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# 🌐 PanelsDB2, FMDB to manage CGP report xml data.

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[dx.doi.org/10.17504/protocols.io.bzvip64e](https://dx.doi.org/10.17504/protocols.io.bzvip64e)

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PanelsDB2, FMDB to manage CGP report xml data.  
The description about DB usage.

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**protocols.io**<https://dx.doi.org/10.17504/protocols.io.bzvip64e>

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## introduction

- 1 Here I will show you here how to manage the report xml data for Foundation One CDx and NCC Oncopanel that have been insured in Japan.  
It is very difficult to manage patient mutation data as a pdf report, but in Japan this is provided as xml data, and if you read xml, you can manage this as structured data.  
This is description of system using Filemaker pro to manage xml data from F1CDx and NCC oncopanel.

## caution

- 2 ## COI

Most of this FMDB was created when I was a hired researcher in a donation course established jointly by each company, including Chugai Pharmaceutical, which is the domestic implementation body of F1CDx.

I have not received any particular instructions or requests from Chugai when creating the FMDB, but I would like to mention here that it was created based on such a relationship.

## ## Support

You may freely use, and modify this DB and xslt associated with it for medical treatment and research at your own risk for non-commercial purposes. The license for redistribution shall be the same as the license for this DB.

Since the core of the reading part has been created, I hope that you can modify it according to the user's environment.

I don't have any support resources. The user is solely responsible for the use, and modification of this DB.

## environment

- 3 PC: This will work laptop PC with small capacity. I think that there is no hard calculation or disk access and memory usage.  
OS: Windows (I created this windows 10)  
FM version: 16 +2. (I created this FM pro 16 adv. Please check this by trial version of FM before buy it.)

repo:

<https://github.com/fk506cni/panelsdb2>



## concept

- 4 The purpose of this DB is to centrally store the xml data returned by the panel inspection while

maintaining the structure as much as possible. For example, when searching for past cases by narrowing down to a specific gene, it depends on the motive such as wanting to avoid the situation of reviewing the PDF.

It is developed for the purpose of swallowing xml data collectively, and it is not assumed that users will register other variables of interest together and analyze related things on the DB. It is recommended to create another table or collect data separately for the research.

This DB is designed to swallow the new xml under the above parent folder every time. This is due to the circumstances of our environment.

If you want to link with the patient ID etc., please write the name of the child folder containing the case xml as 20200105\_patientidxyzz. This database is designed to swallow before and after cutting with an underscore according to the report information.

If you have the above id, you may be able to merge it with a suitable research table later.

The structure of F1CDx and NOP xml itself is not explained here. I created a slide separately, so please check it. Clinicians will find out by comparing the report with xml.

The notes are as follows.

- i. No drug information about the mutation is attached.
- ii. The format is completely different for F1 and NOP.
- iii. TMB has a decimal point.
- iv. It does not hold a LOH score.

Regarding research use, I think that you can use it freely at your own risk, but if you use R or Python, I think that it is smart to obtain data with an odbc connection for various analyzes.

## 5 ## Usage

Please download panelsdb2/xml2fm.zip and extract it.

You need to install FM to your PC before use this.

## Admin User Account

name: Admin

PW: DR>ba)4W&L

It is not assumed that the password will be memorized or manually entered. Please change to a password suitable for each facility.

### Directory setting

## 6 ## dir setting

this require file setting as bellow.

parent\_dir.

+---f1l\_parent\_dir

| +---idaaa\_yymmdd03

| | a1.xml

| |

| \---idbbb\_yymmdd03

| y2.xml

|

+---f1\_parent\_dir

| +---idxxx\_yymmdd01

| | x1.xml

```

| |
| \---idyyy_yymmdd02
|   x2.xml
|
+---g360_parent_dir
|   patient_summary.csv
|
\---nccop_parent_dir
    +---idbbb_yymmdd03
    |   y2.xml
    |
    \---idddd_yymmdd05
        a1.xml

```

here demostructure with dummy data.



## Importing

7 Top is bellow



8 If importing xmls, you should click bottuns and chose paretn dir.



- 9 After importing several platforms, you can create whole platform report and variants data from make AiIV button.



- 10 You can see several info from xml from here



11 you can delete imported data with forbidden word "unko".



12 you can view all patient after make AiIV

