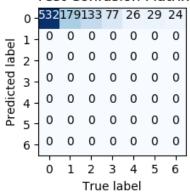


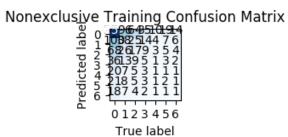


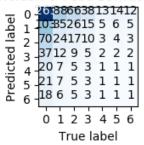


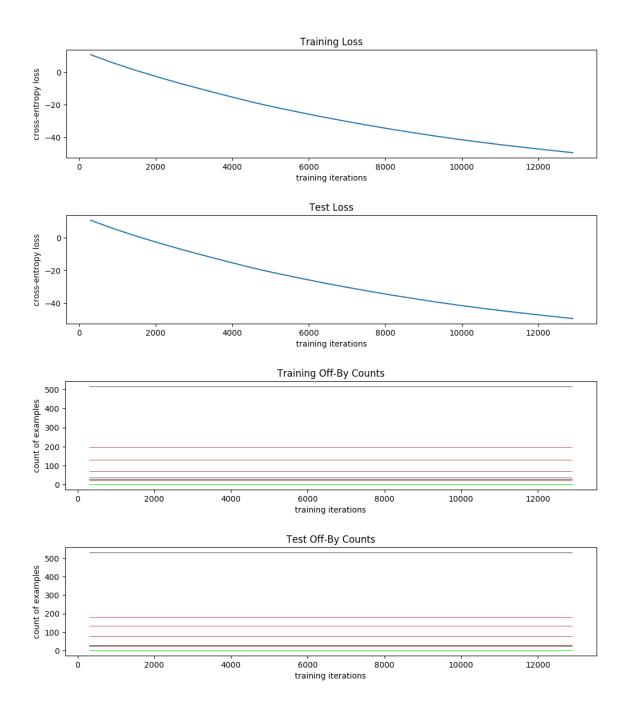


Test Confusion Matrix

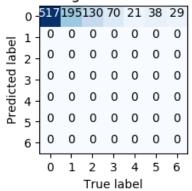


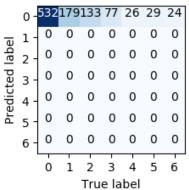


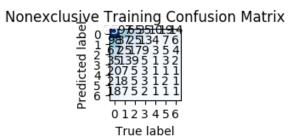




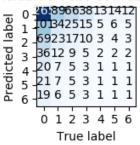


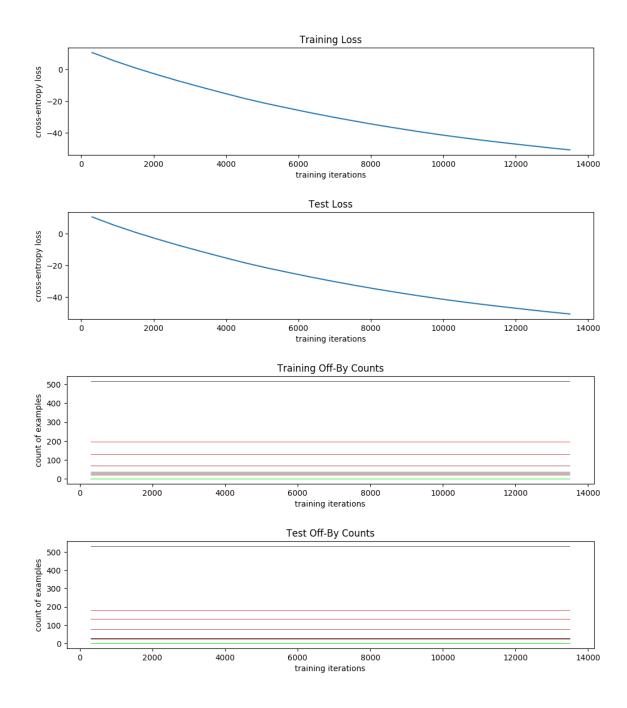




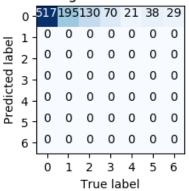


Nonexclusive Test Confusion Matrix

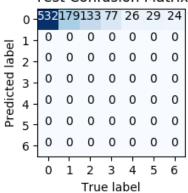


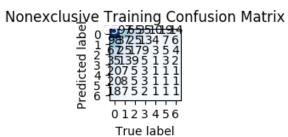


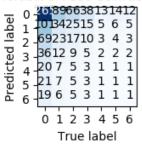


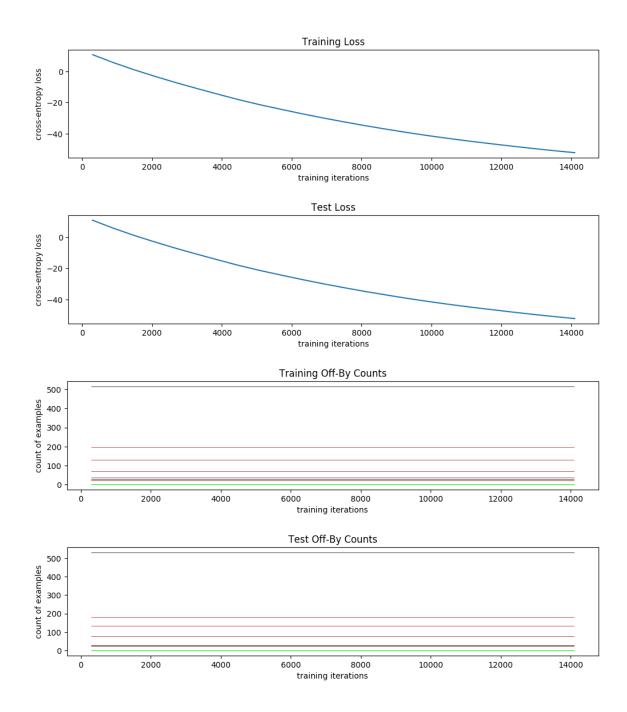


Test Confusion Matrix

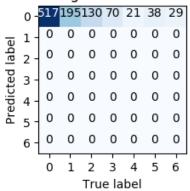


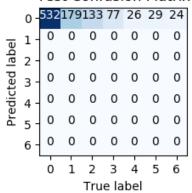


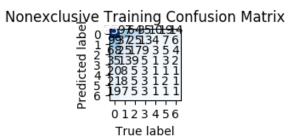




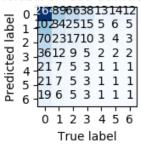


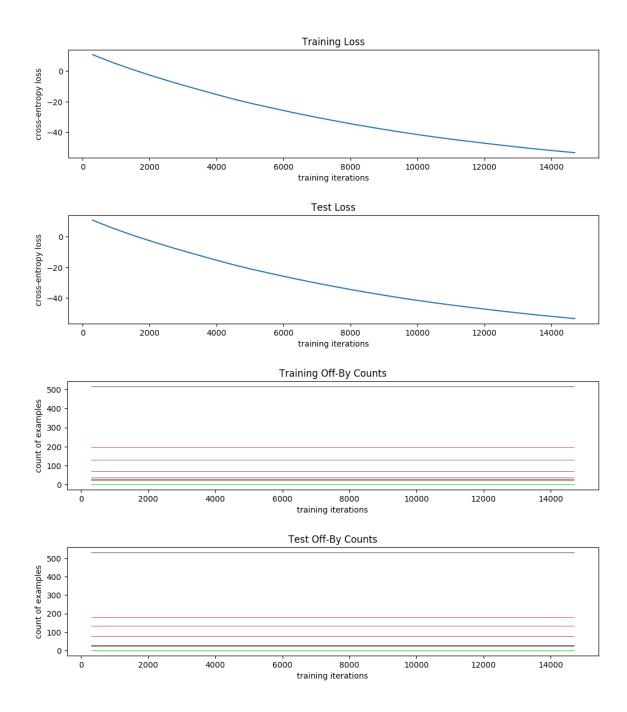




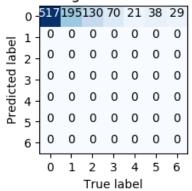


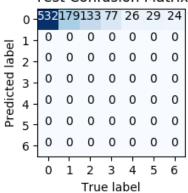
Nonexclusive Test Confusion Matrix

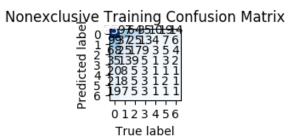




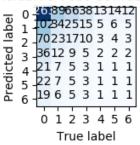


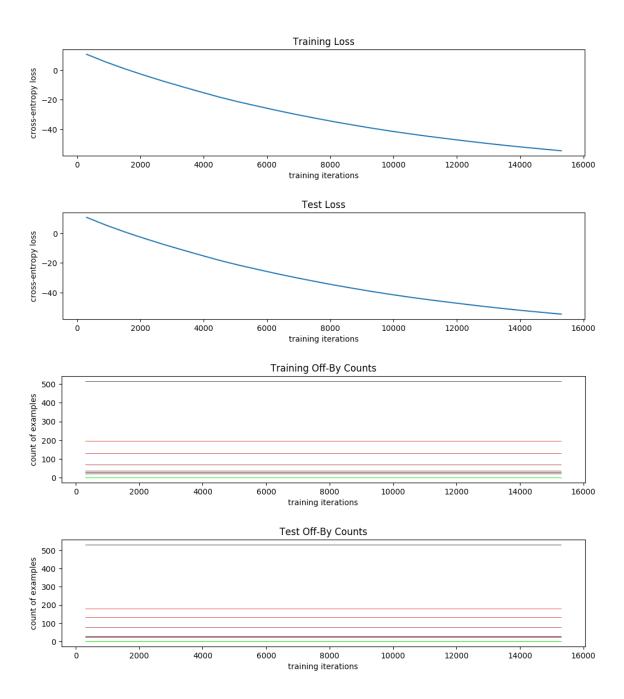




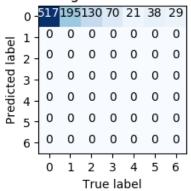


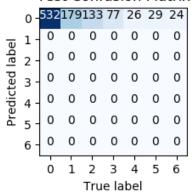
Nonexclusive Test Confusion Matrix

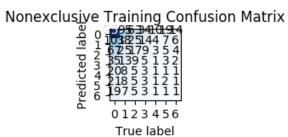




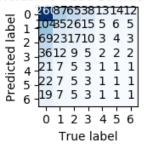


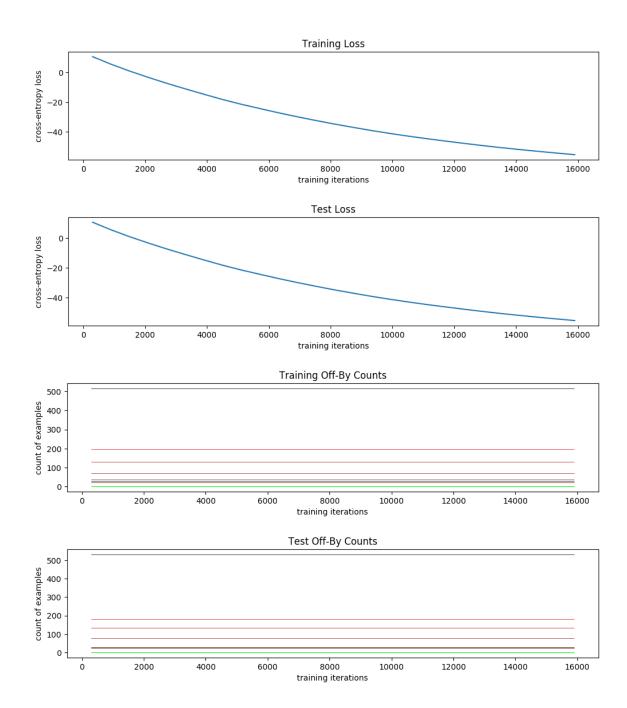




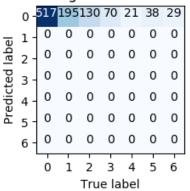


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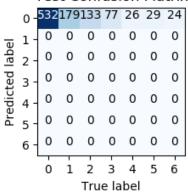


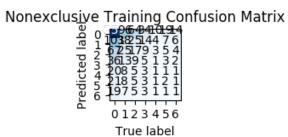


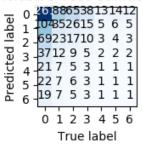


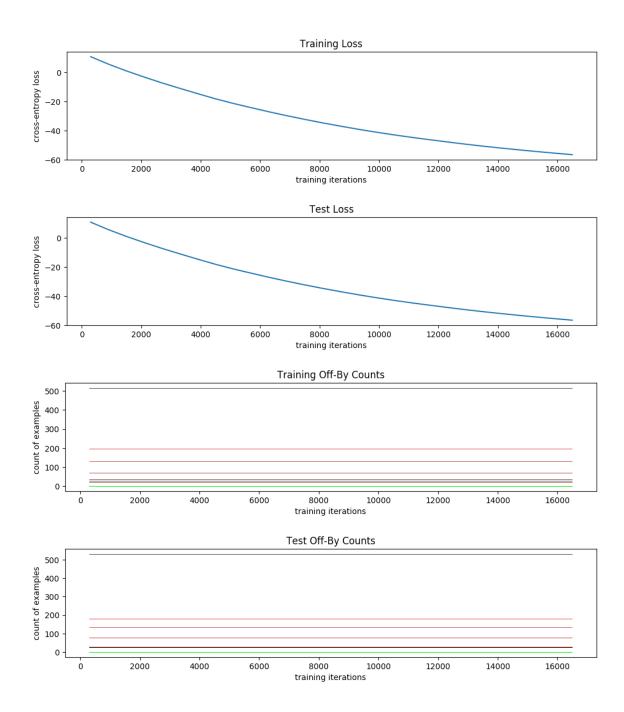


Test Confusion Matrix

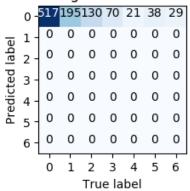


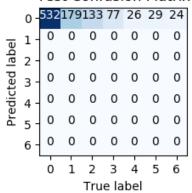


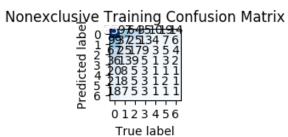




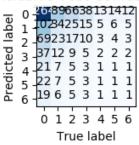


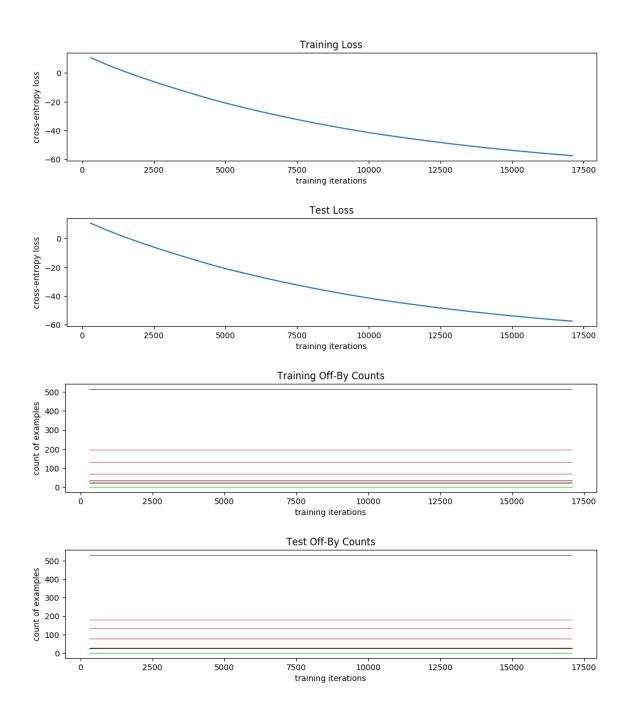




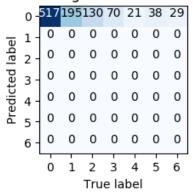


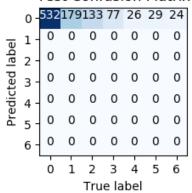
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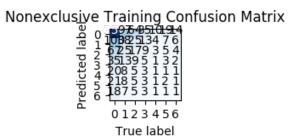




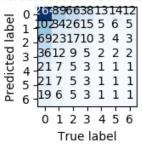


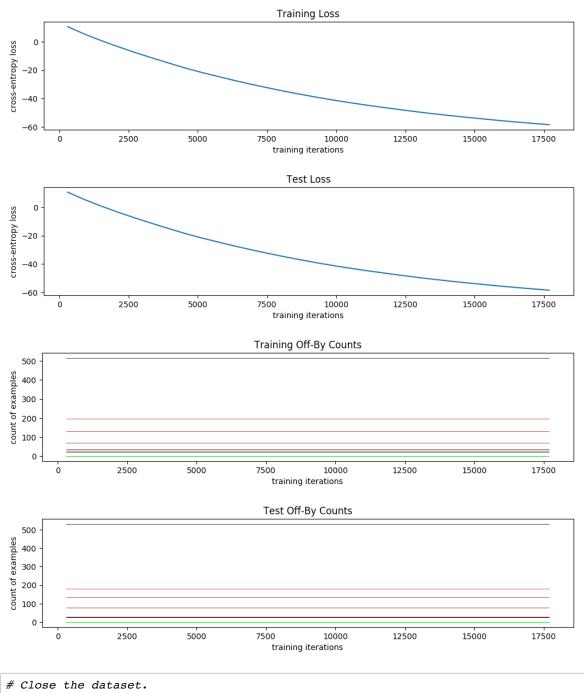






Nonexclusive Test Confusion Matrix





In []: # Close the dataset.
 microbia_segments.close()