FleXScan User Guide

for version 1.1

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http://www.niph.go.jp/soshiki/gijutsu/index_e.html

Introduction

The FlexScan software has been developed to analyze spatial count data using the flexible spatial scan statistic developed by Tango and Takahashi (2005) and Kulldorff's circular spatial scan statistic (1997). It looks like the SaTScan software (2005) developed by Kulldorff together with Information Management System Inc. but its current version is restricted to spatial analyses. As Kulldorff's circular spatial scan statistic uses a "circular window" with variable size to define the potential cluster area, it is difficult to correctly detect noncircular clusters such as those along a river. Most geographical areas are noncircular. Tango and Takahashi's flexible spatial scan statistic, on the other hand, is designed so that the detected cluster is allowed to be flexible in shape while at the same time the cluster is confined within relatively small neighborhoods of each region.

It is a free software program designed for any of the following interrelated purposes:

1) To evaluate reported spatial disease clusters, to see if they are statistically significant.
2) To test whether a disease is randomly distributed over space.
3) To perform geographical surveillance of disease, to detect areas of significantly high rates.

FleXScan uses a Poisson model, where the number of events in an area is Poisson distributed according to a known underlying population at risk. The data may be either aggregated at the census tract, zip-code, county or other geographical level. FleXScan can adjust for the underlying inhomogeneity of a background population and for any number of categorical covariates provided by user.

References

- Tango T. and Takahashi K. (2005). A flexibly shaped spatial scan statistic for detecting clusters. International Journal of Health Geographics 2005, **4**:11. [Open Access] http://www.ij-healthgeographics.com/
- Kulldorff M. (1997). A spatial scan statistic. Communications in Statistics: Theory and Methods, 26:1481-1496.
- Kulldorff M. and Information Management Services, Inc (2005). SaTScan™ v6.0: Software for the spatial and space-time scan statistics. http://www.satscan.org/

Downloading and Installation

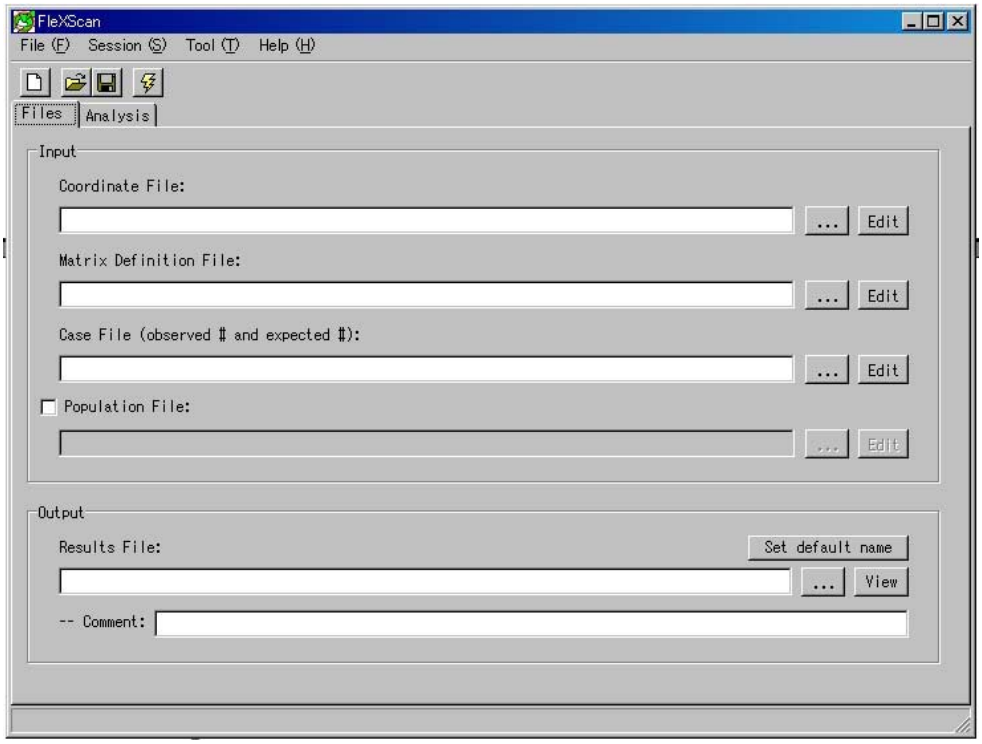
To install FleXScan, go to the Department of Technology Assessment and Biostatistics, National Institute of Public Health Web site at :

http://www.niph.go.jp/soshiki/gijutsu/index_e.html

and select the download link. After downloading the FleXScan installation executable to your PC, click on its icon and install the software by following the step-wise instructions.

System requirements:

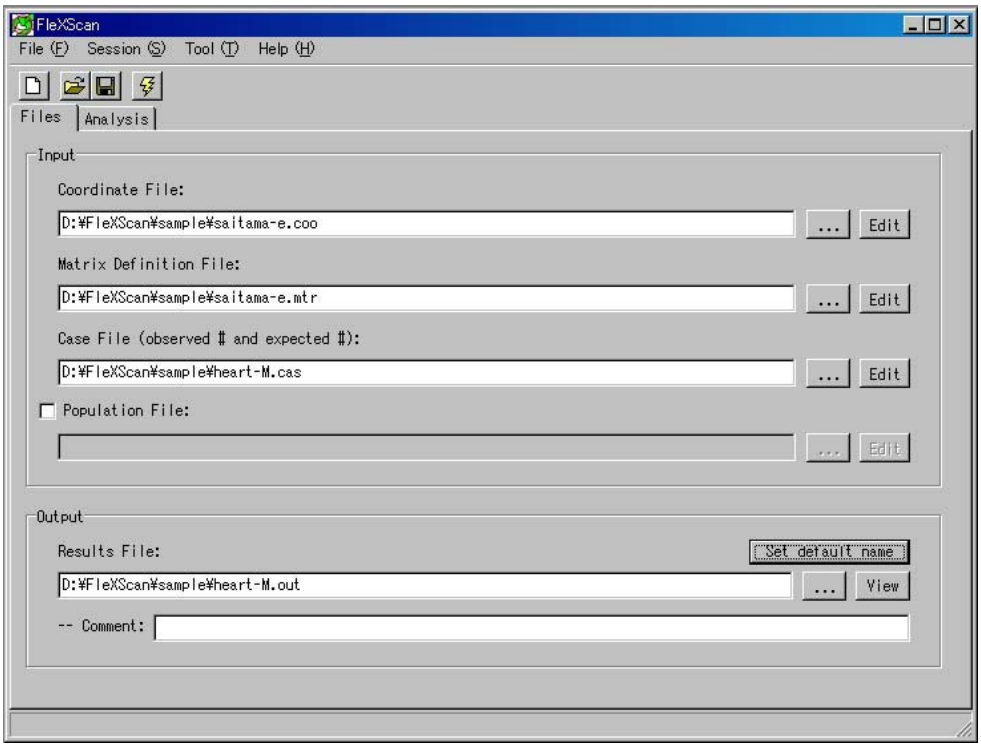
- Intel® Pentium® processor III or higher
- Microsoft® Windows® 2000 or Windows XP
- 256MB of RAM (recommended)



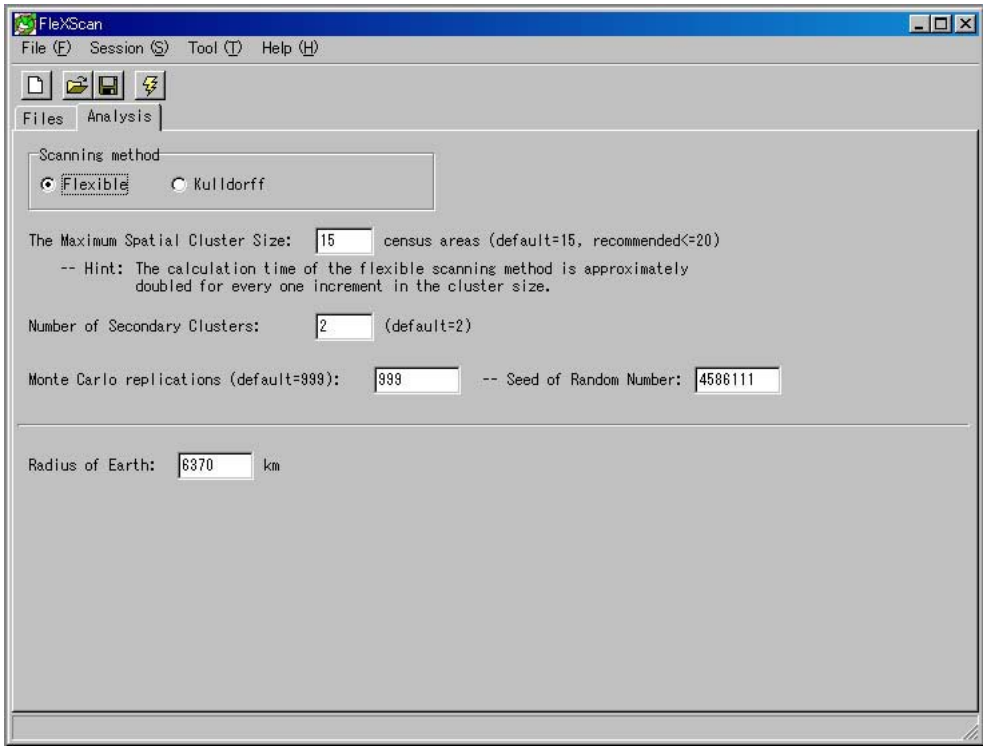
Test Run

Before using your own data, we recommend trying the sample data set provided with the software. To perform a test run:

1. Click on the FleXScan application icon.
2. Select the following files in the sample folder (C:/Program Files/FleXScan/sample, default) as input data.
   ① Coordinate File: “saitama-e.coo”
   ② Matrix Definition File: “saitama-e.mtr”
   ③ Case File: “heart-M.cas” or any cas files.
   ④ Keep Population File: check off.
3. Click on ‘Set default name’ or input any file name to output the results.



4. Next, click on ‘Analysis’ tab and select ‘Flexible’ or ‘Kulldorff’ in the ‘Scanning method.’



5. Click on ‘Run’ button ( ) or select ‘Session’ - ’Run’.
6. After a while, the results file and the results map will appear.

Results:

‘MOST LIKELY CLUSTER’

Census areas included. : kawaguchi, souka, koshigaya,…

are regions detected as the most likely cluster, and its significance is also given by

P-value .....: 0.001

Regardless of the p-value, the most likely cluster is shown on the map with red color.

heart-M.out - メモ帳

ファイル(F)　編集(E)　書式(O)　表示(V)　ヘルプ(H)

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------------------------------------------------
            FleXScan ver.1.1
------------------------------------------------

Scanning method: Flexible spatial scan by data length.

Program run on: Fri Jan 14 20:56:31 2005

Purely Spatial analysis
scanning for clusters with
high rates using the Poisson model.

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SUMMARY OF DATA

Limit length of cluster: 15
Number of census areas.: 92
Total cases ...........: 16462

---------------------------------------------------------

MOST LIKELY CLUSTER

1.Census areas included .: kawaguchi, souka, koshigaya, warabi, hatogaya, yoshikawa, sugito, matsubushi, syouwa
  Maximum distance.......: 24.2393 km (areas: kawaguchi to sugito)
  Number of cases .......: 3097          (2812.38 expected)
  Overall relative risk .: 1.1012
  Log likelihood ratio ..: 16.9276
  Monte Carlo rank ......: 1/1000
  P-value ...............: 0.001

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SECONDARY CLUSTERS
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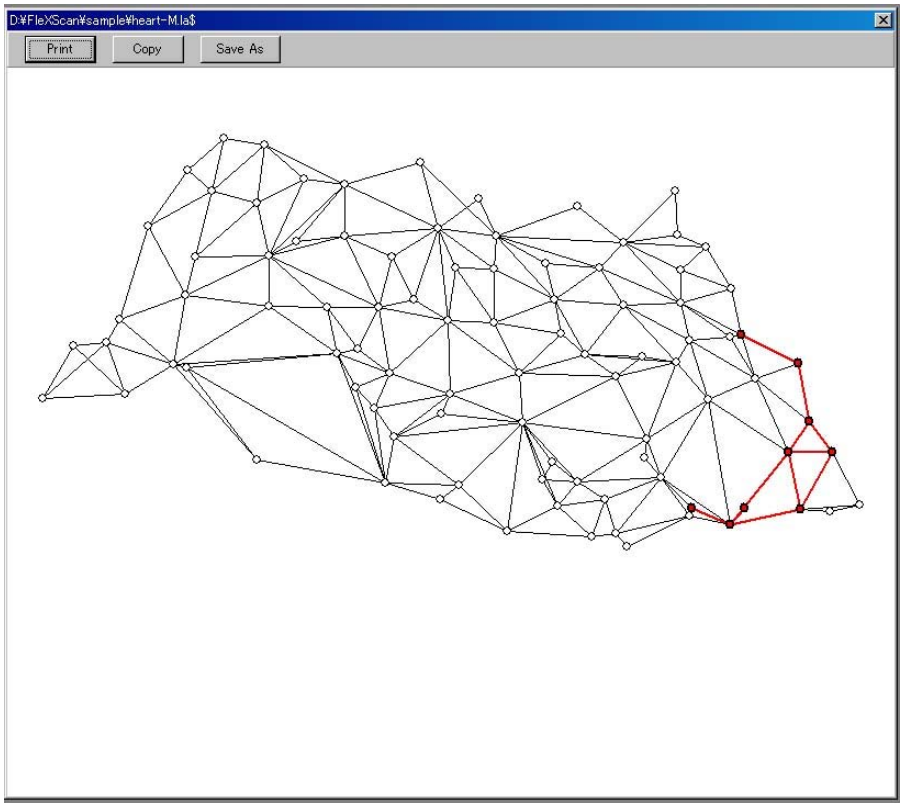
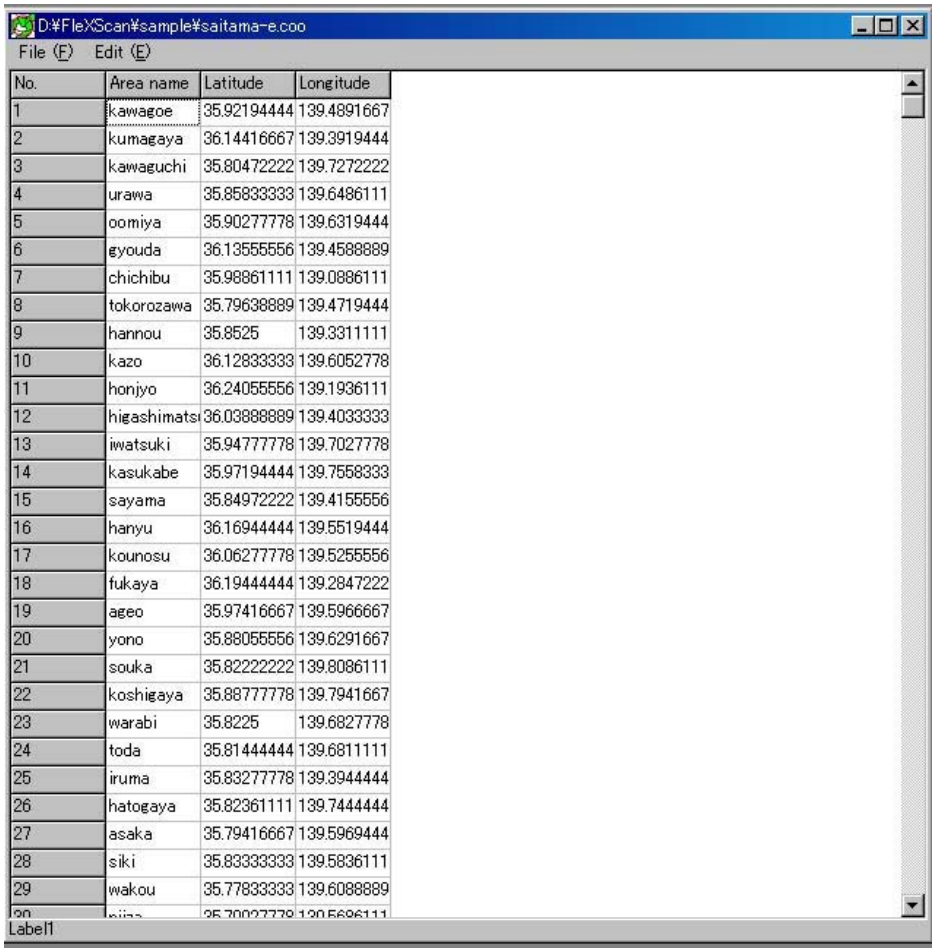


Sample Data Sets and Data Input Form

To analyze your own data using FleXScan, you need to prepare at least three data files: 1) Coordinate File, 2) Matrix Definition File, and 3) Case File. The detailed structure of each file is explained in the following section showing sample data files for Saitama prefecture in Japan (automatically installed in your 'sample' folder).

1) Coordinate File (coo)

- Format : <Area name or code> <Latitude> <Longitude>
  Each data line includes area name, latitudes, and longitudes, respectively. Latitudes and longitudes should be entered as decimal numbers of degrees. You can convert latitudes and longitudes expressed in degrees, minutes, and seconds to decimal number of degrees by the following formula:
  xx (degrees) yy (minutes) zz (seconds) → xx + yy/60 + zz/3600 (degrees).


D:¥FleXScan¥sample¥saitama-e.coo

File (F) Edit (E)

No.	Area name	Latitude	Longitude
1	kawagoe	35.92194444	139.4891667
2	kumagaya	36.14416667	139.3919444
3	kawaguchi	35.80472222	139.7272222
4	urawa	35.85833333	139.6486111
5	oomiya	35.90277778	139.6319444
6	gyouda	36.13555556	139.4588889
7	chichibu	35.98861111	139.0886111
8	tokorozawa	35.79638889	139.4719444
9	hannou	35.8525	139.3311111
10	kazo	36.12833333	139.6052778
11	honjyo	36.24055556	139.1936111
12	higashimats	36.03888889	139.4033333
13	iwatsuki	35.94777778	139.7027778
14	kasukabe	35.97194444	139.7558333
15	sayama	35.84972222	139.4155556
16	hanyu	36.16944444	139.5519444
17	kounosu	36.06277778	139.5255556
18	fukaya	36.19444444	139.2847222
19	ageo	35.97416667	139.5966667
20	yono	35.88055556	139.6291667
21	souka	35.82222222	139.8086111
22	koshigaya	35.88777778	139.7941667
23	warabi	35.8225	139.6827778
24	toda	35.81444444	139.6811111
25	iruma	35.83277778	139.3944444
26	hatogaya	35.82361111	139.7444444
27	asaka	35.79416667	139.5969444
28	siki	35.83333333	139.5836111
29	wakou	35.77833333	139.6088889

Label1

2) Matrix Definition File　(mtr)

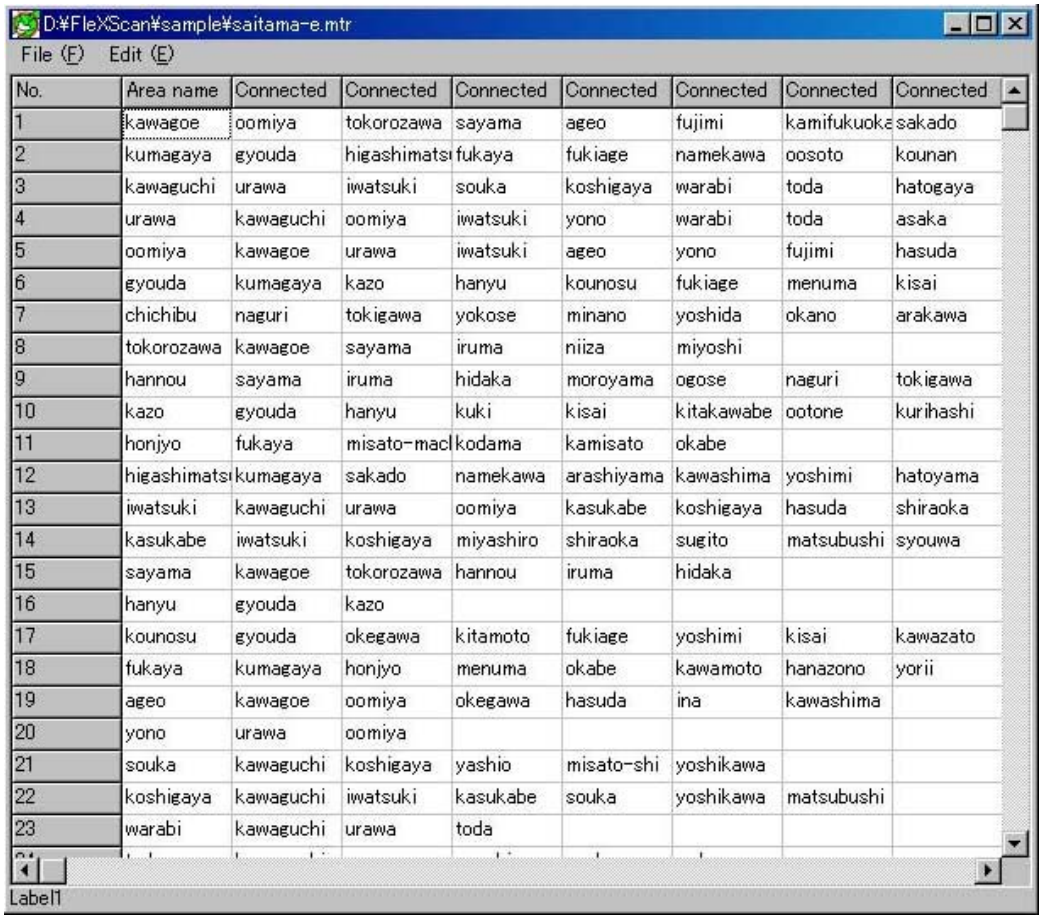
- Format :　<Area name or code>　<Area 1>　<Area 2> …

The first column of each line is the area name, which must be identical to that in Coordinate File. The following columns specify the area name(s) that are adjacent to (i.e., borders on) the area described in the first column. For example, kawagoe, sayama, iruma, niiza, and miyoshi areas are adjacent to tokorozawa (see row No.8 of the figure below).

When Area1 is adjacent to Area3 and Area5, the mtr file should be:

Area1　Area3　Area5
Area2　….
Area3　Area1 …
…

Note that "Area1" also appears in the line of "Area3" in this case (and vice versa), and the matrix must be symmetrical, otherwise an error occurs. The 'Check symmetry' tool in the File menu is available to check the symmetry of the matrix.


D:¥FleXScan¥sample¥saitama-e.mtr

File (F)　Edit (E)

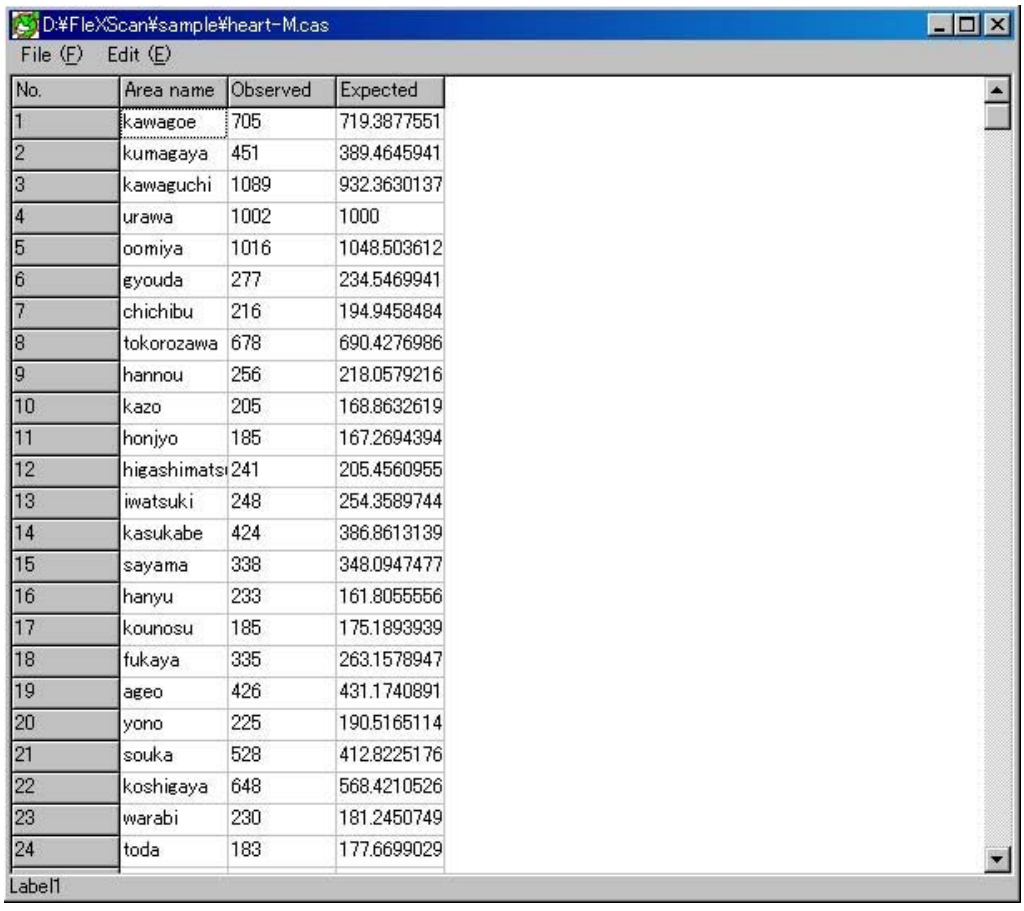
No.	Area name	Connected	Connected	Connected	Connected	Connected	Connected	Connected
1	kawagoe	oomiya	tokorozawa	sayama	ageo	fujimi	kamifukuoka	sakado
2	kumagaya	gyouda	higashimatsu	fukaya	fukiage	namekawa	oosoto	kounan
3	kawaguchi	urawa	iwatsuki	souka	koshigaya	warabi	toda	hatogaya
4	urawa	kawaguchi	oomiya	iwatsuki	yono	warabi	toda	asaka
5	oomiya	kawagoe	urawa	iwatsuki	ageo	yono	fujimi	hasuda
6	gyouda	kumagaya	kazo	hanyu	kounosu	fukiage	menuma	kisai
7	chichibu	naguri	tokigawa	yokose	minano	yoshida	okano	arakawa
8	tokorozawa	kawagoe	sayama	iruma	niiza	miyoshi		
9	hannou	sayama	iruma	hidaka	moroyama	ogose	naguri	tokigawa
10	kazo	gyouda	hanyu	kuki	kisai	kitakawabe	ootone	kurihashi
11	honjyo	fukaya	misato-mach	kodama	kamisato	okabe		
12	higashimatsu	kumagaya	sakado	namekawa	arashiyama	kawashima	yoshimi	hatoyama
13	iwatsuki	kawaguchi	urawa	oomiya	kasukabe	koshigaya	hasuda	shiraoka
14	kasukabe	iwatsuki	koshigaya	miyashiro	shiraoka	sugito	matsubushi	syouwa
15	sayama	kawagoe	tokorozawa	hannou	iruma	hidaka		
16	hanyu	gyouda	kazo					
17	kounosu	gyouda	okegawa	kitamoto	fukiage	yoshimi	kisai	kawazato
18	fukaya	kumagaya	honjyo	menuma	okabe	kawamoto	hanazono	yorii
19	ageo	kawagoe	oomiya	okegawa	hasuda	ina	kawashima	
20	yono	urawa	oomiya					
21	souka	kawaguchi	koshigaya	yashio	misato-shi	yoshikawa		
22	koshigaya	kawaguchi	iwatsuki	kasukabe	souka	yoshikawa	matsubushi	
23	warabi	kawaguchi	urawa	toda				

Label1

3) Case File (observed # and expected #)　(cas)

- Format:　<Area name or code>　<Observed no.>　<Expected no.>

The frequency of disease in each area is described in Case File. The first column of each line is the area name, which must be identical to that in the Coordinate File. The second column is the observed number of diseases, and the 3rd column is the expected number of diseases under the null hypothesis. You need to calculate the expected number by yourself, for example, in the same manner as standardized mortality ratio (SMR). In kawagoe (see No.1 row of the figure) there were 705 deaths and the age-standardized expected number of deaths was 719.4 (i.e., SMR = 719.4 / 705 = 1.02).



No.	Area name	Observed	Expected
1	kawagoe	705	719.3877551
2	kumagaya	451	389.4645941
3	kawaguchi	1089	932.3630137
4	urawa	1002	1000
5	oomiya	1016	1048.503612
6	gyouda	277	234.5469941
7	chichibu	216	194.9458484
8	tokorozawa	678	690.4276986
9	hannou	256	218.0579216
10	kazo	205	168.8632619
11	honjyo	185	167.2694394
12	higashimatsu	241	205.4560955
13	iwatsuki	248	254.3589744
14	kasukabe	424	386.8613139
15	sayama	338	348.0947477
16	hanyu	233	161.8055556
17	kounosu	185	175.1893939
18	fukaya	335	263.1578947
19	ageo	426	431.1740891
20	yono	225	190.5165114
21	souka	528	412.8225176
22	koshigaya	648	568.4210526
23	warabi	230	181.2450749
24	toda	183	177.6699029

We recommend you to prepare the above mentioned dataset 1), 2), and 3) to analyze your data. But, if you do not need standardization (e.g., you are interested in the crude death rate), an alternative approach is possible by preparing data set 1) and 2) plus the following 3') and 4). To use this approach, check the 'Population File' check-box.

3') Case File (observed #) (cas)

- Format: <Area name or code> <Observed no.>

  Create a Case File that contains only area name and observed number of diseases in the same manner as 3), but the expected no. is not needed.

4) Population File (pop)

- Format : <Area name or code> <Population>

  The first column of each line is the area name, which must be identical to that in the Coordinate File. The second column is the population of the area.

Important Note:

- All area names or codes and their order must be identical among 'Coordinate File,' 'Matrix Definition File,' 'Case File,' and 'Population File' (if necessary).

- The area name or code cannot include a space character. Use an under score or a hyphen in stead of a space character.

  Good … 10001

  Good … New_York

  N.G. … New York

Editing your data set

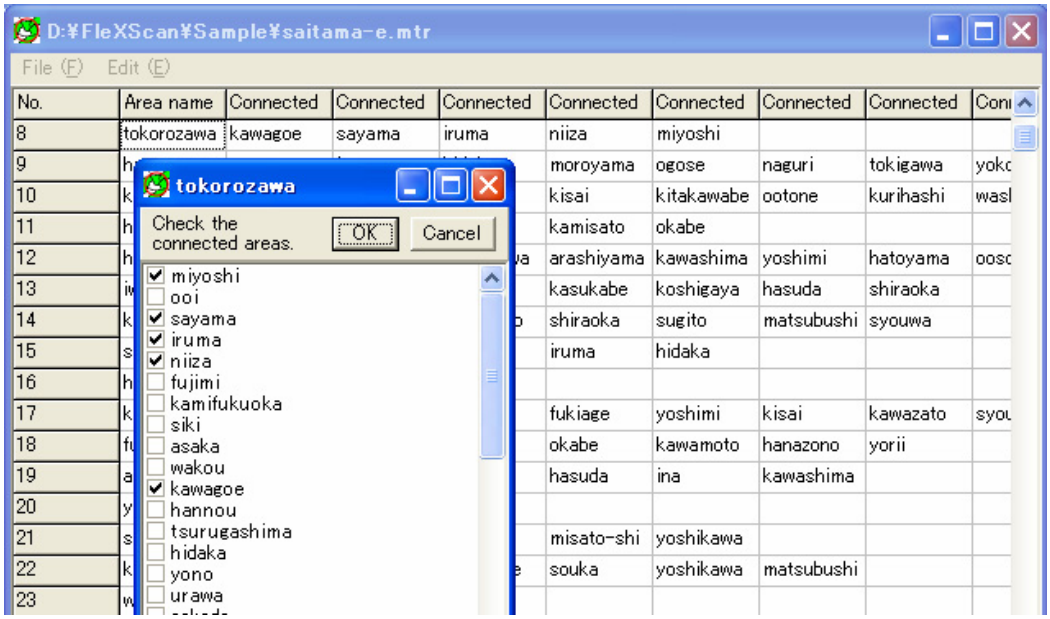
The data files 1) to 4) can be edited using FleXScan data editor. Enter the file name and click 'Edit' button to execute the data editor. You can copy and paste your data from other software such as MS-Excel. It may be convenient to input your data on MS-Excel and copy and paste it to FleXScan data editor.

1) Editing Coordinate File (coo).

- Input the area name and its latitude and longitude in each column.
- 'Save & return' to finish editing data.

2) Editing Matrix Definition File (mtr).

- Coordinate File must be made before starting to edit Matrix Definition File.
- Input the area name, which must be identical to that of Coordinate File. It will be convenient to Copy & Paste all the area names from Coordinate File to Matrix Definition File.
- Select an area name and execute 'Edit – Area List,' then a list of area names will appear in the order of distance from the selected area. Check the check-box of areas that are adjacent to the selected area. By clicking 'OK' button, the checked areas will be automatically added to the 'Adjacent' columns (see the figure below).



- The symmetry can be tested by executing 'File – Check symmetry.' If the information is not symmetry (e.g., Area3 is selected as an adjacent area to Area1, but Area1 is not selected as an adjacent area to Area3), an error message will appear.

Supplementary technical information:

The Matrix Definition File is designed as a user-friendly format. FleXScan automatically convert it to a Connection Information Matrix File (mt0 file) and utilize it for the calculation. You can see the format of mt0 file by a text editor. Conversely, if you already have the area connection data in the format of mt0 file, it can be converted to mtr file by executing 'Tool – Matrix-file converter.'

3) Editing Case File (cas).

4) Editing Population File (pop).

- Coordinate File must be made before starting to edit Case File and Population File.
- Case File and Population File can be edited in the same manner as Coordinate File.

Parameters

You can change several parameters for the analysis on the 'Analysis' tab panel.

- Scanning method
  (1) Flexible : flexible scan statistic by Tango and Takahashi
  (2) Kulldorff : circular scan statistic by Kulldorff

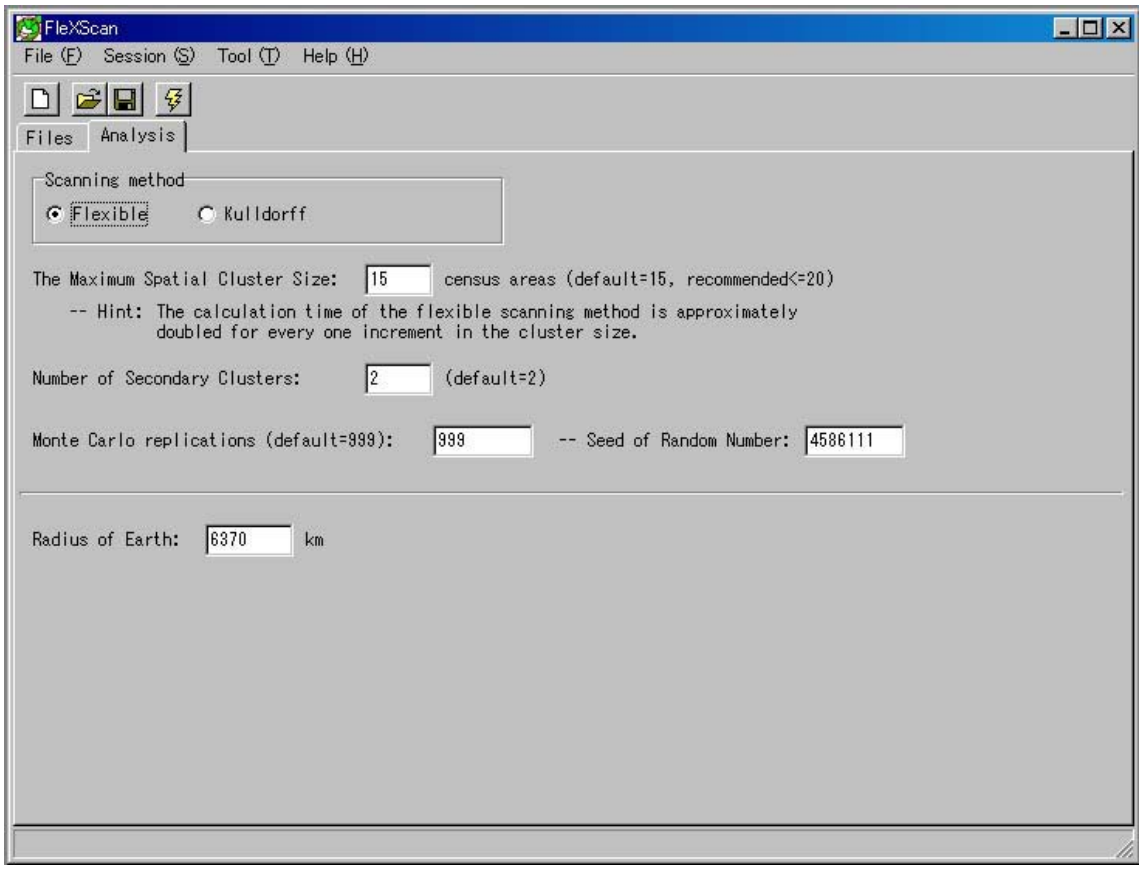
- The Maximum Spatial Cluster Size :
  The number of maximum spatial cluster size to scan. See the reference article for details.

- Number of Secondary Clusters
  The number of secondary clusters to scan. See the reference article for details.

- Monte Carlo replications
  The number of Monte Carlo replications to calculate a p-value for statistical test. For example, if this number is set to 999, the p-value is calculated from the simulated 999 plus 1 observed log-likelihood ratio values (999+1=1000 in total).

- Seed of Random Number
  The seed for generating random numbers in the Monte Carlo simulation.

- Radius of Earth
  Radius of Earth to calculate a distance between two sets of latitude and longitude. It is approximately 6370 km in Japan.


FleXScan
File (F) Session (S) Tool (T) Help (H)
Files
Analysis
Scanning method
Flexible
Kulldorff
The Maximum Spatial Cluster Size: 15 census areas (default=15, recommended<=20)
-- Hint: The calculation time of the flexible scanning method is approximately doubled for every one increment in the cluster size.
Number of Secondary Clusters: 2 (default=2)
Monte Carlo replications (default=999): 999 -- Seed of Random Number: 4586111
Radius of Earth: 6370 km

Software Licenses

- The FleXScan software may be used freely, with proper references to both the software and the statistical methods papers. The suggested citations are:

  Tango T. and Takahashi K. A flexibly shaped spatial scan statistic for detecting clusters. International Journal of Health Geographics 2005, **4**:11.

  Takahashi K, Yokoyama T and Tango T. FleXScan v1.1: Software for the Flexible Scan Statistic. National Institute of Public Health, Japan, 2005.

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