

```
mape_gap100 = list()
                                                                             for seed in tqdm(seed_points):
    start = seed
    end = seed-99
    data_with_missing = data.copy()
    data_with_missing = createGap(data_with_missing,start,end)
                                                                                                        imputed data = obj.impute(data with missing,1)
                                                                                                        mad = obj.mad(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][star
ioa = obj.index_agreement(np.asarray(imputed_data['GlucoseValue')[start:end-1].tolist()),np.asarray(data['GlucoseValue']
fb = obj.fracBias(np.asarray(imputed_data['GlucoseValue')[start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist(),np.asarray(data['GlucoseValue'][start:end-1].tolist(),np.asarray(data['GlucoseValue'][start:end-1].tolist(),np.asarray(data['Glucos
                                                                                                        mad_gap100.append(mad)
ioa_gap100.append(ioa)
fb_gap100.append(fb)
rmse_gap100.append(rmse)
                                                                                                        mape gap100.append(mape)
                                                                       executed in 2.15s, finished 14:06:22 2020-10-14
                                                                         100%
                                                                                                                                                                                                                                                                                        6/6 [00:04<00:00, 1.36it/s]
 for seed in tqdm(seed_points):
    start = seed
    end = seed+49
                                                                                                          data_with_missing = data.copy()
data_with_missing = createGap(data_with_missing,start,end)
                                                                                                        imputed_data = obj.impute(data_with_missing,1)
                                                                                                        mad = obj.mad(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][star
ioa = obj.index_agreement(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue']
fb = obj.trascBias(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['Glucose
                                                                                                      mad_gap50.append(mad)
ioa_gap50.append(ioa)
fb_gap50.append(fb)
rmse_gap50.append(rmse)
mape_gap50.append(mape)
                                                                       executed in 1.25s, finished 14:06:23 2020-10-14
                                                                         100%
                                                                                                                                                                                                                                                                    6/6 [00:02<00:00, 2.66it/s]
for seed in tqdm(seed_points):
    start = seed
    end = start=29
    data_with_missing = data.copy()
    data_with_missing = createCap(data_with_missing,start,end)
                                                                                                          imputed_data = obj.impute(data_with_missing,1)
                                                                                                        mad = obj.mad(np.asarray(imputed_data('GlucoseValue')[start:end-1].tolist()),np.asarray(data('GlucoseValue')[startioa = obj.index_agreement(np.asarray(imputed_data['GlucoseValue')[start:end-1].tolist()),np.asarray(data['GlucoseValue']
fb = obj.fracBias(np.asarray(imputed_data['GlucoseValue')[start:end-1].tolist()),np.asarray(data['GlucoseValue']
mrse = obj.rmse(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['Gl
                                                                                                      mad_gap30.append(mad)
ioa_gap30.append(ioa)
fb_gap30.append(fb)
rmse_gap30.append(rmse)
mape_gap30.append(mape)
                                                                       executed in 909ms, finished 14:06:24 2020-10-14
                                                                                                                                                                                                                                                   6/6 [00:01<00:00, 5.89it/s]
   for seed in tqdm(seed_points):
    start = seed
                                                                                                          start seed
end = start+14
data_with_missing = data.copy()
data_with_missing = createGap(data_with_missing,start,end)
                                                                                                          imputed_data = obj.impute(data_with_missing,1)
                                                                                                        mad = obj.mad(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][star
ioa = obj.index_agreement(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValu
                                                                                                          mad_gap15.append(mad)
                                                                                                          ioa_gap15.append(ioa)
fb_gap15.append(fb)
rmse_gap15.append(rmse)
mape_gap15.append(mape)
                                                                     executed in 597ms, finished 14:06:25 2020-10-14
                                                                                                                                                                                                                                                6/6 [05:39<00:00, 56.52s/it]
   for seed in tqdm(seed_points):
                                                                                                        start seed
end = start+4
data_with_missing = data.copy()
data_with_missing = createGap(data_with_missing,start,end)
                                                                                                        imputed data = obi.impute(data with missing.1)
```

```
mad = obj.mad(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][star
ioa = obj.index_agreement(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['Glucose
fb = obj.index_agreement(np.asarray(imputed_data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['GlucoseValue'][start:end-1].tolist()),np.asarray(data['Glu
                                                                  mad_gap5.append(mad)
ioa_gap5.append(ioa)
fb_gap5.append(fb)
rmse_gap5.append(rmse)
mape_gap5.append(mape)
                                            executed in 402ms, finished 14:06:25 2020-10-14
                                                                                                                                                                                         6/6 [00:04<00:00, 1.28it/s]
  In [113]: IOA = pd.DataFrame({'Gap:5':ioa_gap5, 'Gap:15':ioa_gap15, 'Gap:30':ioa_gap30, 'Gap:50':ioa_gap50, 'Gap:100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap100':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':ioa_gap10':
                                            executed in 78ms, finished 14:06:25 2020-10-14
 Out[113]:
                                                                Gap:5 Gap:15 Gap:30 Gap:50 Gap:100
                                             0 0.524590 0.732829 0.794466 0.688385 0.633212
                                                   1 0.282136 0.599247 0.496989 0.514146 0.471362
                                              2 0.418301 0.846204 0.910656 0.851831 0.619313
                                              3 0.444444 0.730517 0.683936 0.419430 0.440915
                                             4 0.830189 0.929628 0.783506 0.754882 0.461313
                                              5 0.512315 0.639980 0.680301 0.605894 0.318035
In [114]: 1 import matplotlib.pyplot as plt import matplotlib.ticker as ticker import seaborn as sns
                                            executed in 6ms, finished 14:06:25 2020-10-14
         In [ ]: 1
                                            executed in 11ms, finished 14:05:48 2020-10-14
         In [ ]: 1
                                            executed in 8ms, finished 14:05:45 2020-10-14
 In [119]: 1
                                                                   plt.figure(figsize=(14,8))
sns.set(style="white")
fig = sns.leneplot(x = seed_points, y = IOA['Gap:5'], data = IOA, palette="tabl0", linewidth=1.25)
sns.despine()
                                            fig.set_xlabel('Gap Seeds')
fig.set_ylabel('IOA value')
executed in 848ms, finished 14:10:52 2020-10-14
 Out[119]: Text(0, 0.5, 'IOA value')
                                                     0.4
                                                     0.3
                                                                                                                                                                                                                                               1000
Gap Seeds
 In [120]: 1
                                                                   plt.figure(figsize=(14,8))
                                                                   Sans.set(style='white')
fig = sns.lineplot(x = seed_points, y = IOA['Gap:15'], data = IOA, palette="tabl0", linewidth=1.25)
sns.despine()
                                                               ed in 1.02s, finished 14:11:45 2020-10-14
 Out[120]: Text(0, 0.5, 'IOA value')
                                                     0.90
                                                     0.85
                                               <u>6</u> 0.75
                                                     0.70
                                                     0.65
 In [121]: 1
                                                                   plt.figure(figsize=(14,8))
sns.set(style="white")
fig = sns.leneplot(x = seed_points, y = IOA['Gap:30'], data = IOA, palette="tabl0", linewidth=1.25)
sns.despine()
                                                                   fig.set_xlabel('Gap Seeds')
fig.set_ylabel('IOA value')
                                                               ed in 815ms, finished 14:11:51 2020-10-14
 Out[121]: Text(0, 0.5, 'IOA value')
                                                                                                                                                                                                                                                   Λ
```

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0.6
In [122]: 1
                     plt.figure(figsize=(14,8))
sns.set(style="white")
fig = sns.leeplot(x = seed_points, y = IOA['Gap:50'], data = IOA, palette="tabl0", linewidth=1.25)
sns.despine()
              7 fig.set_xlabel('Gap Seeds')
8 fig.set_ylabel('IOA value')
executed in 1.15s, finished 14:11:56 2020-10-14
Out[122]: Text(0, 0.5, 'IOA value')
                 0.5
                                                                             1000
Gap Seeds
In [123]: 1
                     plt.figure(figsize=[14,8))
sns.set(style="white")
fig = sns.lineplot(x = seed_points, y = IOA['Gap:100'], data = IOA, palette="tabl0", linewidth=1.25)
sns.despine()
                     fig.set_xlabel('Gap Seeds')
fig.set_ylabel('IOA value')
              executed in 843ms, finished 14:12:04 2020-10-14
Out[123]: Text(0, 0.5, 'IOA value')
                 0.60
                 0.55
                 0.50
                 0.40
                 0.35
  In [ ]: 1
   In [ ]: 1
 In [73]: MAD = pd.DataPrame(('Gap:5':mad_gap5, 'Gap:15':mad_gap15, 'Gap:30':mad_gap30, 'Gap:50':mad_gap50, 'Gap:100':mad_gap10 MAD
              executed in 47ms, finished 13:25:47 2020-10-14
 Out[73]:
                    Gap:5 Gap:15 Gap:30 Gap:50 Gap:100
              0 4.333333 4.692308 6.428571 10.520833 17.091837
              1 6.333333 2.846154 5.178571 10.041667 14.704082
              2 5.333333 13.307692 21.250000 25.750000 24.551020
              3 2.000000 11.538462 12.142857 8.833333 9.163265
              4 1.333333 8.076923 11.535714 14.645833 12.540816
              5 5.333333 17.230769 22.428571 21.875000 16.387755
 In [74]: FB = pd.DataFrame({'Gap:5':fb_gap5, 'Gap:15':fb_gap15, 'Gap:30':fb_gap30, 'Gap:50':fb_gap50, 'Gap:100':fb_gap100})
FB = pd.DataFrame({'Gap:5':fb_gap5, 'Gap:15':fb_gap15, 'Gap:30':fb_gap30, 'Gap:50':fb_gap50, 'Gap:100':fb_gap100})
              executed in 42ms, finished 13:25:47 2020-10-14
 Out[74]:
                    Gap:5 Gap:15 Gap:30 Gap:50 Gap:100
              0 0.031083 0.035674 0.051890 0.088006 0.149169
              1 0.069425 0.030546 0.052337 0.091316 0.124905
              2 0.038118 0.103091 0.170869 0.209447 0.198190
              3 0.017316 0.108942 0.114510 0.082013 0.085342
              4 0.010479 0.066834 0.097473 0.125138 0.106183
              5 0.047094 0.162981 0.216415 0.210963 0.155640
  To 1751. and DataBusman/[[Car.5].wmon was 5 [Car.16].wmon was 15 [Car.26].wmon was 20 [Car.56].wmon was 50 [Car.160].wmon was 100
```

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TH [/3]: | pu.nacarrame(; wap:: cimse_gap), wap:: cimse_gap10, wap:: cimse_gap20, wap:: c
                            executed in 44ms, finished 13:25:47 2020-10-14
 Out[75]:
                                            Gap:5 Gap:15 Gap:30 Gap:50 Gap:100
                            0 4.725816 5.650051 8.053393 12.470799 19.849176
                                1 6.350853 3.562627 6.657434 13.288466 17.827690
                            2 5.597619 16.462078 24.834452 28.605798 27.065680
                              3 2 449490 13 716918 13 907860 11 011358 11 471349
                             4 1.825742 9.227884 13.238202 16.149690 14.067258
                                5 5.416026 18.757563 23.503799 23.116553 18.599429
 In [76]: |.DataFrame(('Gap:5':mape_gap5, 'Gap:15':mape_gap15, 'Gap:30':mape_gap30, 'Gap:50':mape_gap50, 'Gap:100':mape_gap100})
                             executed in 44ms, finished 13:25:47 2020-10-14
Out[76]:
                                            Gap:5 Gap:15 Gap:30 Gap:50 Gap:100
                              0 3.152333 3.657676 5.416582 9.402892 16.687821
                                 1 6.708753 2.997509 5.413667 9.864004 13.746207
                              2 3.733897 11.190585 19.467499 24.221142 22.700530
                                3 1.709402 11.807833 12.392205 8.738206 9.132209
                              4 1.056410 6.992134 10.447777 13.577102 11.397967
                                5 4.826840 18.081855 24.602487 23.999033 17.393321
In [19]: # IOA.to_csv("-/Desktop/NCSA_genomics/Python - notebooks/GlucoCheck/Metrics/IOA.csv")
# PB.to_csv("-/Desktop/NCSA_genomics/Python - notebooks/GlucoCheck/Metrics/PB.csv")
# RMSE.to_csv("-/Desktop/NCSA_genomics/Python - notebooks/GlucoCheck/Metrics/RMSE.csv"
# MAPL.to_csv("-/Desktop/NCSA_genomics/Python - notebooks/GlucoCheck/Metrics/MAPL.csv")
# MAPL.to_csv("-/Desktop/NCSA_genomics/Python - notebooks/GlucoCheck/Metrics/MAPL.csv")
                              executed in 17ms, finished 22:08:20 2020-10-13
In [20]: v # getting model metrics
                             executed in 9ms, finished 22:08:20 2020-10-13
   In [ ]: 1
                                  print("Model loss on training set:")
print(np.mean(obj.model_history.history['loss']))
print("Model Accuracy on training set:")
print("Model Accuracy on training set:")
print("Model loss on validation set:")
print("Model loss on validation set:")
print("Model accuracy on validation set:")
print("Model accuracy on validation set:")
print("Model accuracy on validation set:")
 In [21]:
                              executed in 1.66s, finished 22:08:21 2020-10-13
                              Model loss on training set:
66.09112285241825
Model Accuracy on training set:
0.09277845
                              Model loss on validation set:
                             KeyError

*ipython-input-21-eac7f6462949> in <module>
4    print(np.mean(obj.model_history.history['accuracy']))
5    print("Model loss on validation set:")
---> 6    print(np.mean(obj.model_history.history['val_loss']))
7    vint("Model accuracy on validation set:")
                                                                                                                                                                  Traceback (most recent call last)
                                            7 print("Model accuracy on validation set:")
8 print(np.mean(obj.model_history.history['val_accuracy']))
                              KeyError: 'val_loss'
 In []: from matplotlib import pyplot
# plot train and validation loss
pyplot.plot(obj.model_history.history['loss'])
pyplot.plot(obj.model_history.history['val_loss'])
pyplot.vlabel('model train vs validation loss')
pyplot.vlabel('loss')
pyplot.vlabel('loss')
pyplot.legend(['loss')
pyplot.legend(['train', 'validation'], locs'upper right')
pyplot.show()
                                executed in 47m 19s, finished 22:08:21 2020-10-13
   In []: * # plot train and validation accuracy
pyplot.plot(obj.model.history.history['accuracy'])
pyplot.plot(obj.model.history.history['val_accuracy'])
pyplot.vlolep['model train vs validation accuracy')
pyplot.vlabel('loss')
pyplot.vlabel('loss')
pyplot.legend(['train', 'validation'], loc='upper right')
pyplot.legend(['train', 'validation'], loc='upper right')
                                executed in 47m 19s, finished 22:08:21 2020-10-13
   In [ ]:
```