Release Information for CNAG 3.3.0.0 (Beta version)

Product:	CNAG 3.3.0.0 (Beta)
Release Number:	3.3.0.0
Release Date:	2009-July-23
Array types	Mapping10K_Xba131 Mapping10K_Xba142 Mapping50K_Hind240 Mapping50K_Xba240 Mendel_Nsp Mendel_Sty Mapping250K_Nsp Mapping250K_Sty Agilent244K GenomeWideSNP_5 (Only SNP and Both SNP+CN probes) GenomeWideSNP_6 (Only SNP and Both SNP+CN probes)
Customer Support:	For more information or support, please visit our website http://www.genome.umin.jp/ or email us at cnag@umin.ac.jp

Introduction

This document contains the release notes for CNAG version 3.3.0.0. The following sections describe the release in detail and provide late-breaking or other information that supplements the main documentation.

This is an intermediate release for wide evaluation and usage. Your feedback is important to us, please help us make this the best product possible. Keep in mind that we are continuing to work on CNAG and things may change in the future.

What's new:

1. CNAG 3.2.0.0 is deprecated. It have some bugs for CN+SNP probes.
2. Allele based analysis at SNP+CN probes
3. SNP Call bar at SNP+CN probes

Installation and Upgrade Notes

Installation

CNAG_3.3.0.0_beta.msi is only one file which you need to install. It can be downloaded from our website. http://www.genome.umin.jp/

IMPORTANT: You must completely uninstall any previous "developer release" or "early access" version of this product before installing this release.

Manifest

This release consists of the following items:

- Release notes (this file)
- Product installer binary

After installation guide:

1. After installing CNAG 3.3.0.0_beta, go to **start** > **All Programs** > **UMIN** > **CNAG**

2. Choose **Parameter** > **Default Setting** or click on **Setting** icon ( ) at toolbar, **Program Setting** dialog box will appear, please select the **Folders** tab:
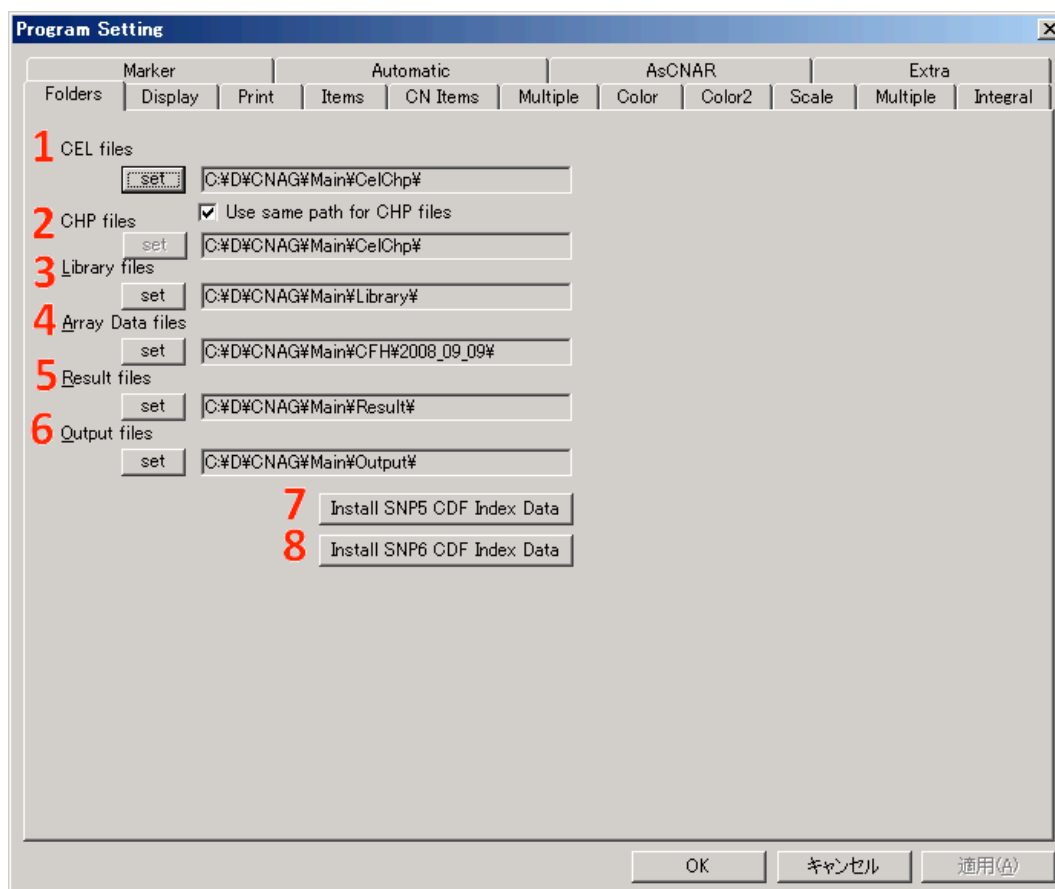

figure 1

CNAG 3.3.0.0 extracts the array data from .CHP and .CEL files created by GCOS, GTYPE or Genotype Console using array information defined by .CDF files (library files), which are provided from Affymetrix and which can be downloaded from the Affymetrix website. The extracted data and result data are stored at different paths. There need to specify the paths.

- **CEL files**: You need to specify the directory containing these files by clicking the "set" buttons that appear under "CEL files" tag.

- **CHP files**: If CEL and CHP files are available at same directory please select the check box **"use same path for CHP files"**, otherwise deselect this checkbox and set the path of CHP files by clicking the "set" button that appear under "CHP files" tag.

- **Library files**: Specify and "Library files" when CNAG is installed on the same PC where GCOS and GTYPE (or GDAS) or Genotype Console are working, these files should be found in the directories accessible from the PC and thus, can be specified by toggling with the Windows file manager. If the destination PC have not available GCOS, GTYPE (or GDAS) or Genotype Console, please download CDF files from Affymetrix website and select the directory of downloaded CDF files by clicking the "set" button that appear under "CDF files" tag.

- **Array Data files**: Select the path to store extracted data (i.e. CFH, CNCFH files) by clicking the "set" button that appear under "Array Data files" tag.

- **Result files**: Select the path to store result data (CFA, CFN, CFS, CNCFA, CNCFN, CNCFS files) by clicking the "set" button that appear under "Result files" tag.

- **Output files**: Select the directory to store results as text and IGB format by clicking the "set" button that appear under "Output files" tag

There are found 4 CDF files for Genome Wide SNP 5.0 array:
GenomeWideSNP_5.Full.cdf, GenomeWideSNP_5..Full.r2.cdf,
GenomeWideSNP_5.r2.cdf, GenomeWideSNP_5.cdf.
And there are found 2 CDF files for Genome Wide SNP 6.0 array:
GenomeWideSNP_6.cdf and GenomeWideSNP_6.Full.cdf.
To choose CDF files for SNP 5.0 or SNP 6.0 array, please follow the following steps

figure 2

- **Install SNP5 CDF index Data**: You need to click at "Install SNP 5 index data" button and select one of the file for SNP 5.0 array from file dialog box and wait for

Installation complete massage box. as shown at figure 2

- **Install SNP6 CDF index Data**: You need to click at "Install SNP 6 index data" button and select one of the file for SNP 6.0 array   and wait for Installation complete massage box as shown at figure 2

Minimum System Requirements

System Processor:	Intel 32-bit 1 GHz
System Memory:	1 GB
Free Disk Space:	500MB
Operating System:	Windows 2000, Windows XP
Networking:	Internet access

Known Problems and Workarounds

Unable to detect StyI or NspI enzyme type for SNP5.0 and SNP6.0
For details please check at http://center2.umin.ac.jp/ml/archive/M04624/

Future improvement of CNAG

- GUI versions of CNAG at Intel based Mac OS X, Linux and Unix Operation Systems