

How To Use CalMorph

Yoshikazu OHYA

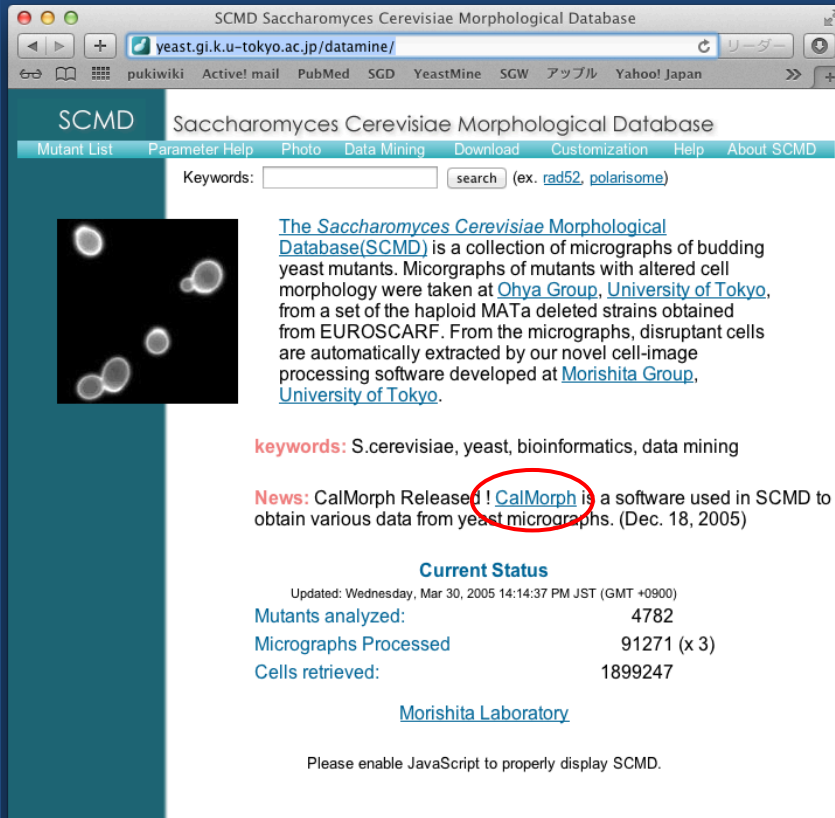
Univ. Tokyo

Topics

- Download
- Start CalMorph
- Set Input Files
- Set Output Folder
- Set Analysis Option
- Start Image Analysis
- Check Output files
- Requirements
- Helps

Access to SCMD

<http://scmd.gi.k.u-tokyo.ac.jp/datamine/>



SCMD Saccharomyces Cerevisiae Morphological Database

Keywords: search (ex. rad52, polarisome)

The Saccharomyces Cerevisiae Morphological Database(SCMD) is a collection of micrographs of budding yeast mutants. Micrographs of mutants with altered cell morphology were taken at [Ohya Group, University of Tokyo](#), from a set of the haploid MATa deleted strains obtained from EUROSCARF. From the micrographs, disruptant cells are automatically extracted by our novel cell-image processing software developed at [Morishita Group, University of Tokyo](#).

keywords: S.cerevisiae, yeast, bioinformatics, data mining

News: CalMorph Released!! [CalMorph](#) is a software used in SCMD to obtain various data from yeast micrographs. (Dec. 18, 2005)

Current Status

Updated: Wednesday, Mar 30, 2005 14:14:37 PM JST (GMT +0900)

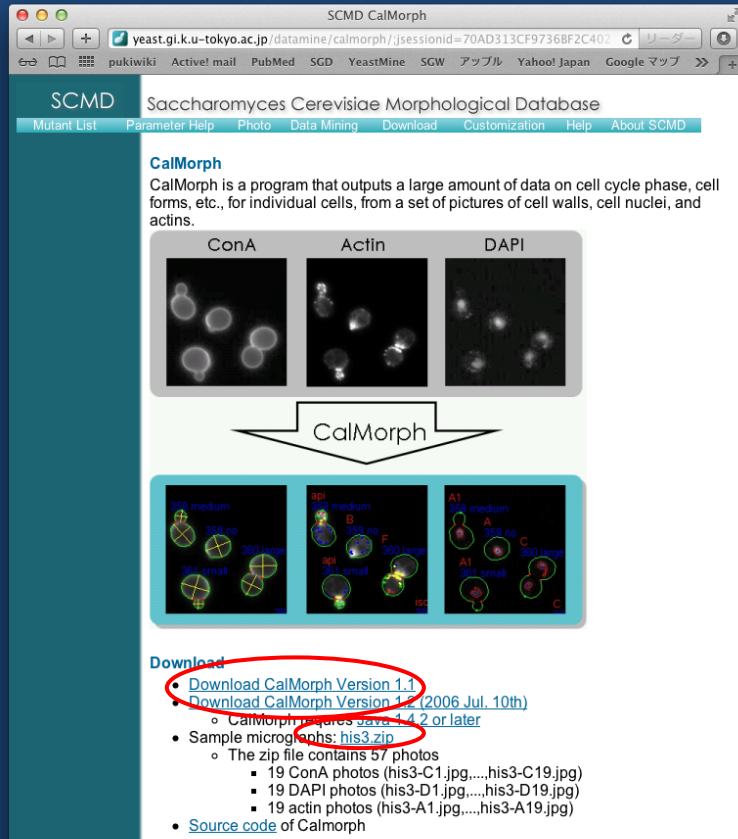
Mutants analyzed:	4782
Micrographs Processed	91271 (x 3)
Cells retrieved:	1899247

[Morishita Laboratory](#)

Please enable JavaScript to properly display SCMD.

- You can see a home page of SCMD
 - Saccharomyces Cerevisiae Morphological Database
- Click CalMorph at the middle of the page

Download CalMorph from SCMD



SCMD CalMorph

yeast.gi.k.u-tokyo.ac.jp/datamine/calmorph/

SCMD Saccharomyces Cerevisiae Morphological Database

Mutant List Parameter Help Photo Data Mining Download Customization Help About SCMD

CalMorph

CalMorph is a program that outputs a large amount of data on cell cycle phase, cell forms, etc., for individual cells, from a set of pictures of cell walls, cell nuclei, and actins.

ConA Actin DAPI

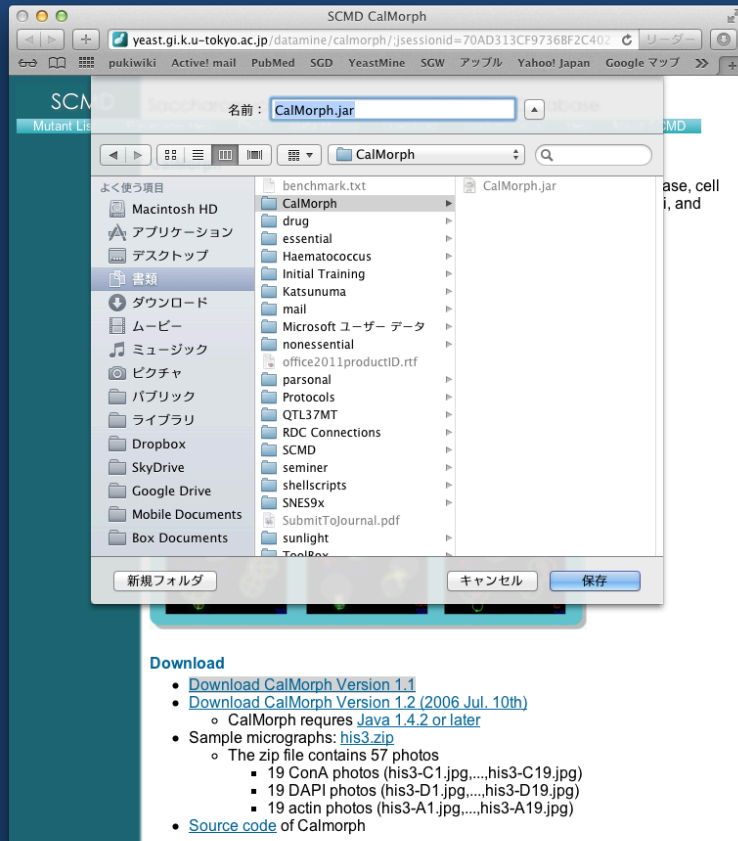
CalMorph

Download

- [Download CalMorph Version 1.1](#)
- [Download CalMorph Version 1.2 \(2006 Jul. 10th\)](#)
 - CalMorph requires ImageJ 4.2 or later
- Sample micrographs: [his3.zip](#)
 - The zip file contains 57 photos
 - 19 ConA photos (his3-C1.jpg, ..., his3-C19.jpg)
 - 19 DAPI photos (his3-D1.jpg, ..., his3-D19.jpg)
 - 19 actin photos (his3-A1.jpg, ..., his3-A19.jpg)
- [Source code](#) of Calmorph

- Click “Download CalMorph Version 1.1”
- Click “his3.zip”
 - Test images

Save “CalMorph.jar” and “his3.zip”



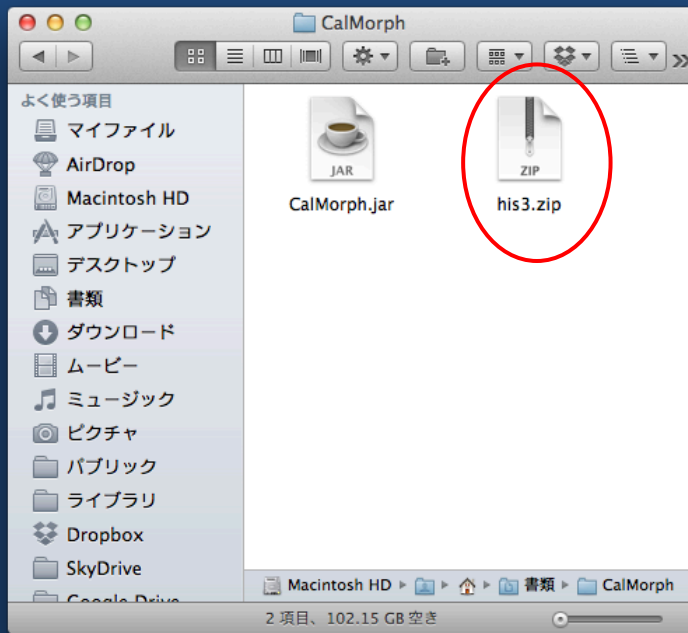
The screenshot shows a web browser window with the address bar displaying `yeast.gi.k.u-tokyo.ac.jp/datamine/calmorph/`. A file download dialog box is open, showing the file name `CalMorph.jar` and a list of files in the `CalMorph` directory. The list includes `benchmark.txt`, `CalMorph`, `drug`, `essential`, `Haematococcus`, `Initial Training`, `Katsunuma`, `mail`, `Microsoft ユーザー データ`, `nonessential`, `office2011productID.rtf`, `personal`, `Protocols`, `QLT37MT`, `RDC Connections`, `SCMD`, `seminer`, `shellscripts`, `SNES9x`, `SubmitToJournal.pdf`, `sunlight`, and `ToolBox`. The dialog box has buttons for `新規フォルダ`, `キャンセル`, and `保存`.

Download

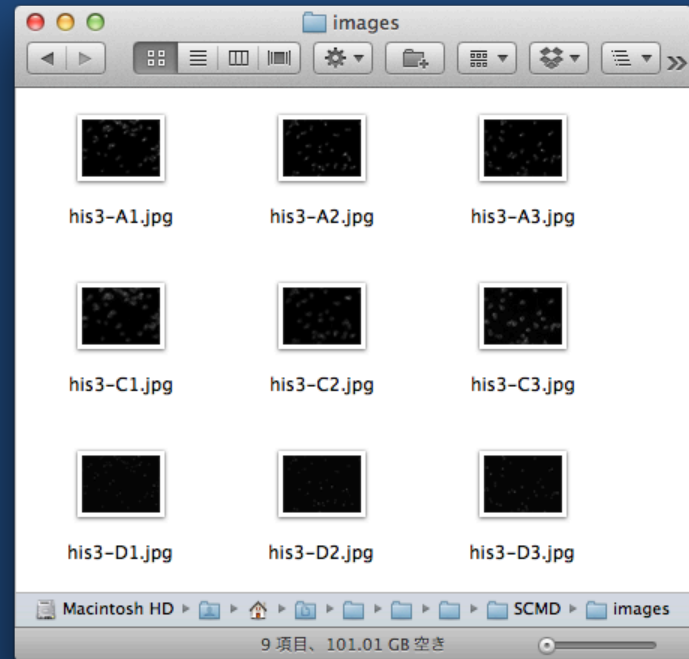
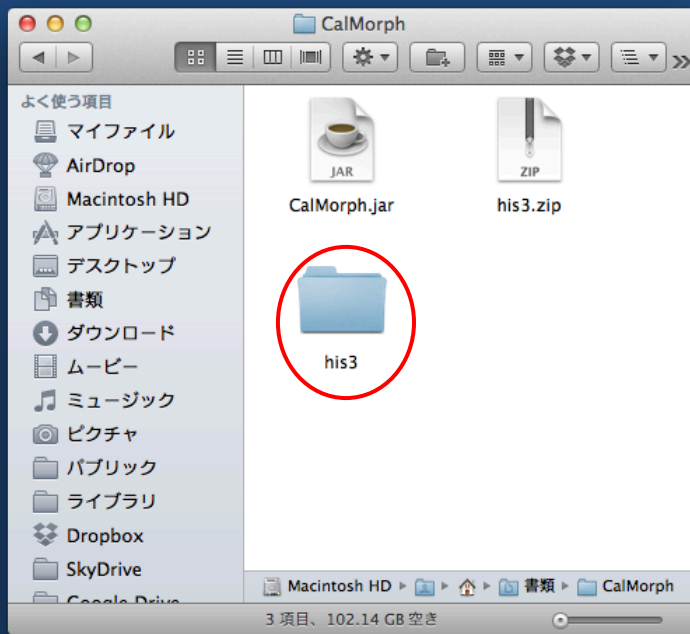
- [Download CalMorph Version 1.1](#)
- [Download CalMorph Version 1.2 \(2006 Jul. 10th\)](#)
 - CalMorph requires [Java 1.4.2 or later](#)
- Sample micrographs: [his3.zip](#)
 - The zip file contains 57 photos
 - 19 ConA photos (his3-C1.jpg, ..., his3-C19.jpg)
 - 19 DAPI photos (his3-D1.jpg, ..., his3-D19.jpg)
 - 19 actin photos (his3-A1.jpg, ..., his3-A19.jpg)
- [Source code](#) of Calmorph

- In this case, the files are saved at `~/Documents/CalMorph`

Unzip “his3.zip”



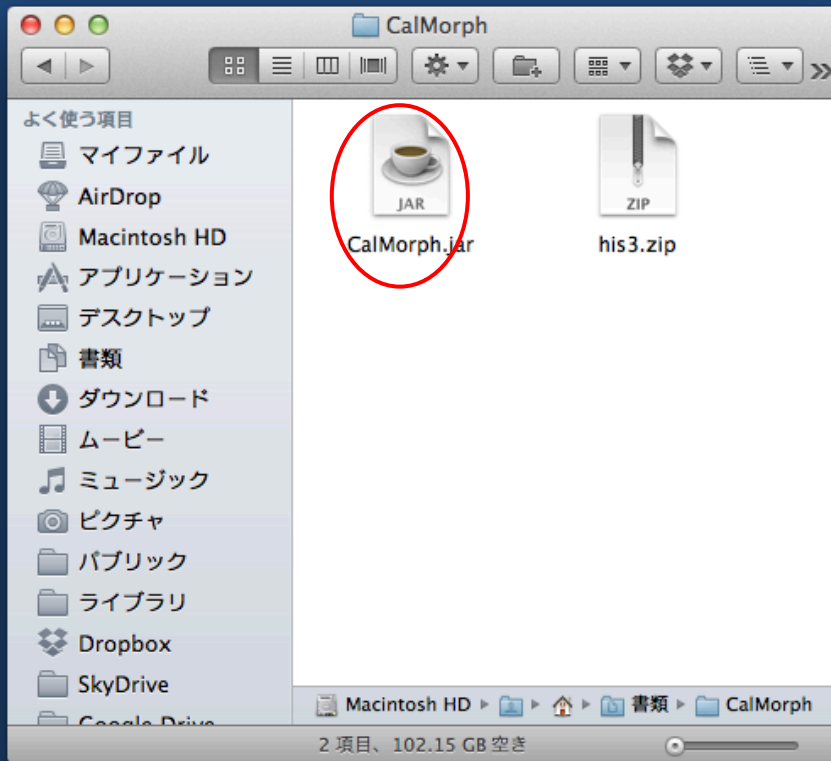
Check file names



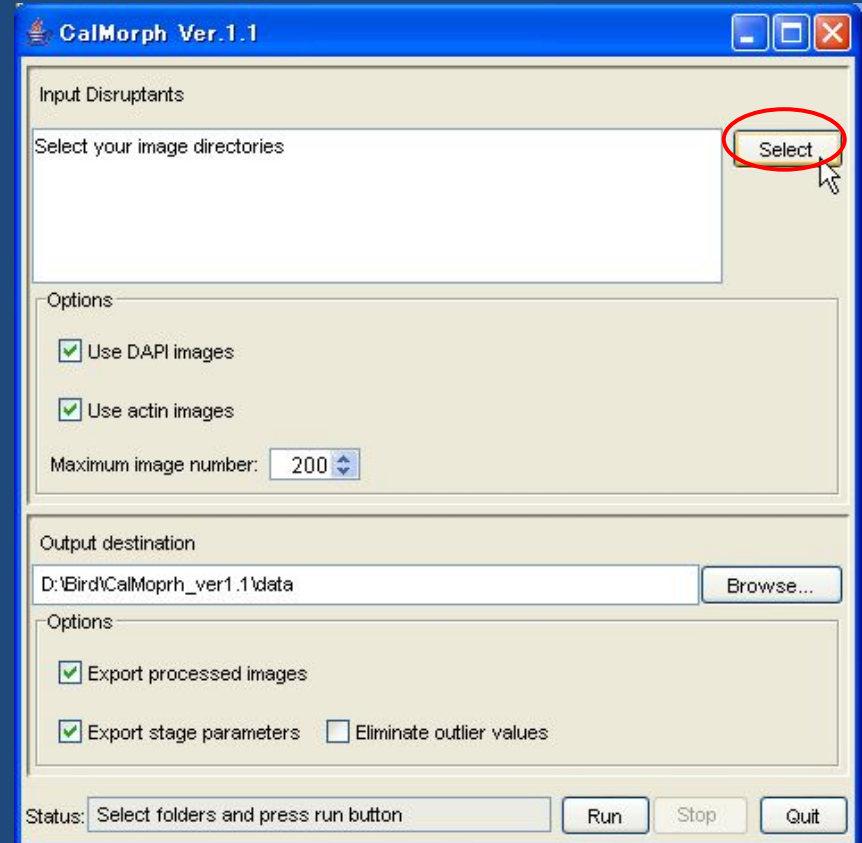
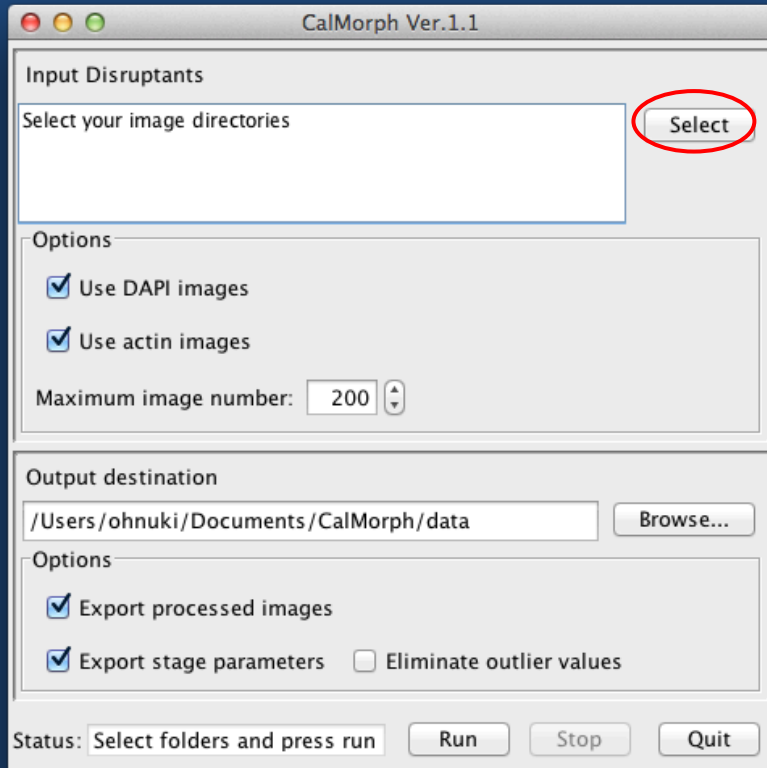
[folder name]-[A|C|D][number].jpg

Start CalMorph

- Double click “CalMorph.jar”

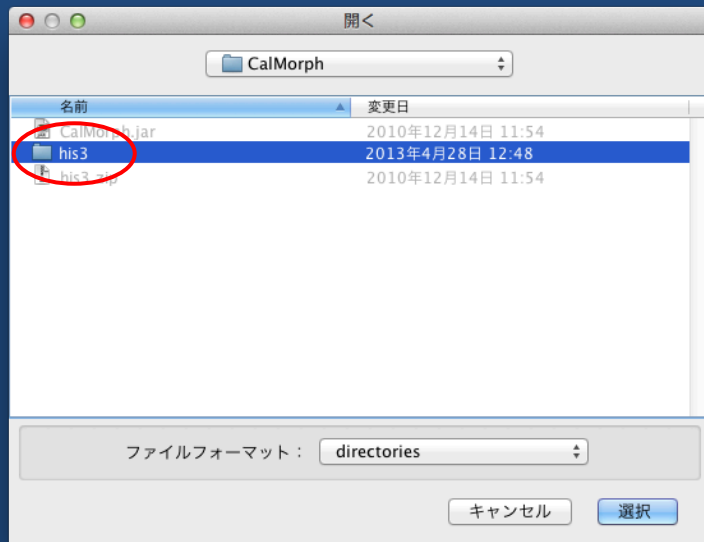


Set Input Files



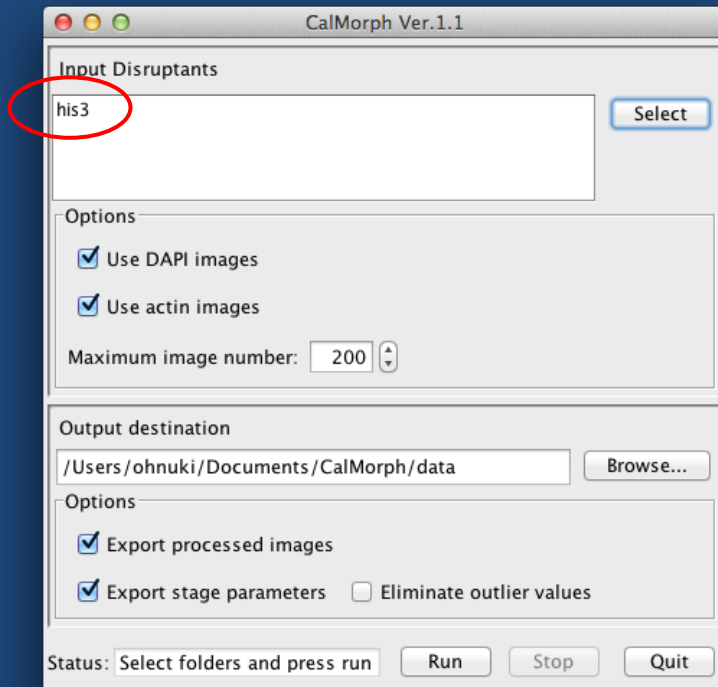
Select “his3” folder

- If you want to analyze two or more sets of images, you can select multiple folders in this step by saving the folders of images at a same folder in advance



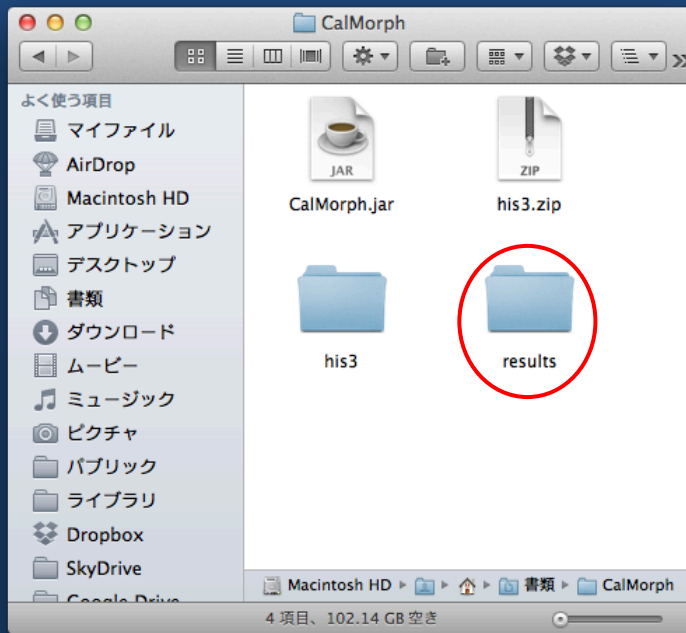
Check the selected folder name

- If you selected multiple folders, all selected folders appear here



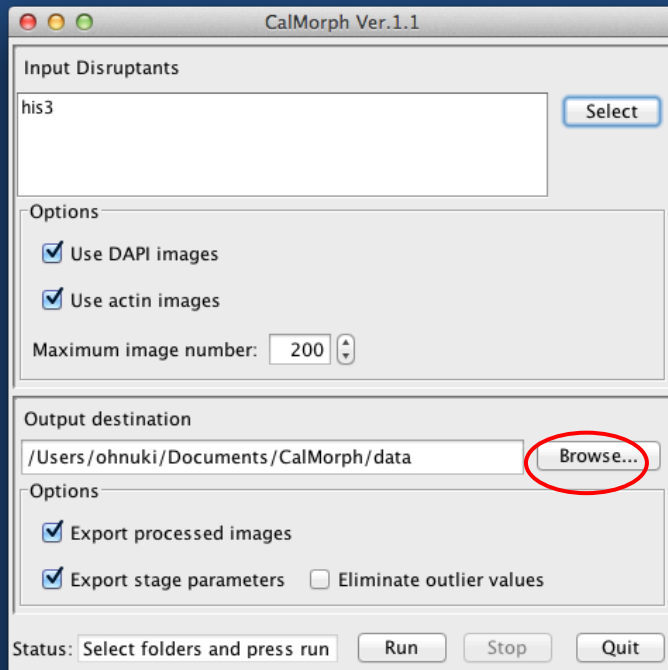
Make a folder “results” for output

- Output files from CalMorph will be stored in this folder

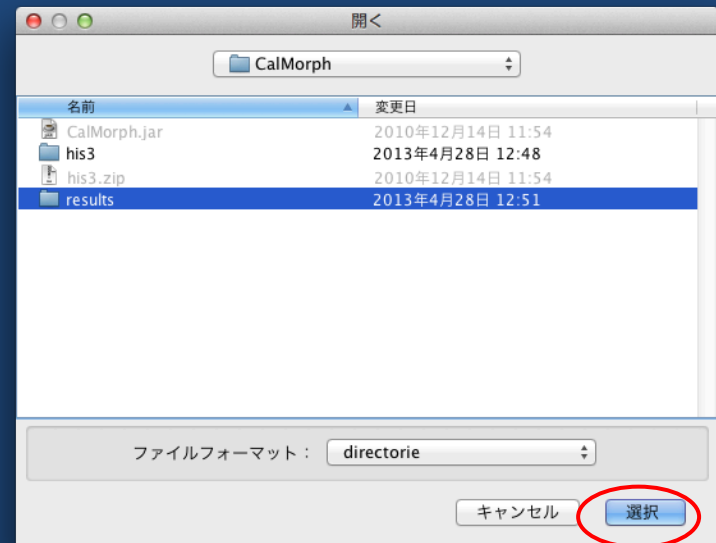


Set Output Folder

Click “Browse” button

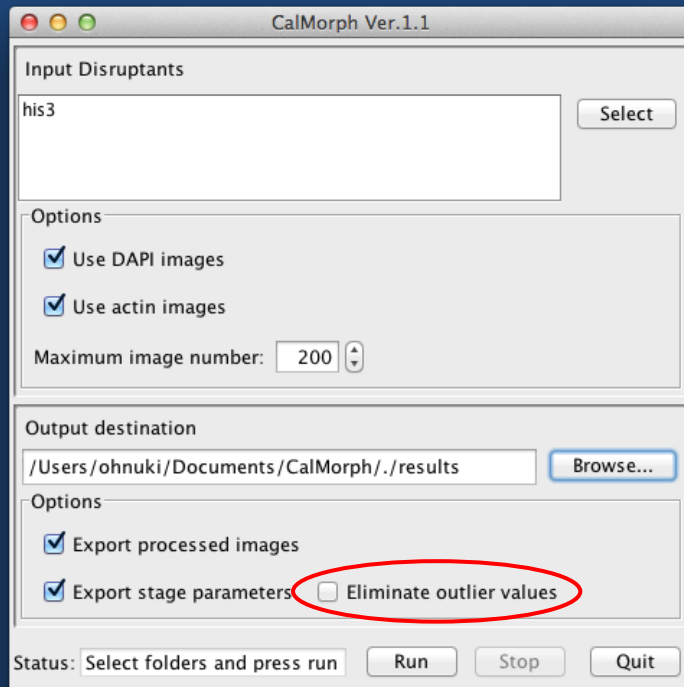


Select output folder



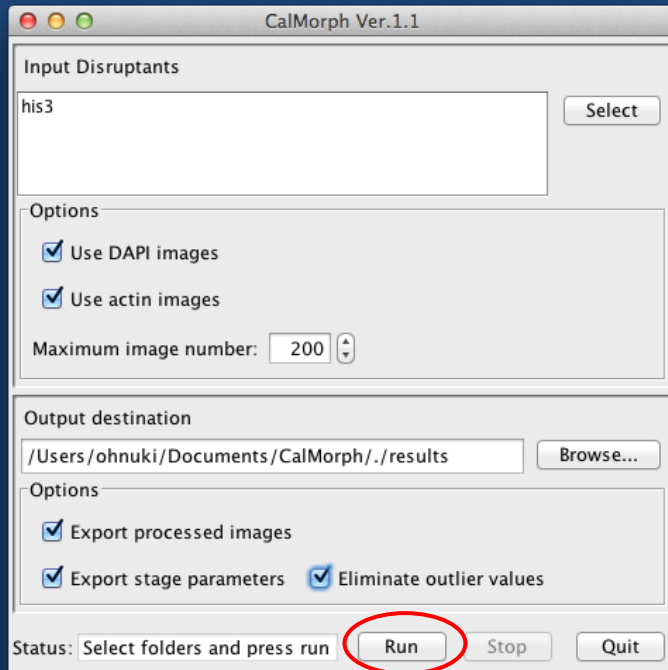
Set Analysis Option

- Select “Eliminate outlier values”
- CalMorph eliminate 1% outliers before calculating mean values in each parameter

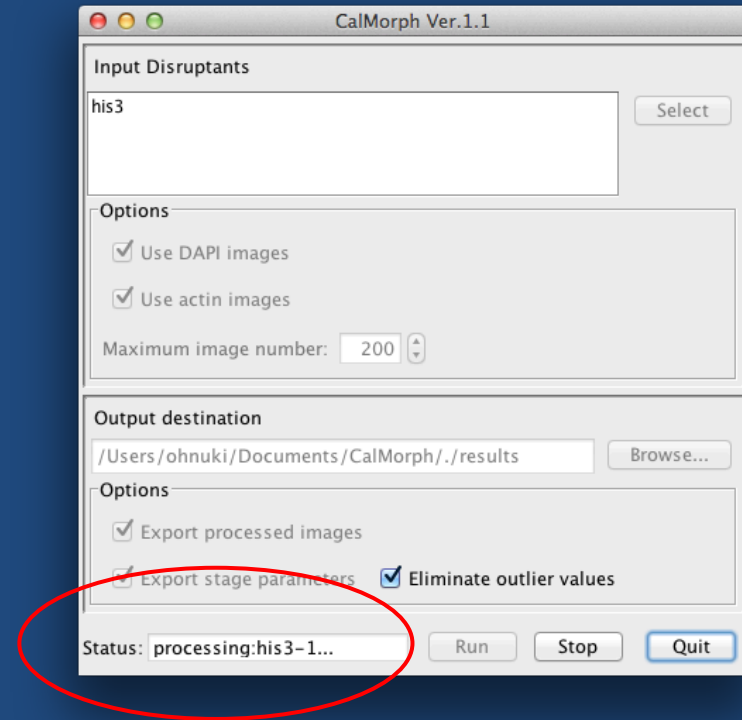


Start Image Analysis

Click “Run” button

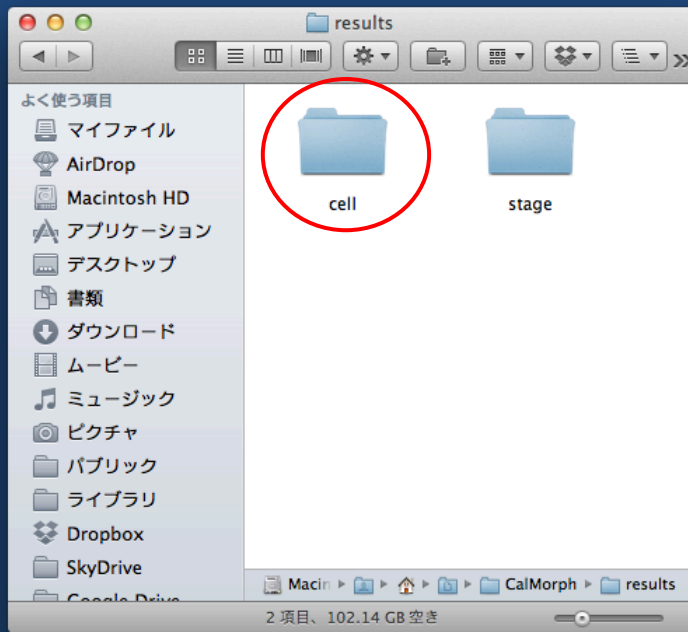


Check status

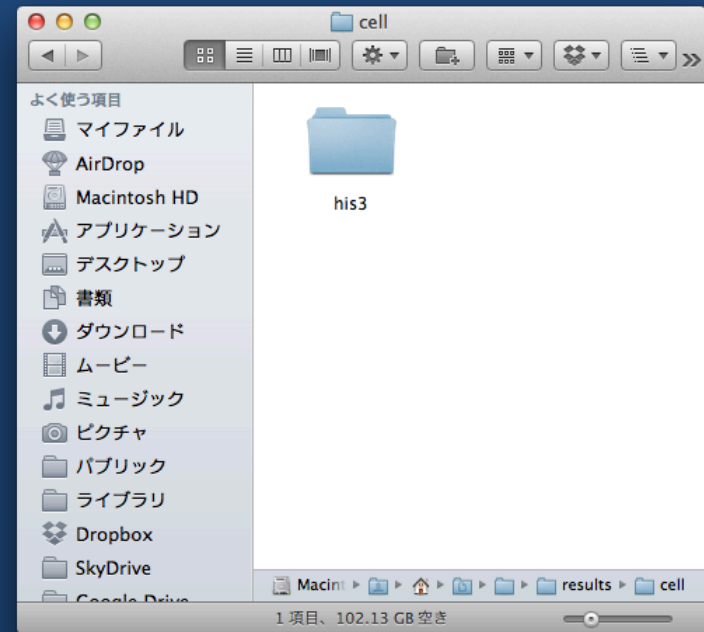


Check Output Files

“results” folder

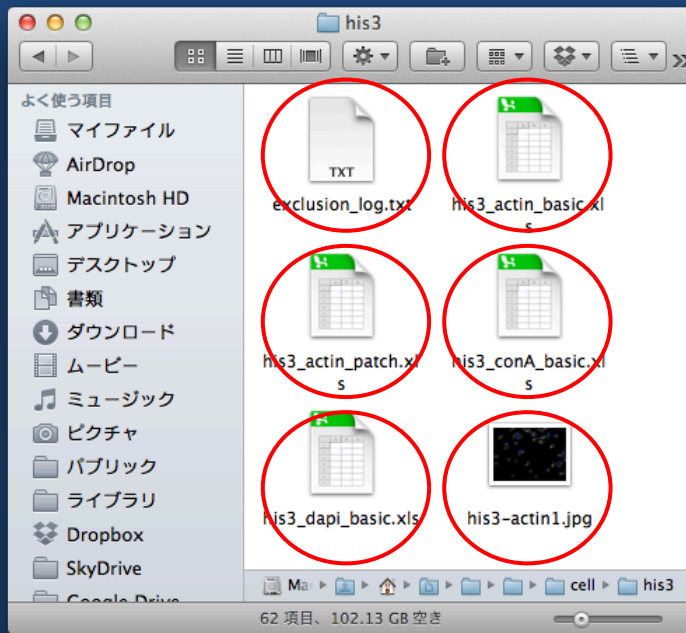


“cell” folder



Folders of same names as inputs will be made in a “cell” folder

“cell” folder



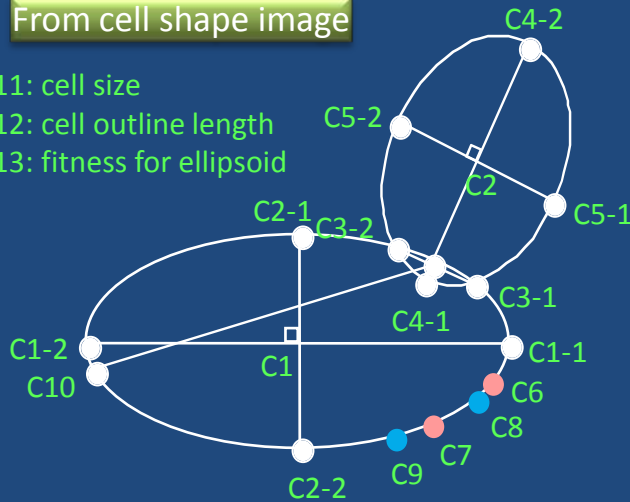
- JPG files of analyzed image
- Error-log file
 - exclusion_log.txt
- Excel files for basic parameter values
 - his3_actin_basic.xls
 - his3_actin_patch.xls
 - his3_conA_basic.xls
 - his3_dapi_basic.xls

Basic Parameters

Feature points that are extracted directly from the images to calculate biologically significant parameters

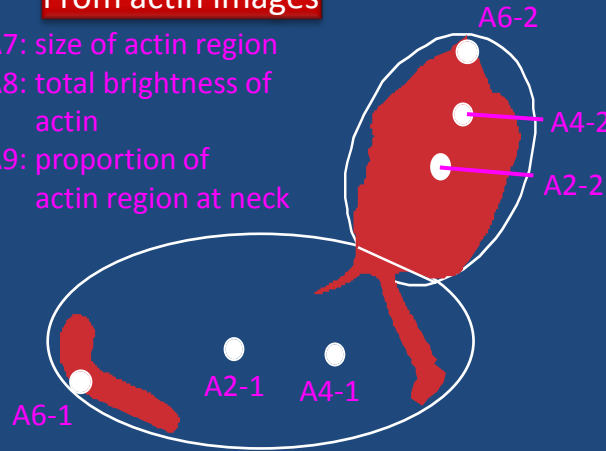
From cell shape image

- C11: cell size
- C12: cell outline length
- C13: fitness for ellipsoid

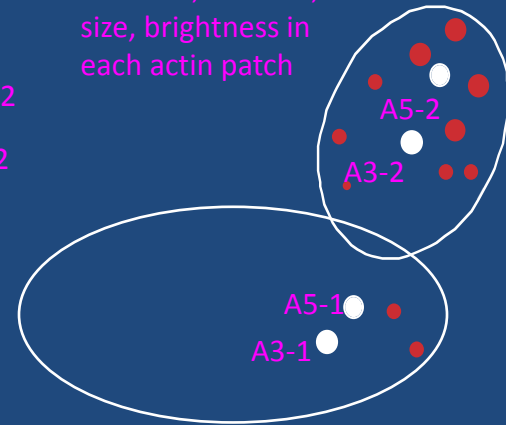


From actin images

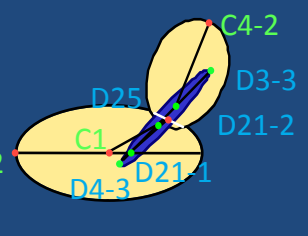
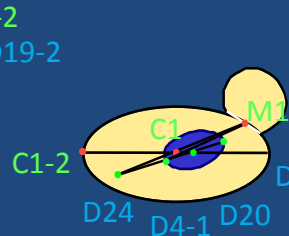
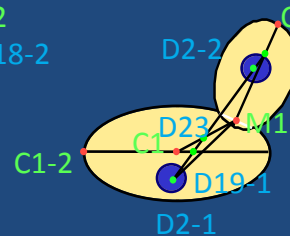
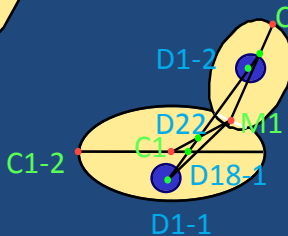
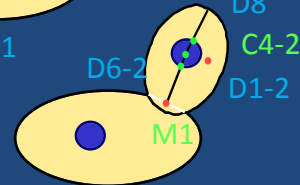
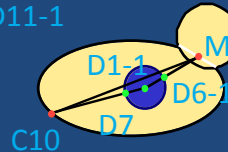
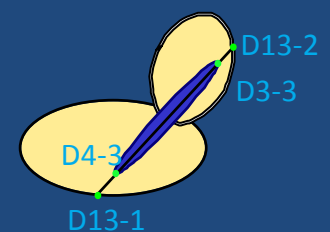
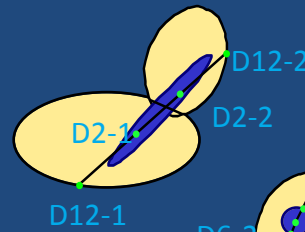
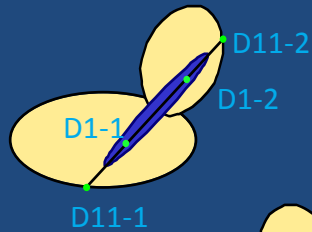
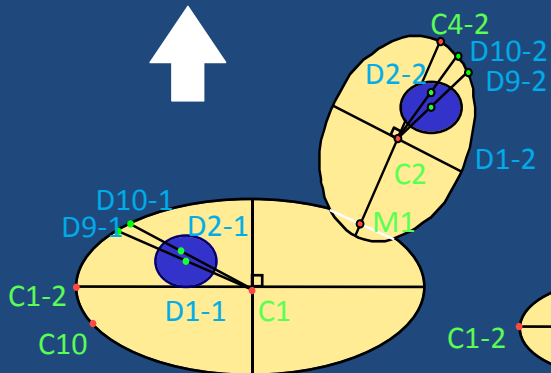
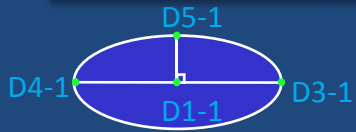
- A7: size of actin region
- A8: total brightness of actin
- A9: proportion of actin region at neck



- A1: Number, location, size, brightness in each actin patch



From nuclear DNA images



- D14: nuclear size
- D15: sum of nuclear brightness
- D16: maximal brightness of nuclei

Biological Parameters

From Cell Shape Image

C101	whole cell size
C102	whole cell outline length
C103	long axis length in mother
C104	short axis length in mother
C105	neck position
C106	bud direction
C107	long axis length in bud
C108	short axis length in bud
C109	neck width
C110	distance between bud tip and mother long axis extension
C111	distance between bud tip and mother short axis extension
C112	distance between middle point of neck and mother center
C113	distance between bud tip and mother long axis
C114	bud axis ratio
C115	mother axis ratio
C116	axis ratio ratio
C117	outline ratio
C118	size ratio

C119	no bud ratio
C120	small bud ratio
C121	medium bud ratio
C122	large bud ratio
C123	small bud ratio to bud
C124	medium bud ratio to bud
C125	large bud ratio to bud
C126	brightness difference
C127	thickness difference
C128	distance between middle point of neck and C10

A107	ratio of budded cells with bud-tip localized actin
A108	ratio of budded cells with actin dispersed in bud
A109	ratio of budded cells with delocalized actin
A110	ratio of budded cells with neck localized actin
A111	ratio of cells with delocalized actin
A112	ratio of cells with localized actin
A113	ratio of cells with no actin
A114	ratio of delocalized actin to budded cells
A115	ratio of localized actin to budded cells
A116	ratio of bud-tip localized actin to budded cells
A117	ratio of dispersed actin to budded cells
A118	ratio of delocalized actin to budded cells
A119	ratio of neck localized actin to budded cells
A120	total length of actin patch link
A121	distance between the most distant patches
A122	the number of bright actin patches
A123	ratio of actin patches to actin region

From Actin Image

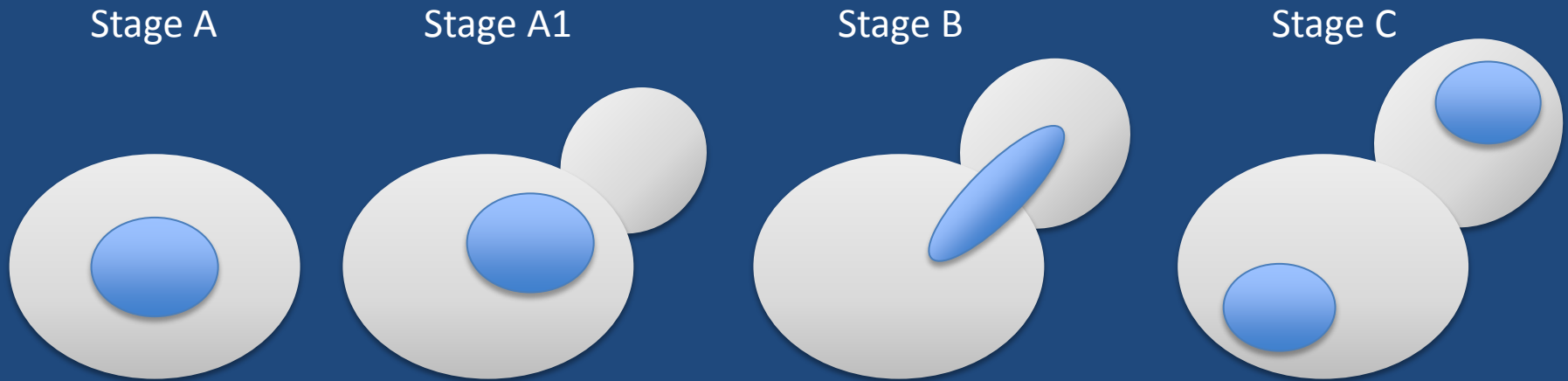
A101	actin region ratio
A102	bud actin region ratio
A103	relative gravity center of weighted actin region in mother
A104	relative gravity center of weighted actin region in bud
A105	ratio of the no bud cells with delocalized actin
A106	ratio of no bud cells with localized actin

From Nuclear DNA Image

D101	D1-1C1-1 or D1-1C1-2	D121	D2-3-2M1	D141	D6-2M1 / D8C4-2	D161	D1-1D3-1	D181	D15-3 / D14-3
D102	D1-1C1-2	D122	D2-1D2-2	D142	\angle D1-1C1C1-2	D162	D1-2D3-2	D182	D16-1 / (D15-1 / D14-1)
D103	D1-1M1	D123	D2-1C1	D143	\angle D2-1C1C1-2	D163	D1-3-1D3-3 or D1-3-2D3-3	D183	D16-2 / (D15-2 / D14-2)
D104	D1-2M1	D124	D2-3-1C1 or D2-3-2C1	D144	\angle D1-2C2C4-2	D164	D3-1D4-1	D184	D16-1 / (D15-1 / D14-1)
D105	D1-3-1M1	D125	D2-2C2	D145	\angle D2-2C2C4-2	D165	D3-2D4-2	D185	D14-2 / D14-1
D106	D1-3-2M1	D126	D2-3-1C2 or D2-3-2C2	D146	\angle D1-1D18-1C1-2	D166	D3-3D4-3	D186	D15-2 / D15-1
D107	D1-1D1-2	D127	D2-2C4-2	D147	\angle D2-1D19-1C1-2	D167	D1-1D5-1	D187	A_ratio
D108	D1-1C1	D128	D2-3-1C4-2 or D2-3-2C4-2	D148	\angle D4-1D20-1C1-2	D168	D1-2D5-2	D188	A1_ratio
D109	D1-3-1C1 or D1-3-2C1	D129	D2-1C10	D149	\angle D4-3D21-1C1-2	D169	D1-3-1D5-3 or D1-3-2D5-3	D189	B_ratio
D110	D1-2C2	D130	D2-3-1C10 or D2-3-2C10	D150	\angle D1-1D22C1	D170	D3-1D4-1 / D1-1D5-1	D190	C_ratio
D111	D1-3-1C2 or D1-3-2C2	D131	D6-1M1	D151	\angle D2-1D23C1	D171	D3-2D4-2 / D1-2D5-2	D191	D_ratio
D112	D1-2C4-2	D132	D6-2M1	D152	\angle D4-1D24C1	D172	D3-3D4-3 / D1-3D5-3	D192	E_ratio
D113	D1-3-1C4-2 or D1-3-2C4-2	D133	D7C10	D153	\angle D4-3D25C1	D173	D1-1D1-2 / D11-1D11-2	D193	F_ratio
D114	D1-1C10	D134	D8C4-2	D154	\angle D1-2D18-2C4-2	D174	D2-1D2-2 / D12-1D12-2	D194	A_ratio_to_no_bud
D115	D1-3-1C10 or D1-3-2C10	D135	D1-1C1 / C1D9-1	D155	\angle D2-2D19-2C4-2	D175	D3-3D4-3 / D13-1D13-2	D195	A1_ratio_to_bud
D116	D2-1C1-1 or D2-1C1-2	D136	D2-1C1 / C1D10-1	D156	\angle D3-3D21-2C4-2	D176	D1-1D2-1	D196	B_ratio_to_bud
D117	D2-1C1-2	D137	D1-2C2 / C2D9-2	D157	\angle D1-1M1C1	D177	D1-2D2-2	D197	C_ratio_to_bud
D118	D2-1M1	D138	D2-2C2 / C2D10-2	D158	\angle D2-1M1C1	D178	D1-3D2-3		
D119	D2-2M1	D139	D6-2M1 / D6-1M1	D159	\angle D4-1M1C1	D179	D15-1 / D14-1		
D120	D2-3-1M1	D140	D6-1M1 / D7C10	D160	\angle D4-3M1C1	D180	D15-2 / D14-2		

501 parameters

Classification of Biological Parameters

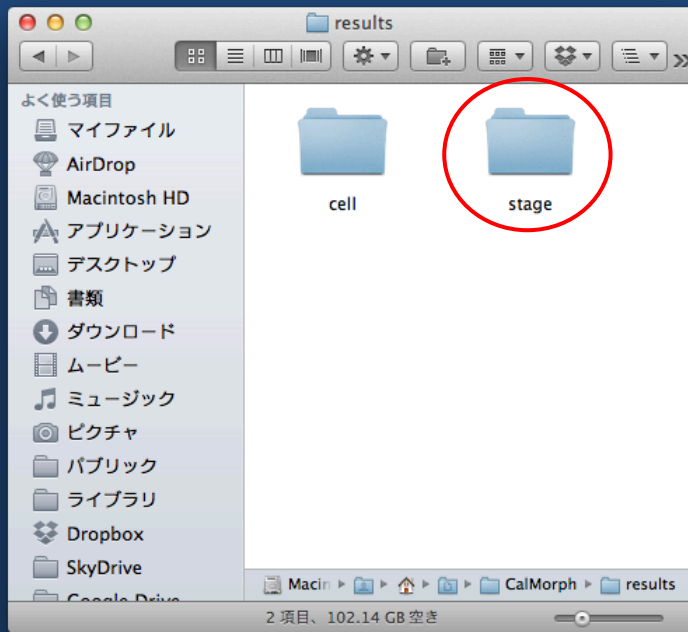


Category of Parameters	Cell Wall	Actin	Nucleus	Total
Stage A	16	17	40	73
Stage A1B	55	32	68	153
Stage C	55	32	148	235
Population	7	15	18	40
Total	133	96	272	501

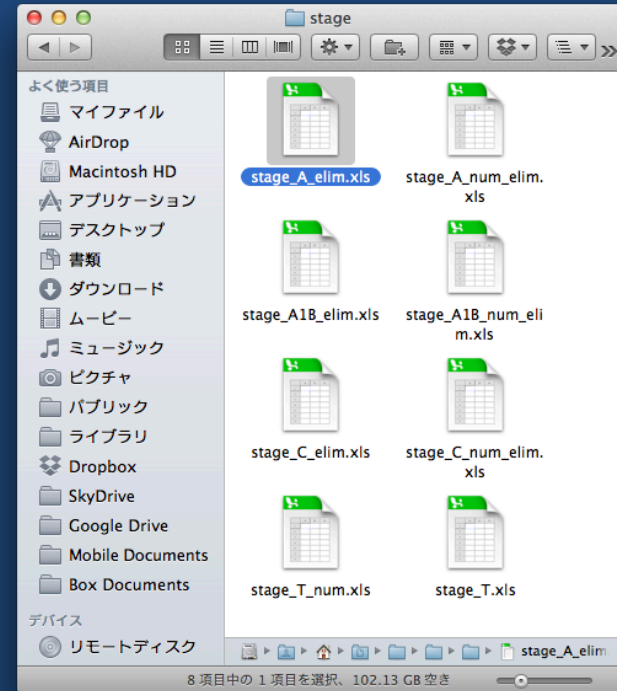
CalMorph outputs 501 parameter values in an Excel format

Check Output Files in “stage” folder

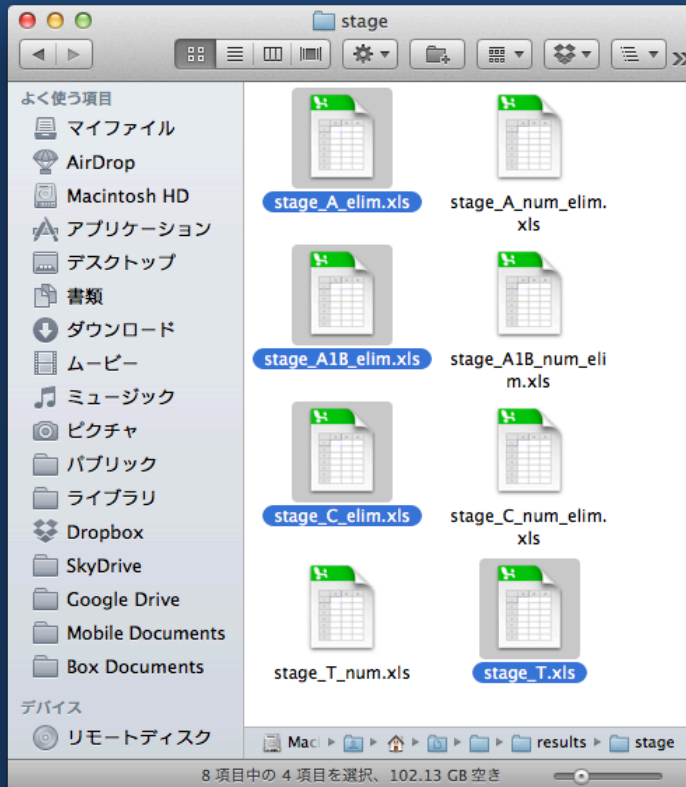
“results” folder



“stage” folder



Files of Biological Parameters



- stage_A_elim.xls
- stage_A_num.xls
- stage_A1B_elim.xls
- stage_A1B_num.xls
- stage_C_elim.xls
- stage_C_num.xls
- stage_T_num.xls
- stage_T.xls

Check Parameter Values

	A	B	C	D	E	F	G	H	
1	Total	C119	C120	C121	C122	C123	C124	C125	A105
2	his3	0.3725	0.215	0.1975	0.215	0.342629482	0.314741036	0.342629482	
3									
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If you input multiple samples by selecting multiple folders, results of each sample will be stored at each row in the files

Requirements of CalMorph

- Java runtime version: 1.4.2 or later
- Image size: 520 x 696 pixels
- Format of image files: 8 bit gray scale JPG
 - Images of cell shape (cell wall stained by FITC-ConA)
 - Three images for each view window
- Format of file names:
 - [folder name]-[A|C|D][number].jpg
- Pixel size: 0.129 x 0.129 $\mu\text{m}^2/\text{pixel}$
 - x100 object lens
 - 2 x 2 binning
 - CCD of 6.45 $\mu\text{m}/\text{pixel}$ (ex. Photometrix CoolSNAP HQ)

Helps for CalMorph

Saccharomyces cerevisiae morphological database

SCMD Saccharomyces Cerevisiae Morphological Database

Keywords: search (ex. rad52, polarisome)

The *Saccharomyces Cerevisiae* Morphological Database(SCMD) is a collection of micrographs of budding yeast mutants. Micrographs of mutants with altered cell morphology were taken at [Ohya Group, University of Tokyo](#), from a set of the haploid MATa deleted strains obtained from EUROSCARF. From the micrographs, disruptant cells are automatically extracted by our novel cell-image processing software developed at [Morishita Group, University of Tokyo](#).

keywords: S.cerevisiae, yeast, bioinformatics, data mining

News: CalMorph Released ! [CalMorph](#) is a software used in SCMD to obtain various data from yeast micrographs. (Dec. 18, 2005)

Current Status
Updated: Wednesday, Mar 30, 2005 14:14:37 PM JST (GMT +0900)

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[Morishita Laboratory](#)

Please enable JavaScript to properly display SCMD.

CalMorph User Manual

CalMorph

User Manual

<http://scmd.gi.k.u-tokyo.ac.jp/datamine/>

Available at download page of SCMD

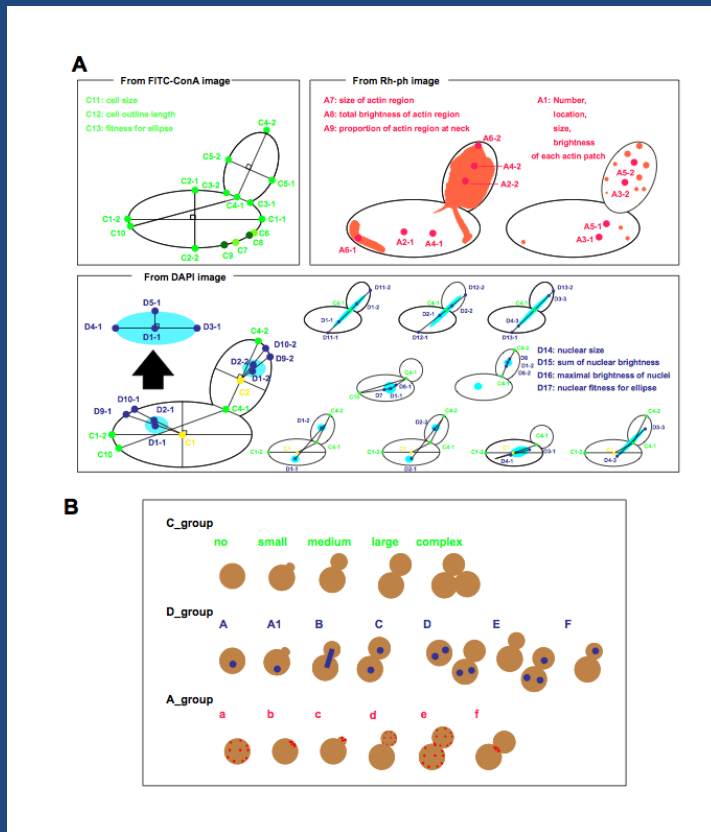
Helps for Parameters

High-dimensional and large-scale phenotyping of yeast mutants

Ohya et al., 2005, PNAS

Figure 5 for Basic Parameter

Table 1 for Biological Parameter



Gene ID	Description	Reference
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Thank you for your attention!

<http://scmd.gi.k.u-tokyo.ac.jp/datamine/>