

MinimalMarker

Installation Guide and Manual

Version 3

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Step 1: Visit the website of ActiveState

<http://www.activestate.com/activeperl>


Webpage Screenshot

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Step 2: Download ActivePerl

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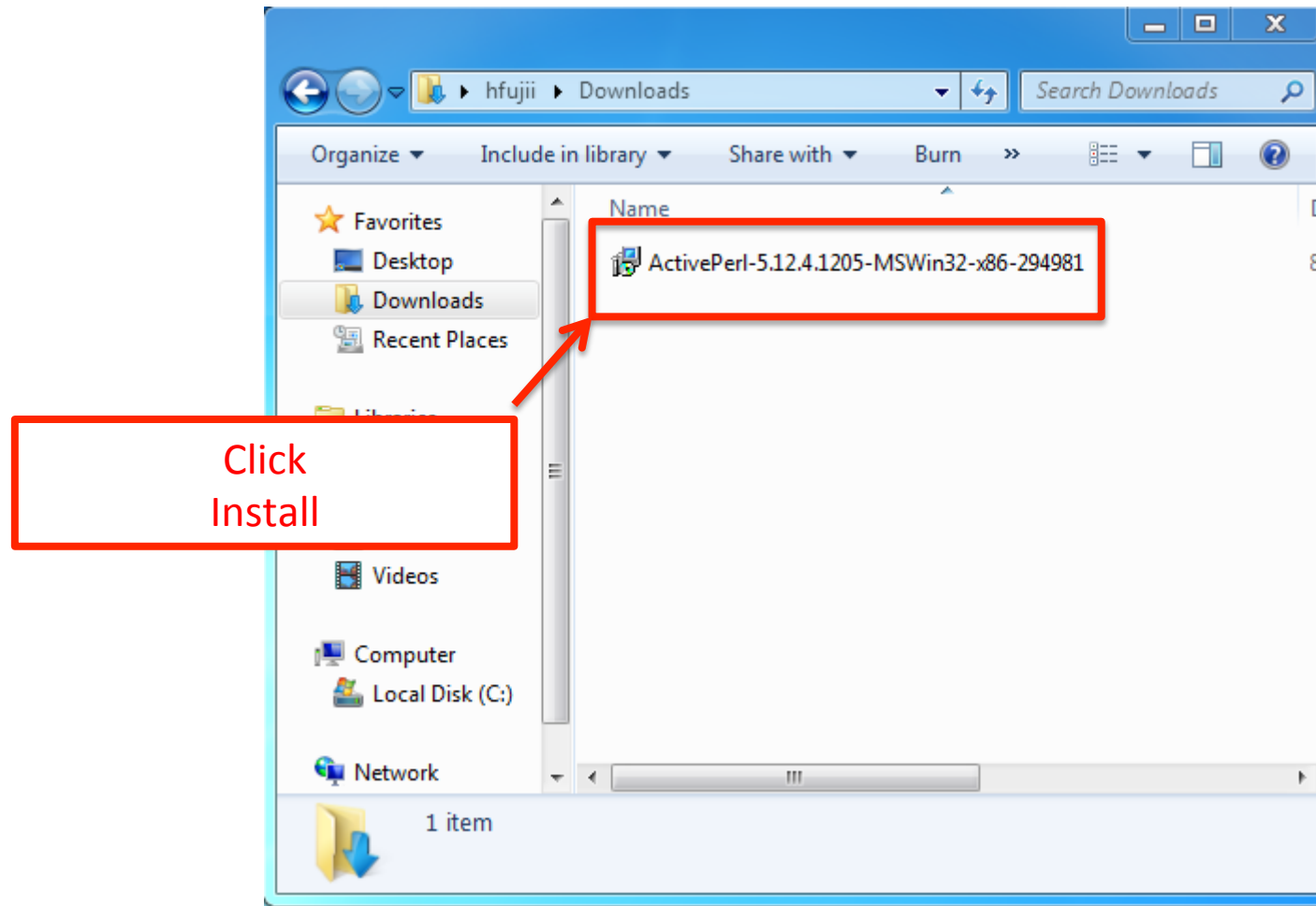
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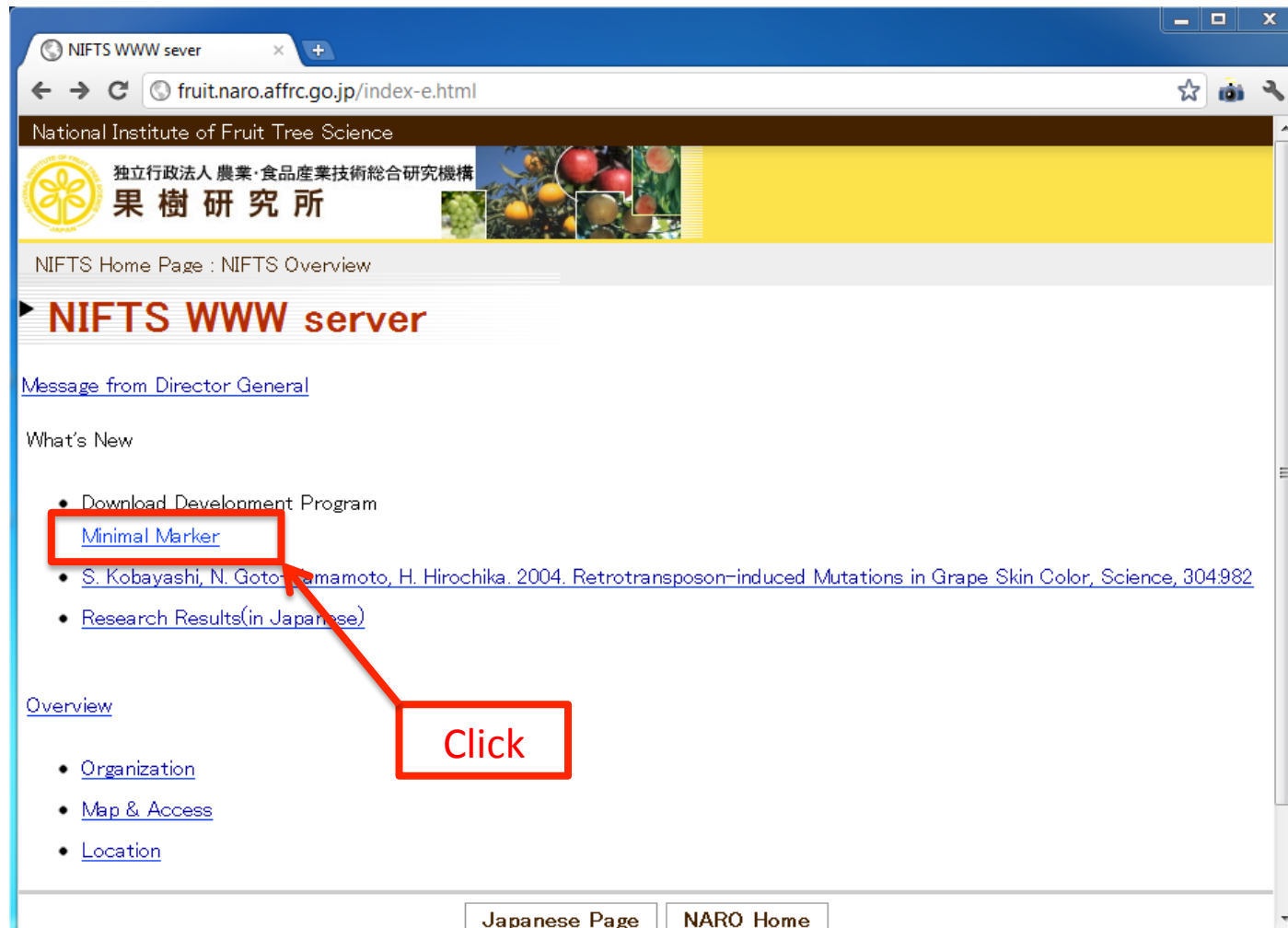
<http://www.activestate.com/activeperl/downloads>

Step 3: Install ActivePerl



Step 4: Visit the website of NIFTS

<http://fruit.naro.affrc.go.jp/index-e.html>



Step 5: Download MinimalMarker

The image shows two overlapping browser windows from the National Institute of Fruit Tree Science (NIFTS). The background window displays the 'Minimal Marker' page, which includes a description of the software, system requirements, and a disclaimer. The foreground window shows the 'Install the software' section, which lists four steps for installation. A red box highlights the link 'I agree with a policy of disclaimer and copyright in the software and download it.' with an arrow pointing to it from a red box labeled 'Click'. Another red box labeled 'Click' points to the 'Contact us' link at the bottom of the foreground window.

Minimal Marker

The computer program, MinimalMarker, can identify all the appropriate table using a co-dominant marker set or dominant marker set. In many of the markers listed in a variety/marker type table to discriminate is the minimal number of a marker set that can discriminate all varieties by MinimalMarker, one can discriminate varieties efficiently in terms of

System requirement

MinimalMarker runs in the execution environment of Perl5, such as V you have to install Perl5 environment such as ActivePerl (<http://www.activestop.com/>)

Disclaimer

Install the software

1. Identify the path to the Perl execution environment
2. Download the software from the following URL
3. Software is compressed by ZIP format.
4. Compressed file includes 4 files (program source, manual, sample for input data, and sample for output data Put this program on appropriate directory of the computer)

[I agree with a policy of disclaimer and copyright in the software and download it.](#)

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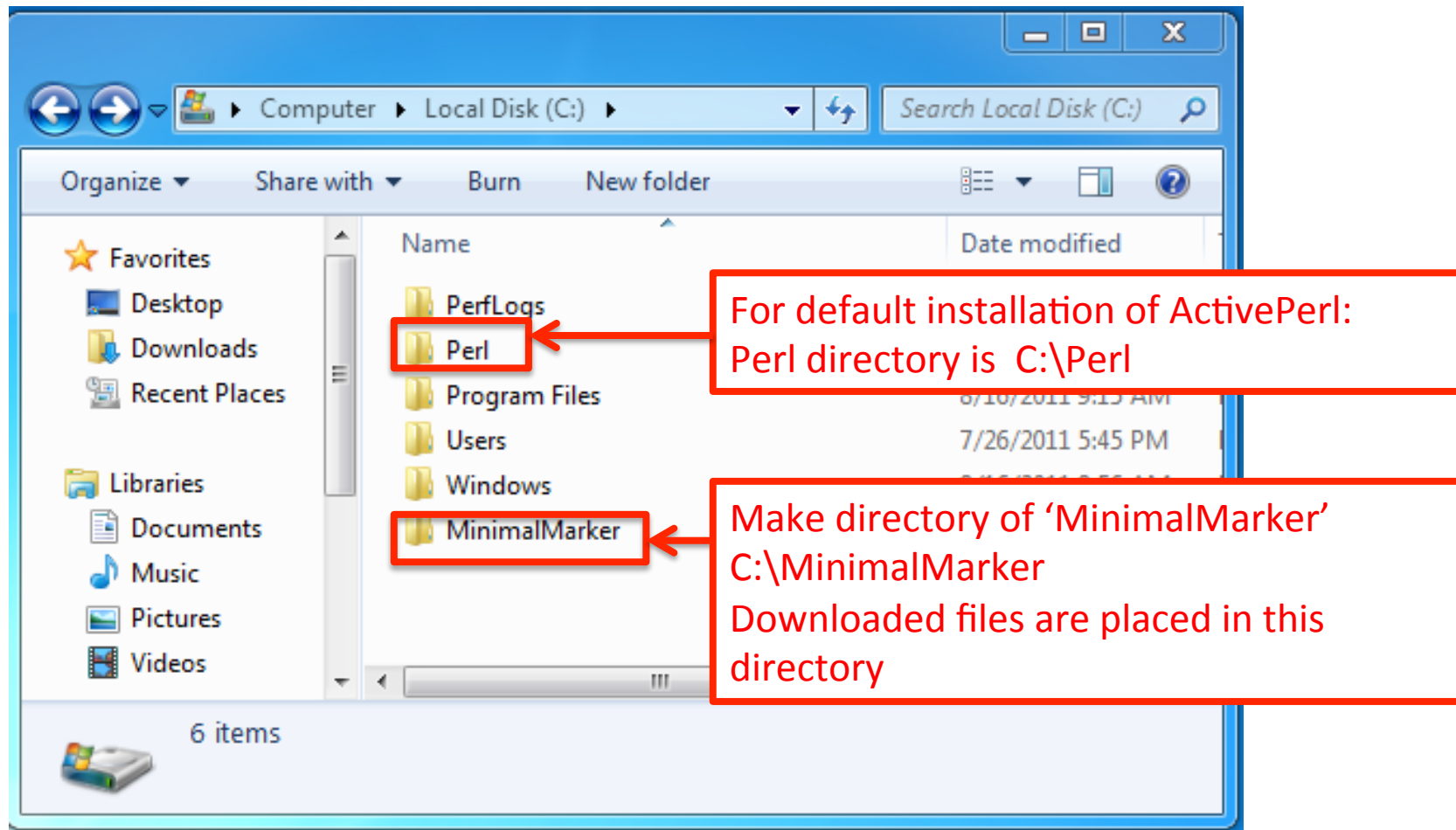
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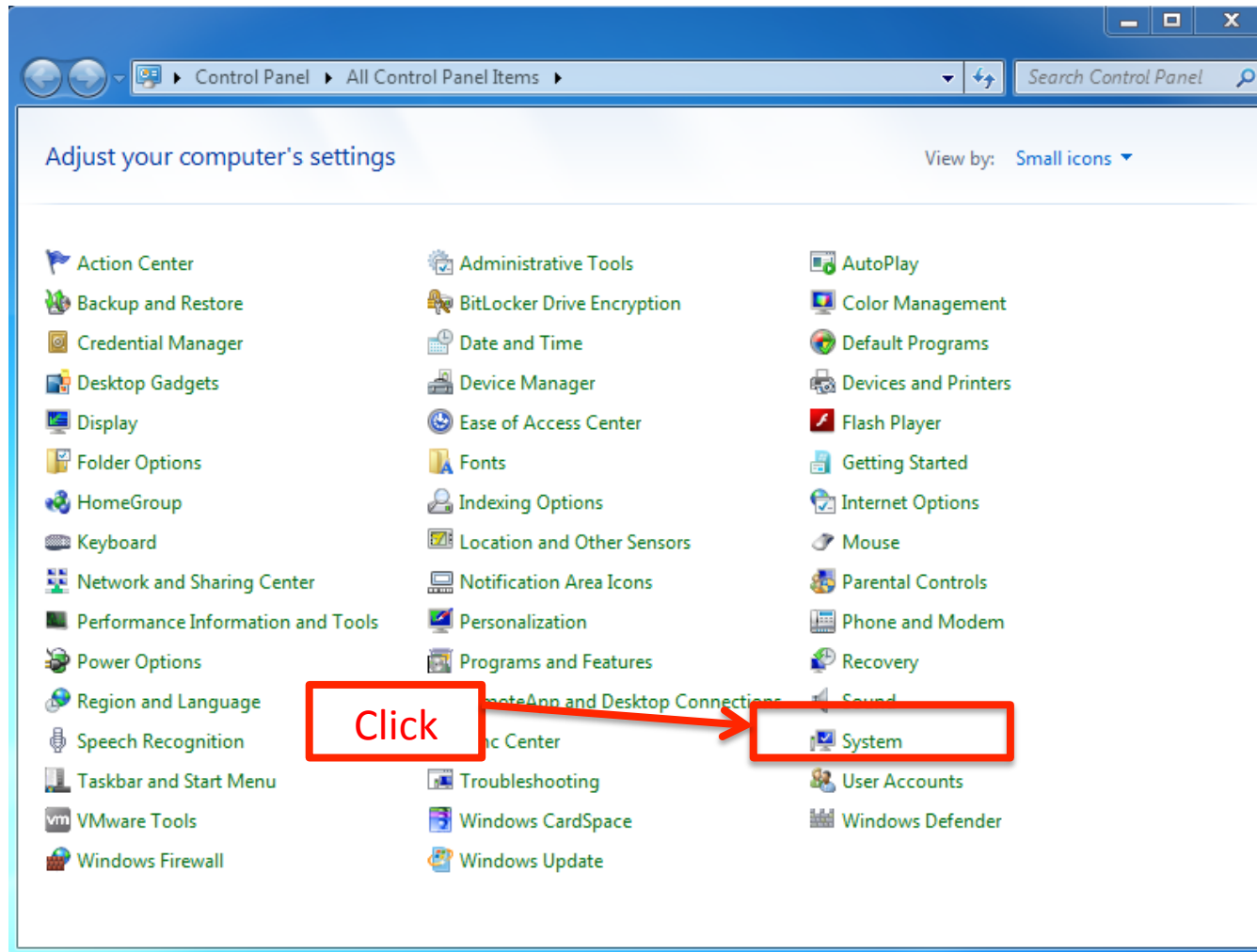
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Step 6: Check Perl directory

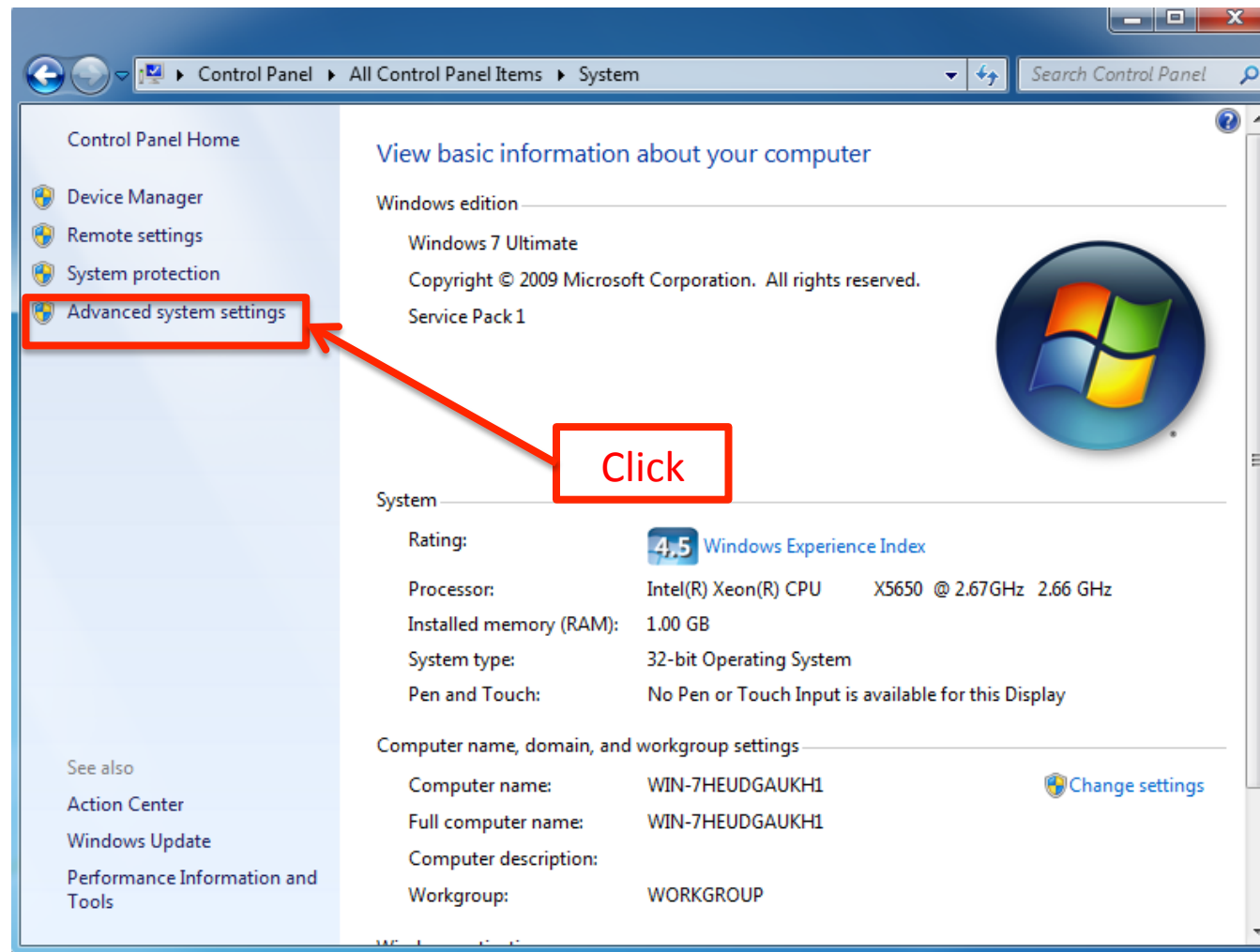
Step 7a: Make directory for MinimalMarker



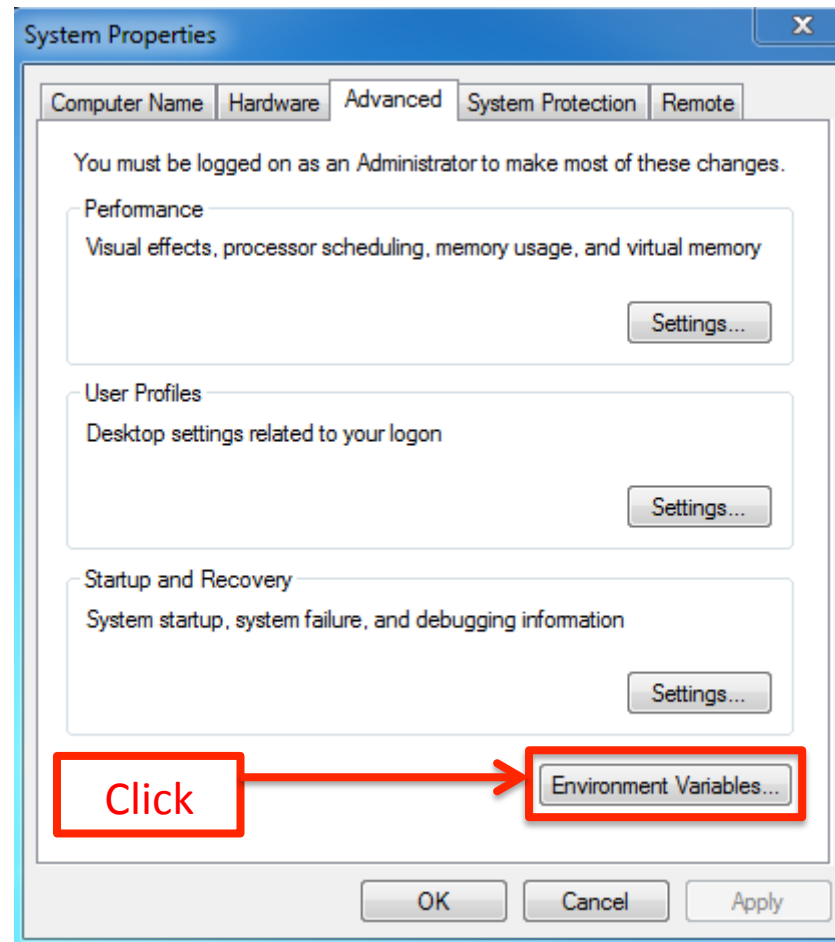
Step 7b: Go to Control Panel > System



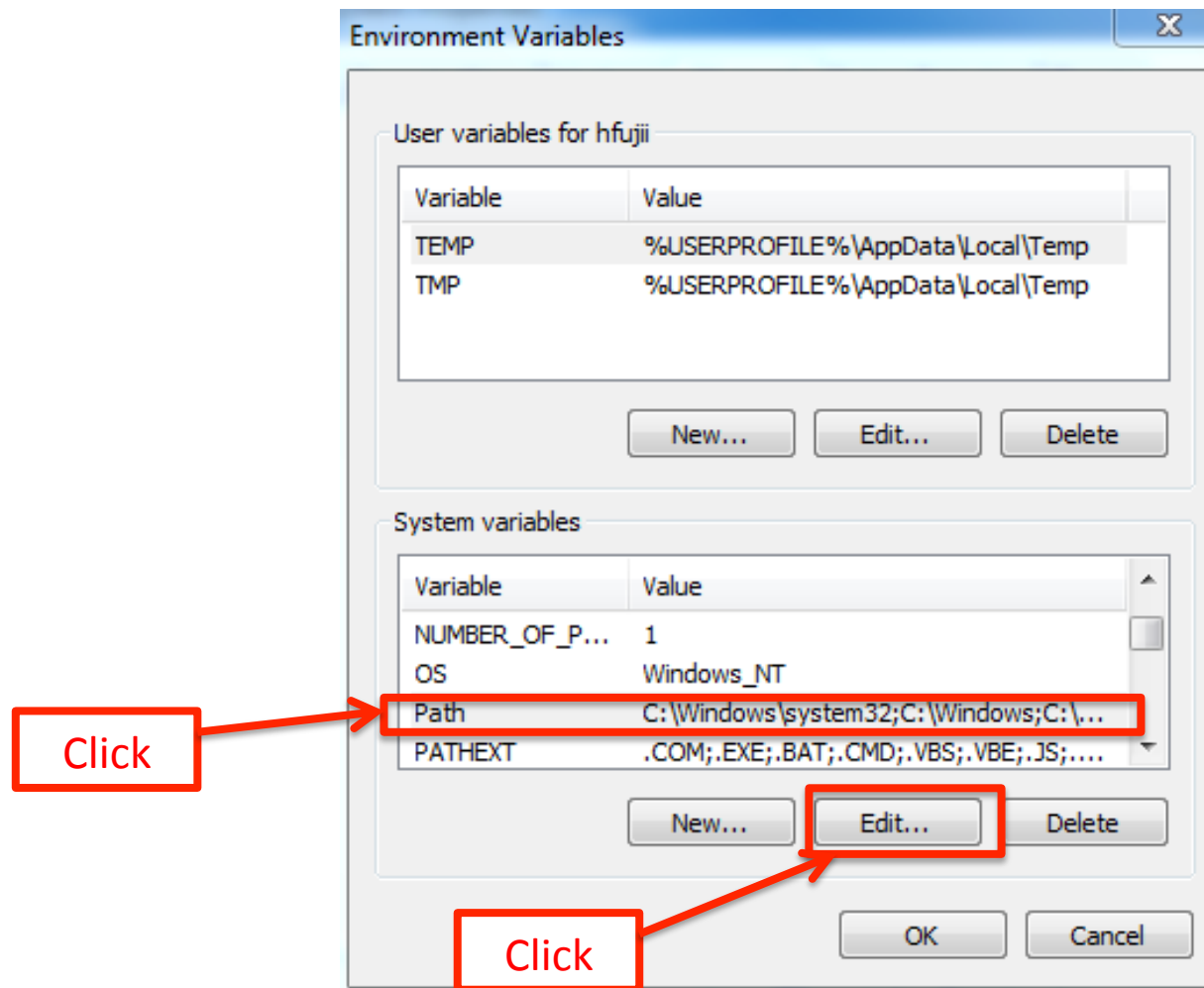
Step 8: Click Advanced system settings



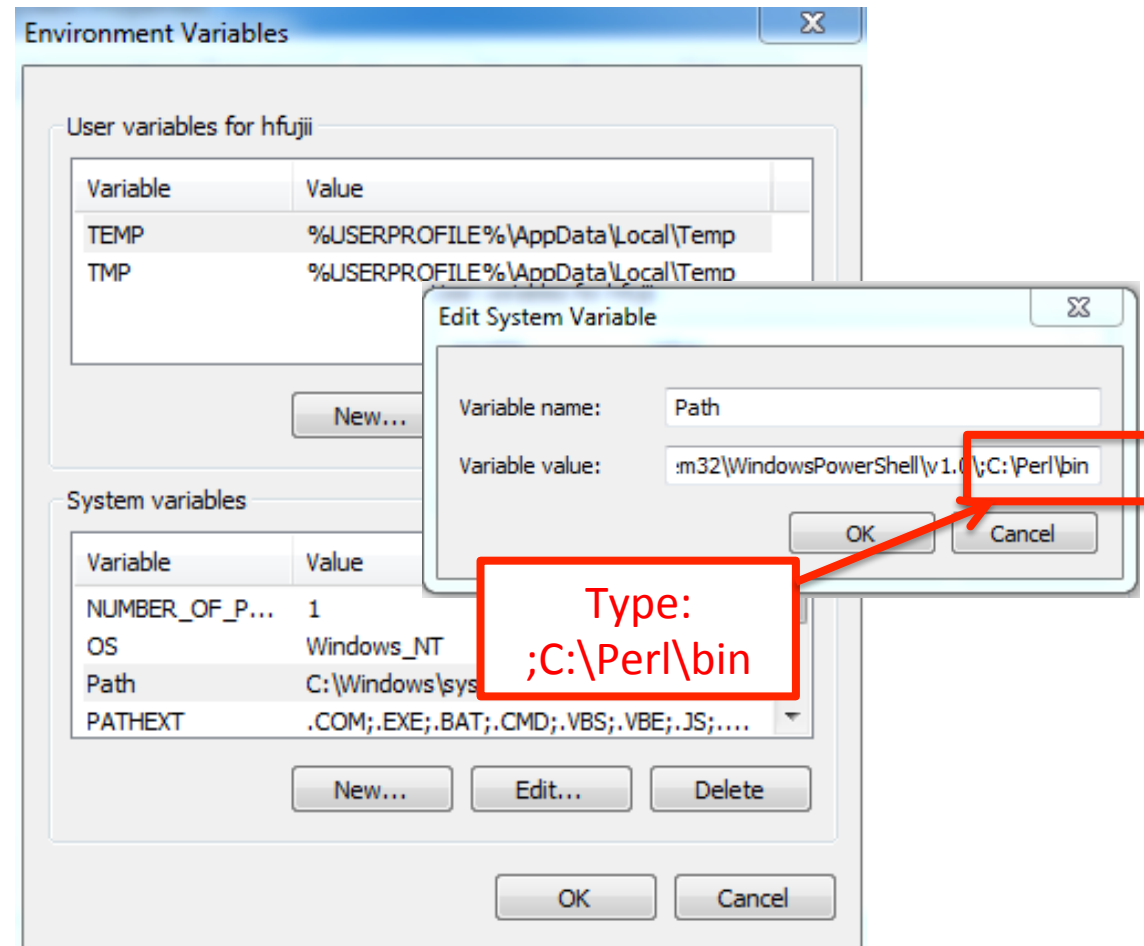
Step 9: Click Environment Variables



Step 10: Select 'Path' and Click 'Edit'



Step 11: Add “;C:\Perl\” to Path



Step 12: Confirmation of Perl

```
Command Prompt
C:\Users\hfujii>perl -h

Usage: C:\Perl\bin\perl.exe [switches] [--] [program]
  -0[octall]      specify record separator (<\0, i
  -a              autosplit mode with -n or -p (<splits $_ into @F>)
  -C[number/list] enables the listed Unicode features
  -c              check syntax only (runs BEGIN and CHECK blocks)
  -d[:debugger]   run program under debugger
  -D[number/list] set debugging flags (argument is a bit mask of alphabets)
  -e program      one line of program (several -e's allowed, omit programf
  -E program      like -e, but enables all optional features
  -f              don't do $sitelib/sitecustomize.pl at startup
  -F/pattern/     split() pattern for -a switch (///'s are optional)
  -i[extension]   edit <> files in place (makes backup if extension suppli
  -Idirectory     specify @INC/#include directory (several -I's allowed)
  -l[octall]      enable line ending processing, specifies line terminator
  -[mM][[-lmodule execute "use/no module..." before executing program
  -n              assume "while (<>) { ... }" loop around program
  -p              assume loop like -n but print line also, like sed
  -s              enable rudimentary parsing for switches after programfil
  -S              look for programfile using PATH environment variable
  -t              enable tainting warnings
  -T              enable tainting checks
  -u              dump core after parsing program
  -U              allow unsafe operations
  -v              print version, subversion (includes VERY IMPORTANT perl
  -V[:variable]   print configuration summary (or a single Config.pm varia
  -w              enable many useful warnings (RECOMMENDED)
  -W              enable all warnings
  -x[directory]   strip off text before #!perl line and perhaps cd to dire
  -X              disable all warnings

C:\Users\hfujii>
```

Use Command Prompt:
Start -> All programs -> Accessories

Type:
Perl -h

Help menu of
Perl appears here

Step 13: Confirmation of MinimalMarker

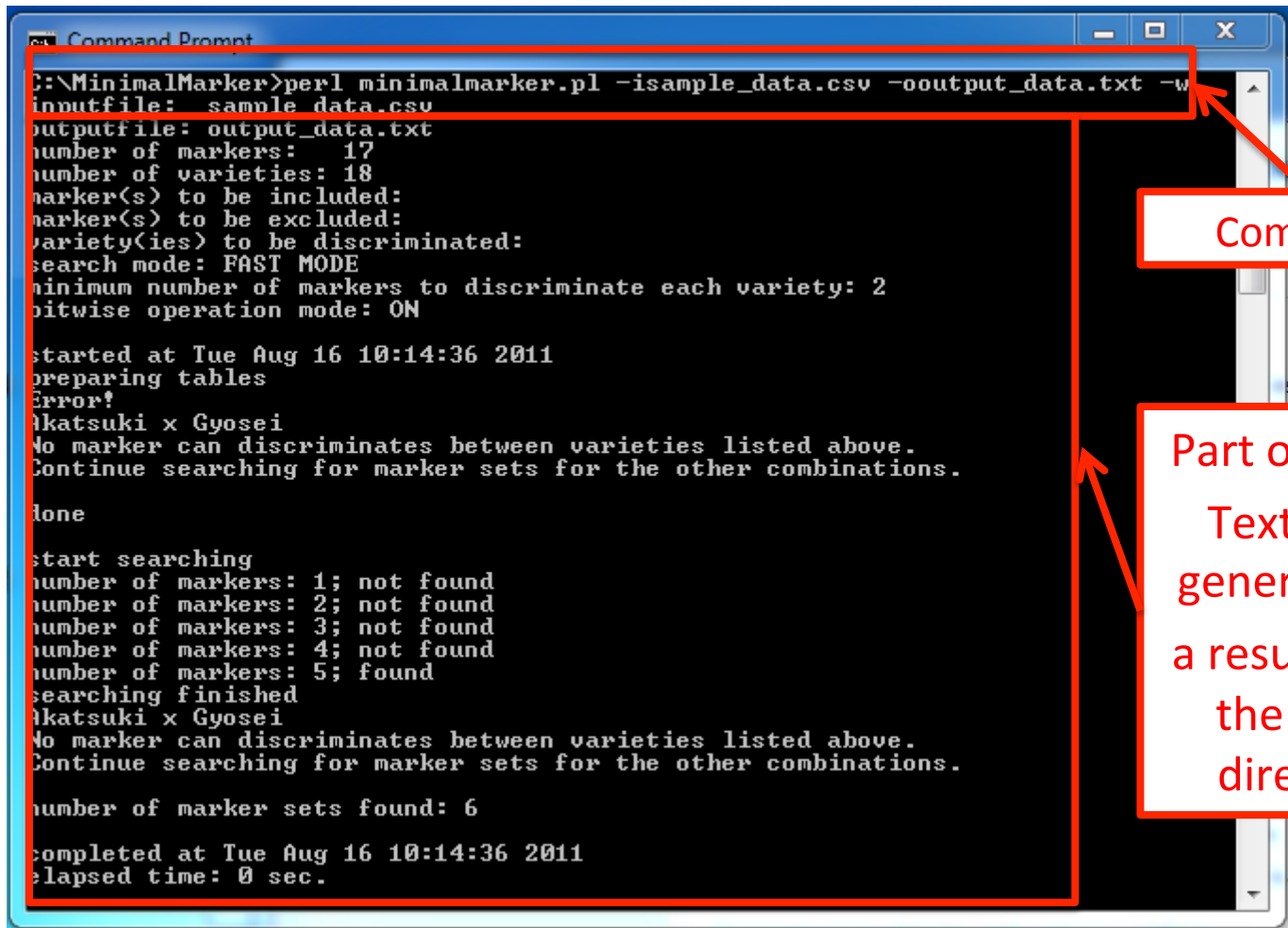
```
CA: Command Prompt
C:\Users\hfujii>cd \minimalmarker
C:\MinimalMarker>perl minimalmarker.pl -h
program name: minimalmarker
a program for identification of discriminating gene marker sets
usage: perl minimalmarker.pl [-switches]
-h          print this message
-g          ignore order of characters in each data
-t          print each marker set instantly after found
-w[number]  discriminate each variety by at least specified
            -w means -w2
-p[1/2]     print data table etc.<1:print and search, 2:print
-m[0/1/2/n] search mode; 0:slow<enumeration method>, 1:fast<default>
            2:heuristic<greedy algorithm>, n:heuristic with n power<n>2>
-b[0/1]     bitwise operation; 0: do not use, 1:use<fast; default>
-d[1/2]     use demo data; 1:Fujii's, 2: in J. Bioinfo. Comput. Biol.
-k[symbol]  symbol for data not determined <case sensitive>
-v[number]  variety to be discriminated
-r[number]  number of distribution to calculate on computers
-a[number]  search marker sets with extra cardinal number
-s[number]  number of markers start searching
-e[number]  number of markers stop searching<-1:search all>
-n[number]  marker to be included in a marker set
-x[number]  marker to be excluded from a marker set
-il[filename] input file name
-ol[filename] output file name
C:\MinimalMarker>
```

Change directory:
Type: `cd \minimalmarker`

Type:
`Perl minimalmarker.pl -h`

Help menu of MinimalMarker appears here

Overview of operation



```
C:\MinimalMarker>perl minimalmarker.pl -isample_data.csv -ooutput_data.txt -w
inputfile: sample_data.csv
outputfile: output_data.txt
number of markers: 17
number of varieties: 18
marker(s) to be included:
marker(s) to be excluded:
variety(ies) to be discriminated:
search mode: FAST MODE
minimum number of markers to discriminate each variety: 2
bitwise operation mode: ON

started at Tue Aug 16 10:14:36 2011
preparing tables
Error!
Akatsuki x Gyosei
No marker can discriminate between varieties listed above.
Continue searching for marker sets for the other combinations.

done

start searching
number of markers: 1; not found
number of markers: 2; not found
number of markers: 3; not found
number of markers: 4; not found
number of markers: 5; found
searching finished
Akatsuki x Gyosei
No marker can discriminate between varieties listed above.
Continue searching for marker sets for the other combinations.

number of marker sets found: 6

completed at Tue Aug 16 10:14:36 2011
elapsed time: 0 sec.
```

Command

Part of result:
Text file is generated as a result file in the same directory

MinimalMarker Manual

- MinimalMarker Manual
-
- Files for this manual:
- Program file: minimalmarker.pl
- Sample data: sample_data.csv (Yamamoto et al., 2003, Breed Sci 2003, 53:35-40)
- Output file of sample data: sample_data_output.txt
-
- The input table should be described in comma separated value (CSV) format as shown in Fig. 1. MinimalMarker is acceptable for co-dominant marker of diploid (Fig. 1A) and dominant marker (Fig. 1B), co-dominant marker with any number of alleles (Fig. 1C) and numerical notation of SSR marker (Fig. 1D) because they can all be dealt with as a problem of character string comparison in the program. In the character notation, the order of the characters can be ignored. It is judged that 'AB' is the same as 'BA'. In the case of numerical notation of co-dominant SSR marker, it must be unified in the descending order or the ascending order and the delimiter such as '/' is necessary between the figures.
- The format of command line is shown in Fig. 2 and an example of output data is shown in Fig. 3. Table 1 shows program options.

MinimalMarker Manual Fig. 1

A	B
Variety,V1,V2,V3,V4,V5 M1,aa,ab,aa,ab,aa M2,aa,ab,ab,aa,bb M3,aa,aa,aa,aa,bb M4,aa,aa,ab,ab,aa M5,ab,ab,bb,ab,aa	Variety,V1,V2,V3,V4,V5 M1,+,+,+,+,+ M2,+,-,-,-,+ M3,+,+,+,- M4,+,-,+,- M5,-,+,-,-,+
C	D
Variety,V1,V2,V3,V4,V5 M1,ab,ad,ae,bf,cg M2,aa,bb,cc,dd,ee M3,ab,cd,ef,gh,hi M4,bc,cd,ac,de,dd M5,ab,ab,bb,ab,aa	Variety,V1,V2,V3,V4,V5 M1,80/84,80/84,84/84,80/84,80/84 M2,78/94,78/94,78/88,88/94,80/94 M3,193/197,193/197,195/197,195/201,193/197 M4,177/195,195/195,177/195,177/177,177/195 M5,136/136,136/136,132/136,136/136,136/136

Fig. 1. Data input format to MinimalMarker. The program requires input files in comma separated value (CSV) format. First term of the data should be 'Variety' in the first line and following it names of variety must be written in first line. After second line, names of markers must be written in first column and following maker types. Any words are permitted in the variety names and the marker names instead of 'V1' or 'M1'. (A) Character notation of co-dominant marker of diploid and it is the input example of sample data shown in Table1. (B) +/- notation of dominant marker. (C) co-dominant marker with any number of alleles, (D) Numerical notation of SSR marker of diploid. 2 figures must be separated by delimiter such as '/'.

MinimalMarker Manual Fig. 2

Format:

```
>perl minimalmarker.pl [option switch] -i[input filename(s)] -o[output filename(s)]
```

Example:

```
>perl minimalmarker.pl -p1 -w -g -m1 -b1 -s3 -n1 -n2 -x3 -x4 -itestin.csv -otestout.txt
```

Fig. 2. Format of command line of MinimalMarker and the example. Input file(s) and Output file(s) must be set. Refer to Table6 for the option switches.

MinimalMarker Manual Fig. 3

```
number of markers: 17
number of varieties: 17
option switches:
-p: 0, -w: OFF, -g: OFF, -m: 1, -b: ON
Akatsuki x Gyosei
No marker(s) can discriminate between varieties listed above
number of marker sets found: 6
list of marker sets found:
M1a,M4c,MA023a
M4c,MA007a,MA023a
M4c,MA007a,MA035a
M4c,MA014a,MA023a
M4c,MA015a,MA027a
M4c,MA027a,MA035a
elapsed time: 0 sec.
```

Fig. 3. Sample data output. Peach data was used as sample data (Yamamoto et al., 2003, Breed Sci 2003, 53:35-40.). The program outputted that SSR genotypes of 'Akatsuki' and 'Gyosei' are identical, and computation was continued. Six minimal marker sets which consist of three markers were outputted.

MinimalMarker Manual Table 1

Table 1 Program options for MinimalMarker

Option	Arguments	Significance
-p[0/1/2]	0: Do not print the table (default) 1: Print the table 2: Print the table and the program quits	The table shows the possibility of discrimination between two varieties by each marker, as in Table 3.
-w		Under the condition that at least two markers are required for discriminating between every pair of cultivars, minimal marker set(s) are searched.
-s[number]	Number of markers which starts search	Specifies the number of markers required to start the search. In case of dominant markers, at least 7 markers are required to identify 100 varieties. In this case, the search is completed quickly using the -s7 option switch.
-e[number]	Number of markers which stops the search -1: Search the total number of markers.	Specifies the number of markers required to end the search. Even if no minimal marker set is identified, the search can be stopped when it is expected that the computation time will be too large to be practical.
-n[number]	Row number of the marker One or more specification is possible (ex. -n1 -n2)	Specifies markers that must be included in the minimal marker sets.
-x[number]	Row number of the marker One or more specification is possible (ex. -x1 -x2)	Specifies markers that must be excluded from the minimal marker sets.
-v[number]	Column number of the variety(ies) One or more specification is possible (ex. -v1 -v2)	Specifies variety(ies) and the minimal marker set(s) that discriminate the specified variety(ies) from other varieties in a variety/marker type table.
-m[0/1/2]	0: Enumeration method 1: Branch-and-bound method (default) 2: Heuristic method	Computation is accelerated using the branch-and-bound method. The same result is obtained by the enumeration method and the branch-and-bound method. Computation is drastically accelerated using the heuristic method, but it does not guarantee whether the marker sets obtained are minimal nor whether all minimal marker set(s) are identified.
-b[0/1]	0: Arithmetic operation 1: Bit operation (default)	Computation is accelerated using the bit operation when the amount of computation time required to obtain the results becomes too large. The same result is obtained by the arithmetic operation and the bit operation.

MinimalMarker

Installation Guide and Manual Version

- June 11 2011 version 1
- August 16 2011 version 2
- September 06 2011 version 3