

## Code to turn data into text files

```
Wgenesample =  
  StringJoin["PCV1num", ToString[InputString["What number individual is this?"]]];  
basepairs = ToString[  
  {InputString["Paste the base pair sequence (ex: AAGCTATGG ) here"]};  
source = ToString[InputString["What's the source? (ex: GenBank: AB043895.5)"]];  
(*SpecialNote=ToString[InputString["Any Special Notes? If not type 'no'. "]]];*)  
  
(* OtherInput = ToString[InputString[" Enter Prompt for OtherInput Here "]]];*)
```

```
lettersample = {basepairs} // ToString;  
LetterDNAToNum[Sample_] := ToExpression[StringReplace[ToString[  
  {StringReplace[StringReplace[ToString[{Sample}], {" " → "", " " → "", "{" → "",  
    "}" → "", "(" → "", ")" → "", "[" → "", "]" → "", ";" → "", ":" → "", "_" → "",  
    "+" → "", "&" → "", "/" → "", "." → "", "RowBox" → "", "Null" → "", "  
    " → "", "  
    " → ""}], {"0" → "0,", "1" → "1,", "2" → "2,",  
    "3" → "3,", "A" → "0,", "C" → "1,", "G" → "2,", "T" → "3,", "a" → "0,",  
    "c" → "1,", "g" → "2,", "t" → "3,", "U" → "3", "u" → "3", "N" → ""}]]]  
  ], ",,}" → "}" ]]  
  
(* N Removed by/in the above code *)  
numgenesample = LetterDNAToNum[lettersample];  
lengthofgeneitself = Length[Flatten[numgenesample]];  
M = numgenesample;
```

To produce a .txt file of the gene run the following (grey) cell

To open the created file include `SystemOpen[txtfilename]`

```
(*txtfilename=  
  StringReplace[StringJoin[StringReplace[StringJoin[Wgenesample, " ", source],  
    {"gene" → "", "." → "_", " " → ""}], ".txt"], {"GenBank:" → "gb"}];  
PCV1directory="C:\\Users\\George\\Documents\\SVD DNA stuff\\PCV1 individuals\\";  
Export[FileNameJoin[{PCV1directory,txtfilename}],Flatten[numgenesample]]  
(*Sends the output to a specific file *)  
  
(*Export[txtfilename,Flatten[numgenesample]]*)  
(*Print["This produced a .txt file with the name ", txtfilename]  
  SystemOpen[txtfilename]*)*)
```

C:\\Users\\George\\Documents\\SVD DNA stuff\\PCV1 individuals\\PCV1num50gbDQ358813\_1.txt

## Reading the data into lists

```
PCV1directory = "C:\\Users\\George\\Documents\\SVD DNA stuff\\PCV1 individuals\\";
```

```

ReadList["C:\\Users\\George\\Documents\\SVD
DNA stuff\\PCV1 individuals\\PCV1num1gbKX816645_1.txt"];

StringJoin[PCV1directory, "PCV1num", "k", "gbKX816645_1.txt"]
C:\\Users\\George\\Documents\\SVD DNA stuff\\PCV1 individuals\\PCV1numkgbKX816645_1.txt

ReadList[StringJoin[PCV1directory, "PCV1num", "2", ToString[____ _], ".txt"]]
$Failed

```

```

PCV1ListofLists =
  Import["C:\\Users\\George\\Documents\\SVD DNA stuff\\PCV1 individuals"]

{PCV1num10gbKC924758_1.txt, PCV1num11gbKC894933_1.txt,
PCV1num12gbKC878437_1.txt, PCV1num13gbKC733436_1.txt, PCV1num14gbJX566507_1.txt,
PCV1num15gbKC447455_1.txt, PCV1num16gbAY099501_1.txt, PCV1num17gbJN133303_1.txt,
PCV1num18gbJN133302_1.txt, PCV1num19gbJN398656_1.txt, PCV1num1gbKX816645_1.txt,
PCV1num20gbGU799575_1.txt, PCV1num21gbHM143844_1.txt, PCV1num22gbU49186_1.txt,
PCV1num23gbAY219836_1.txt, PCV1num24gbAY184287_1.txt, PCV1num25gbGU722334_1.txt,
PCV1num26gbGU371908_1.txt, PCV1num27gbDQ650650_1.txt, PCV1num28gbDQ659154_1.txt,
PCV1num29gbDQ659153_1.txt, PCV1num2gbKJ808815_1.txt, PCV1num30gbDQ494788_1.txt,
PCV1num31gbDQ494787_1.txt, PCV1num32gbDQ472016_1.txt, PCV1num33gbDQ472015_1.txt,
PCV1num34gbDQ472014_1.txt, PCV1num35gbDQ472013_1.txt, PCV1num36gbDQ472012_1.txt,
PCV1num37gbAY699796_1.txt, PCV1num38gbAY660574_1.txt, PCV1num39gbFJ475129_2.txt,
PCV1num3gbKJ746930_1.txt, PCV1num40gbY09921_1.txt, PCV1num41gbAF012107_1.txt,
PCV1num42gbFJ159693_1.txt, PCV1num43gbFJ159692_1.txt, PCV1num44gbFJ159691_1.txt,
PCV1num45gbFJ159690_1.txt, PCV1num46gbFJ159689_1.txt, PCV1num47gbEF533941_1.txt,
PCV1num48gbEF493843_1.txt, PCV1num49gbDQ648032_1.txt, PCV1num4gbKJ746929_1.txt,
PCV1num50gbDQ358813_1.txt, PCV1num5gbKJ408799_1.txt, PCV1num6gbKJ408798_1.txt,
PCV1num7gbAY754015_1.txt, PCV1num8gbAY754014_1.txt, PCV1num9gbKF732857_1.txt}

```

This mixed up the order a bit, but doesn't really matter what order PCV1ListofLists is in since we can just make a new list with these more well-ordered

```

PCV1ListofLists[[2]]
Length[PCV1ListofLists]
PCV1num11gbKC894933_1.txt
50

ReadList[StringJoin[PCV1directory, "PCV1num11gbKC894933_1.txt"]];

ReadList[StringJoin[PCV1directory, PCV1ListofLists[[2]]]];

PCV1Individual1 = ReadList[StringJoin[PCV1directory, PCV1ListofLists[[1]]]];

```

```
Do[PCV1Individualk =  
  ReadList[StringJoin[PCV1directory, PCV1ListofLists[[k]]], {k, 1, 7}]]  
Do[PCV1Individualk = ReadList[StringJoin[PCV1directory, PCV1ListofLists[[k+1]]],  
  {k, 8, 49}]]  
PCV1Samples = Table[PCV1Individualk, {k, 1, 49}];  
(*This is a list of the PCV1 samples with the differently-lengthed one,  
  PCV1ListofLists[[8]], excised *)
```

PCV1Individual<sub>39</sub> – PCV1Individual<sub>49</sub>

(\*Can see a few differences between these two samples\*)

[illegible]



```
(*PCV1pythonformdirectory=
"C:\\Users\\George\\Documents\\SVD DNA stuff\\PCV1SamplesPythonForm\\";
Do[Export[StringJoin[{PCV1pythonformdirectory,"PCV1_Sample_",ToString[k],".txt"}],
PCV1Samples[[k]],{k,1,49}]*)
```

## Compressibility

Initial (some of which unusable) samples, See next section for proper samples

```
PCV1directory = "C:\\Users\\George\\Documents\\SVD DNA stuff\\PCV1 individuals\\";
PCV1ListofLists =
  Import["C:\\Users\\George\\Documents\\SVD DNA stuff\\PCV1 individuals"];
Do[PCV1Individualk = ReadList[StringJoin[PCV1directory, PCV1ListofLists[[k]]]],
{k, 1, 7}]
Do[PCV1Individualk = ReadList[StringJoin[PCV1directory, PCV1ListofLists[[k+1]]]],
{k, 8, 49}]
PCV1Samples = Table[PCV1Individualk, {k, 1, 49}];
(*This is a list of the PCV1 samples with the differently-lengthed one,
PCV1ListofLists[[8]], excised *)
```

The above blue cell defines a list of lists PCV1Samples. Each

PCV1Samples[[k]] for k from 1 to 49 corresponds to the complete genome of a PCV1 individual listed in the folder *PCV1 individuals*.

**NOTE** : The name of these text files have nothing to do with the order of PCV1Samples, since the order in the folder was scrambled when importing it to mathematica

Length[PCV1Samples]

49

PCV1Samples[[1]]

```
{0, 1, 1, 0, 2, 1, 2, 1, 0, 1, 3, 3, 1, 2, 2, 1, 0, 2, 1, 2, 2, 1, 0, 2, 1, 0, 1, 1, 3, 1, 2, 2, 1, 0,
2, 1, 2, 3, 1, 0, 2, 3, 2, 0, 0, 0, 0, 3, 2, 1, 1, 0, 0, 2, 1, 0, 0, 2, 0, 0, 0, 0, 2, 1, 2, 2,
1, 1, 1, 2, 1, 0, 0, 1, 1, 1, 1, 0, 3, 0, 0, 2, 0, 2, 2, 3, 2, 2, 2, 3, 2, 3, 3, 1, 0, 1, 1, 1,
3, 3, 0, 0, 3, 0, 0, 3, 1, 1, 3, 3, 1, 1, 2, 0, 2, 2, 0, 2, 2, 0, 2, 0, 0, 0, 0, 1, 0, 0, 0,
0, 3, 0, 1, 2, 2, 2, 0, 2, 1, 3, 3, 1, 1, 0, 0, 3, 1, 3, 1, 1, 1, 3, 3, 3, 3, 3, 2, 0, 3, 3, 0,
3, 3, 3, 3, 2, 3, 3, 3, 2, 1, 2, 2, 0, 2, 0, 2, 2, 0, 0, 2, 2, 3, 3, 3, 2, 2, 0, 0, 2, 0, 2, 2,
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3, 3, 3, 2, 1, 3, 0, 0, 2, 0, 0, 2, 1, 0, 2, 0, 1, 3, 3, 3, 3, 0, 0, 1, 0, 0, 2, 2, 3, 2, 0, 0,
2, 3, 2, 2, 3, 0, 3, 3, 3, 3, 2, 2, 3, 2, 1, 1, 1, 2, 1, 3, 2, 1, 1, 0, 1, 0, 3, 1, 2, 0, 2, 0,
0, 0, 2, 1, 2, 0, 0, 0, 2, 2, 0, 0, 1, 1, 2, 0, 1, 1, 0, 2, 1, 0, 2, 0, 0, 3, 0, 0, 0, 2, 0,
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1, 2, 2, 2, 0, 0, 2, 0, 3, 2, 1, 0, 2, 1, 0, 2, 1, 2, 3, 2, 0, 3, 3, 2, 2, 0, 0, 2, 0, 1, 0,
```

```

2, 1, 3, 2, 3, 0, 1, 0, 1, 2, 3, 1, 0, 3, 0, 2, 3, 2, 2, 2, 1, 1, 1, 2, 1, 1, 1, 2, 2, 3, 3,
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1, 2, 2, 3, 0, 0, 1, 2, 1, 1, 3, 1, 1, 3, 3, 2, 2, 1, 1, 0, 1, 2, 3, 1, 0, 3, 1, 1, 3, 0, 3,
0, 0, 0, 0, 2, 3, 2, 0, 0, 0, 2, 0, 0, 2, 3, 2, 1, 2, 1, 3, 2, 1, 3, 2, 3, 0, 2, 3, 2, 3, 3}

```

## Comparison of sample ordering

```

testset = {0, 1, 0, 2, 0, 3, 0, 0, -1, -2, -1, -2, 0, 0, -3, 0};
Count[testset, 0]
Length[testset]
Length[testset] - Count[testset, 0] (*Number of nonzero elements *)
8

```

8

```

indivcomparison[k_] := PCV1Individual1 - PCV1Individualk
numofdiffelements[k_] := Length[indivcomparison[k]] - Count[indivcomparison[k], 0]
(*Number of different elements between PCV1Individual1 and PCV1Individualk *)

```

```

Mean[Table[numofdiffelements[k], {k, 1, 49}]] // N
Median[Table[numofdiffelements[k], {k, 1, 49}]] // N
229.878

```

16.

```

Do[If[numofdiffelements[k] > 30, Print[k], 0], {k, 1, 49}]
(*Gives us the k for which the number of different elements is more than 30 *)

```

7

11

12

21

23

29

33

40

43

47

48

```

(*Do[Print[{k,numofdiffelements[k]}],{k,1,49}] (*To check the above*)*)

```

Note that there are 11 samples for which the number of different elements is more than 30, delete these in the python code and rename some others as follows:

Now we remove these and redefine for k of PCV1\_Sample\_k.txt

k= 49 -&gt; 7

46 to 11

45 to 12

44 to 21

42 to 23

41 to 29

39 to 33

So we now have  $49 - 11 = 38$  usable samples

## Usable Samples

```
PCV1Sample[k_] := ReadList[StringJoin[
  "C:\\Users\\George\\Documents\\SVD DNA stuff\\Usable PCV1 Samples\\PCV1_Sample_",
  ToString[k], ".txt"]]
```

```
(*This is a defines PCV1Sample[k] as the list form of PCV1_Sample_k.txt ,
the k-th Usable PCV1 samples,
THE NUMBERS DONT ALL LINE UP WITH THOSE IN PREVIOUS PARTS,
I.E. PCV1_Sample_38.txt here is NOT same as the old PCV1_Sample_38.txt,
renumbered them *)
```

```
Length[ ( PCV1Sample[1] - PCV1Sample[9] ) ] -  
Count[ ( PCV1Sample[1] - PCV1Sample[2] ), 0] (*Number of differences *)
```

30

```
( PCV1Sample[1] - PCV1Sample[9] ) [ [k] ]
```



[illegible]

```
Union[Table[If[(PCV1Sample[1] - PCV1Sample[9])[[k]] == 0, 0, k], {k, 1, 1759}]]
```

(\*Places where these samples differ\*)

$$\{0, 465, 469, 658, 760, 907, 910, 916, 956, 958, 1032, 1216, 1321, 1346, 1378, 1400, 1503, 1510, 1519, 1578, 1587, 1670, 1757\}$$

```

differingbasepairlocations[i_, j_] :=

```

```
Union[Table[If[(PCV1Sample[i] - PCV1Sample[j])[[k]] == 0, 0, k], {k, 1, 1759}]]
```

(\*Places where these samples differ\*)

```
Table[differingbasepairlocations[i, 9], {i, 1, 8}]
```

\$Aborted