

```

Table[{" =num" num, Length[ $\Lambda_{\text{num}}$ ], Length[ $\Lambda_{\text{num}}$ [[1]]]}, {num, 2, 12}]
Table[{" =num" num, Length[ $\Gamma_{\text{num}}$ ], Length[ $\Gamma_{\text{num}}$ [[1]]]}, {num, 2, 12}]

{{2 =num, 4, 1024}, {3 =num, 8, 512}, {4 =num, 16, 256},
 {5 =num, 32, 128}, {6 =num, 64, 64}, {7 =num, 128, 32}, {8 =num, 64, 16},
 {9 =num, 32, 8}, {10 =num, 16, 4}, {11 =num, 8, 2}, {12 =num, 4, 1}}

{{2 =num, 4, 4}, {3 =num, 8, 8}, {4 =num, 16, 16},
 {5 =num, 32, 32}, {6 =num, 64, 64}, {7 =num, 128, 128}, {8 =num, 64, 64},
 {9 =num, 32, 32}, {10 =num, 16, 16}, {11 =num, 8, 8}, {12 =num, 4, 4}}

{2, 4, 8, 16, 32, 64, 32, 16, 8, 4, 2, 1}
{2, 4, 5, 8, 14, 22, 32, 16, 8, 4, 2, 1}
{2, 4, 8, 16, 32, 64, 32, 16, 8, 4, 2, 1} - {2, 4, 5, 8, 14, 22, 32, 16, 8, 4, 2, 1}
{2, 4, 8, 16, 32, 64, 32, 16, 8, 4, 2, 1}

{2, 4, 5, 8, 14, 22, 32, 16, 8, 4, 2, 1}

{0, 0, 3, 8, 18, 42, 0, 0, 0, 0, 0, 0}

```

4 sample case

```

maxbondDim = {{1, 2}, {2, 4}, {3, 8}, {4, 16}, {5, 32},
 {6, 64}, {7, 32}, {8, 16}, {9, 8}, {10, 4}, {11, 2}, {12, 1}};

numofNONzero $\lambda$ of4samplePCV1 = {{1, 2}, {2, 4}, {3, 5}, {4, 8},
 {5, 14}, {6, 22}, {7, 32}, {8, 16}, {9, 8}, {10, 4}, {11, 2}, {12, 1}};

numofNONzero $\lambda$ of4genelengthRandomFilledsampleTrialNum1 = {{1, 2}, {2, 4}, {3, 8},
 {4, 16}, {5, 32}, {6, 64}, {7, 32}, {8, 16}, {9, 8}, {10, 4}, {11, 2}, {12, 1}};
(*Singular values for a given random trial,
filled at end for comparison to filled samples *)
numofNONzero $\lambda$ of4genelengthRandomFilledsampleTrialNum2 = {{1, 2}, {2, 4}, {3, 8},
 {4, 16}, {5, 32}, {6, 64}, {7, 32}, {8, 16}, {9, 8}, {10, 4}, {11, 2}, {12, 1}};
(*Singular values for a DIFFERENT random trial,
filled at end for comparison to filled samples *)
numofNONzero $\lambda$ of4genelengthRandomUNfilledsampleTrialNum1 = {{1, 2}, {2, 4}, {3, 8},
 {4, 16}, {5, 32}, {6, 64}, {7, 32}, {8, 16}, {9, 8}, {10, 4}, {11, 2}, {12, 1}};
numofNONzero $\lambda$ of4genelengthRandomUNfilledsampleTrialNum2 = {{1, 2}, {2, 4}, {3, 8},
 {4, 16}, {5, 32}, {6, 64}, {7, 32}, {8, 16}, {9, 8}, {10, 4}, {11, 2}, {12, 1}};

numofNONzero $\lambda$ of4genelengthLISTOFALL1 = {2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1};
(* bond dimensions but done for a list of all ones [1,1, ..., 1,1]
Also get the same results for a list of all 2's and all 3's*)

numofNONzero $\lambda$ of4genelengthLISTOFALL0 = {0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1};
(* bond dimensions but done for a list of all ones [1,1, ..., 1,1]
get this since the first lambda is just the zero matrix *)

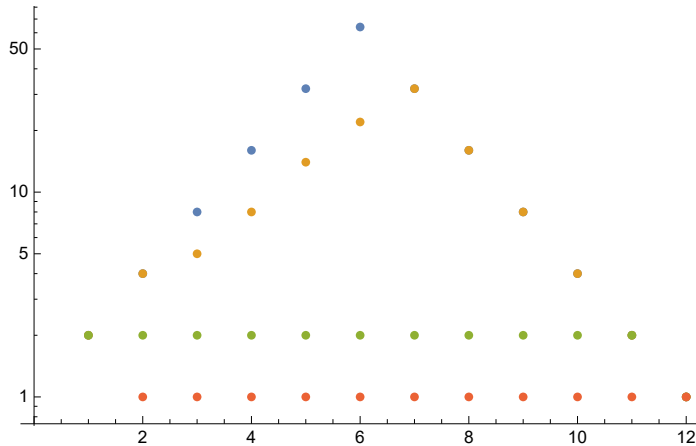
```

Note that the bond dimensions are the same for all the random (and random + filled) trials,

```
maxbondDim - numofNONzeroλof4samplePCV1
```

```
{ {0, 0}, {0, 3}, {0, 8}, {0, 18}, {0, 42}, {0, 0}, {0, 0}, {0, 0}, {0, 0}, {0, 0}, {0, 0} }
```

```
ListLogPlot[{maxbondDim, numofNONzeroλof4samplePCV1,  
numofNONzeroλof4genelengthLISTOFALL1, numofNONzeroλof4genelengthLISTOFALL0}]
```



Key:

Blue - max bond dimensions (also random sets since they overlap)

yellow - combined DNA sample catenation

green - list of all 1 (also same for lists of all 2 and all 3)

red - list of all 0

We test lists of solely one digit (the bottom two bond dimension plots) so as to have something to compare the other stuff to. Importantly, we can see that the algorithm doesn't give the maximal number of bond dimensions in the latter half of the plot for these highly compressible sets. Contrast this with the DNA plot

Note: break the MPS down to 2x1 at end but don't do 1x2 at beginning. This is why it may appear a bit asymmetric, not due to an error.

16 sample case

```
maxbondDim16samplecase = {2, 4, 8, 16, 32, 64, 128, 64, 32, 16, 8, 4, 2, 1};
```

```
numofNONzeroλof16samplePCV1 = {2, 4, 8, 14, 16, 24, 32, 40, 32, 16, 8, 4, 2, 1};
```

```
numofNONzeroλof16geneRandomanalog = {2, 4, 8, 16, 32, 64, 128, 64, 32, 16, 8, 4, 2, 1};
```

```
ListLogPlot[  
  {maxbondDim16samplecase, numofNONzero $\lambda$ of16samplePCV1, numofNONzero $\lambda$ of16geneRandomanalog}]
```

