

2023-08-14

Ontario Institute for Cancer Research

Djerba: A Modular System to Generate Clinical Genome Interpretation Reports for Cancer

Iain Bancarz PhD



Introduction

1. Clinical reporting
2. How Djerba works
3. Going modular

github.com/oicr-gsi/djerba



1. Clinical Reporting

What is a clinical report?

- Report for an individual patient
- **Accredited** for clinical use
- Printable document:
 - Assay results
 - Interpretation
 - Treatment (if any)



Accreditation



ACCREDITATION
CANADA



Centers for Disease Control and Prevention
CDC 24/7: Saving Lives, Protecting People™

Clinical Laboratory Improvement Amendments (CLIA)



OICR is the first lab in
North America to be
accredited with
CAP, ACD and CLIA

Clinical Assays

Main assay

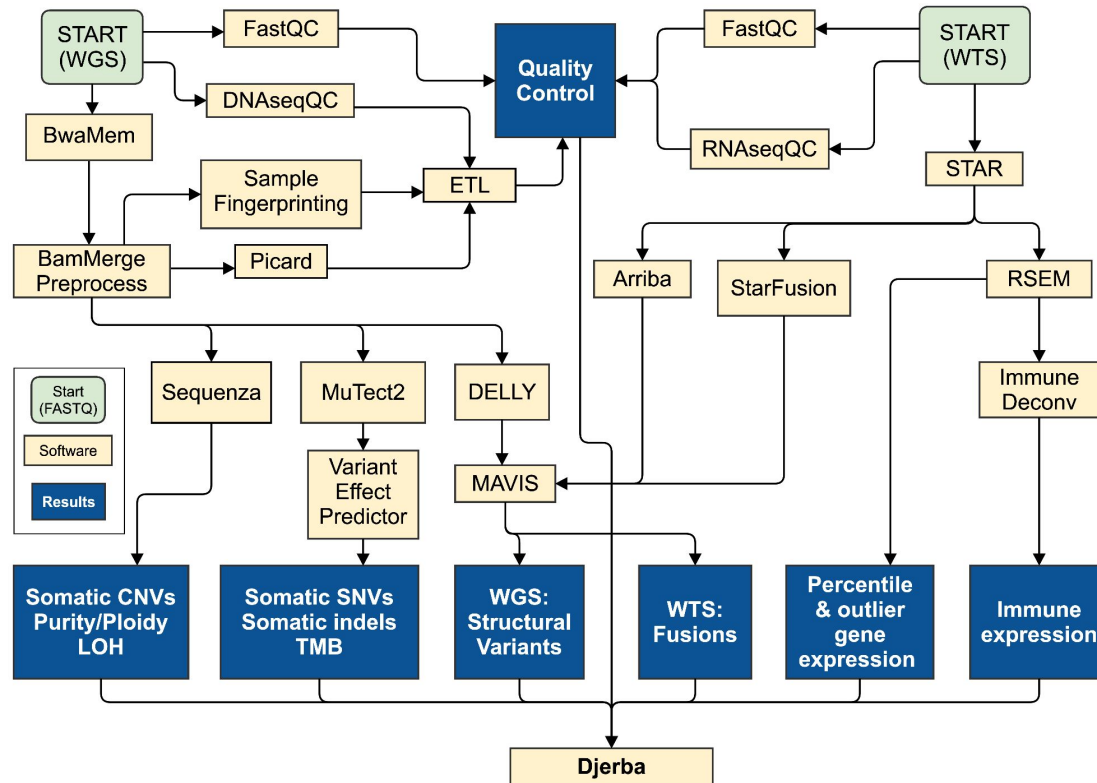
- Whole Genome and Transcriptome Sequencing: WGTS

Others

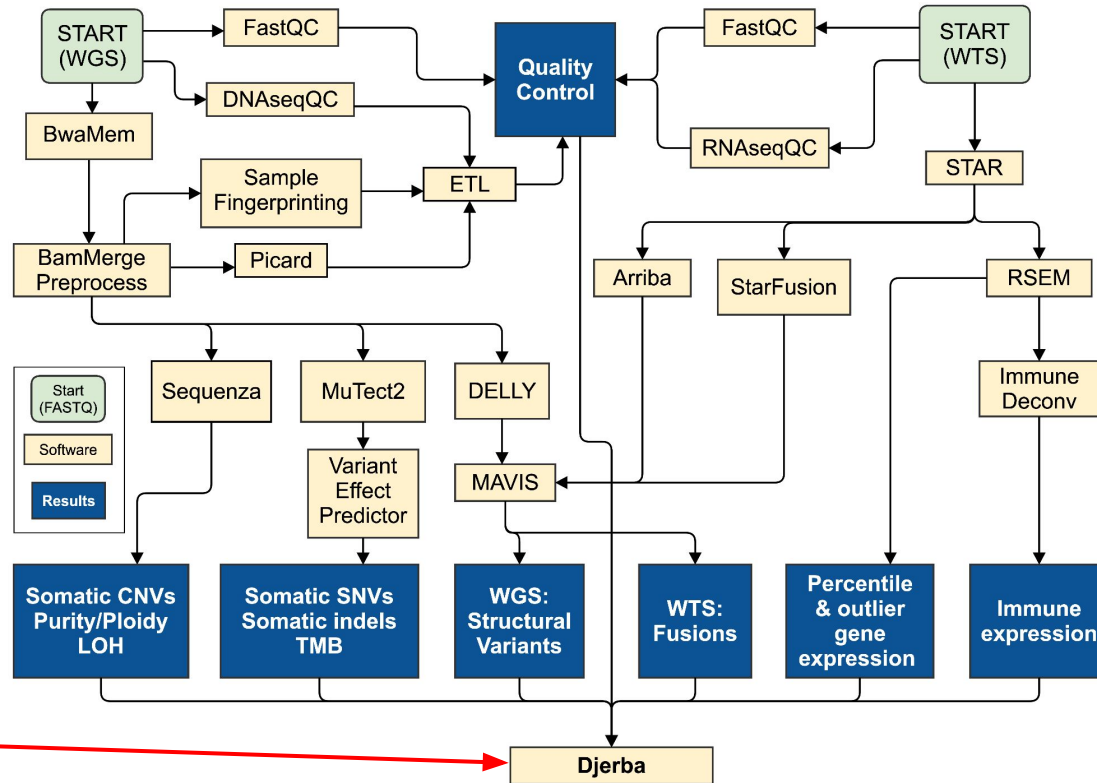
- Plasma Whole Genome Sequencing: PWGS
- Targeted Sequencing: TAR
- Whole Genome Sequencing: WGS



WGTS pipelines: From FASTQ to Clinical Report



WGTS pipelines: From FASTQ to Clinical Report



Djerba

Clinical reporting: Example



Ontario Institute for Cancer Research
c/o Tissue Portal Sample Receiving MaRS Centre
West Tower 661 University Avenue, Suite 6-46
Toronto, Ontario, Canada, M5G 0A3
CAP: 8381376 ACDx: 0730 CLIA: 99D2270792

Director: Trevor Pugh, PhD, FACMG
Phone: 647-468-7844
Main contact: Alexander Fortuna, MSc
Phone: 416-973-8539
Hours of Operation: Mon-Fri, 9:00AM - 5:00PM

Clinical Research Report

PATIENT & PHYSICIAN

Patient Name: LAST, FIRST
Patient Genetic Sex: SEX
Physician Licence #: nnnnnnnn
Physician Phone #: nnn-xxx-xxxx
Patient DOB: yyyy/mm/dd
Requisitioner Email: NAME@DOMAIN.COM
Physician: LAST, FIRST
Physician Hospital: HOSPITAL NAME AND ADDRESS

CASE OVERVIEW

Assay: Whole genome and transcriptome sequencing (WGTS)-80X Tumour, 30X Normal (v3.0)
Primary cancer: Pancreatic Adenocarcinoma
Site of biopsy/surgery: Paravertebral Mass
Study: PLACEHOLDER **Patient Study ID:** PLACEHOLDER
Patient LIMS ID: PLACEHOLDER **Tumour Sample ID:** PLACEHOLDER
Requisition Approved: 2023/01/01 **Blood Sample ID:** PLACEHOLDER
Date of Report: yyyy/mm/dd **Report ID:** PLACEHOLDER-v1

TREATMENT OPTIONS

Review identified 1 mutation(s) indicating an FDA Approved and/or NCCN Recommended Biomarker and 3 mutation(s) indicating investigational therapies.

FDA Approved and/or NCCN Recommended Biomarker:

OncoKB	Treatment(s)	Gene(s)	Alteration
1	Pembrolizumab	Biomarker	MSI-H

Investigational Therapies:

OncoKB	Treatment(s)	Gene(s)	Alteration
3B	Enasidenib, Vorasidenib	IDH2	p.R172M
4	Palbociclib, Ribociclib, Abemaciclib	CDKN2A	Deletion
4	Erdafitinib, AZD4547	FGFR1, PLAG1	Fusion

RESULTS SUMMARY

The patient has been diagnosed with Pancreatic Adenocarcinoma and has been referred for the OICR Genomics WGTS assay through the PLACEHOLDER study. This test uncovered 1 out of 4 most commonly altered genes in pancreatic cancer ([DOI:10.1038/nature14169](https://doi.org/10.1038/nature14169)): a *CDKN2A* deletion (9p21.3, with proximal deletions of *CDKN2B* and *MTAP*). While there are no FDA-approved therapeutic options for these mutations in PAAD, laboratory data suggest that loss-of-function alterations of *CDKN2A* may

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Patient metadata

Sample info

Summary text

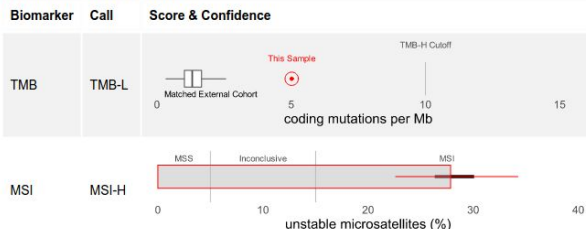
Therapies

... and much more!

Clinical Reporting: Continued Example

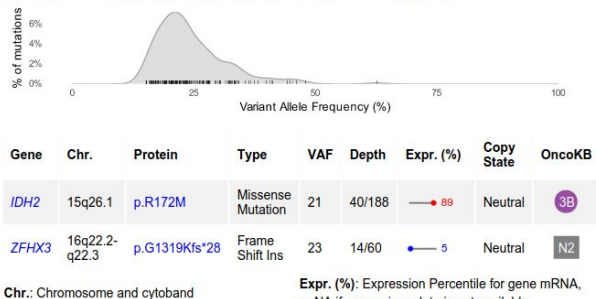
GENOMIC LANDSCAPE

Tumour Mutation Burden (TMB) was **5.02** coding mutations per Mb (187 mutations) which corresponded to the 71st percentile of the pan-cancer cohort and classifies it as **Tumour Mutational Burden Low (TMB-L, < 10 coding mutations / Mb)**. This TMB places the tumour in the 99th percentile of the COMPASS cohort. The microsatellite status is **Microsatellite Instability High (MSI-H)**. This tumour has **55,699** candidate SNVs for ctDNA screening, making the sample **eligible** for OICR's plasma WGS assay (minimum of 4,000 SNVs required).



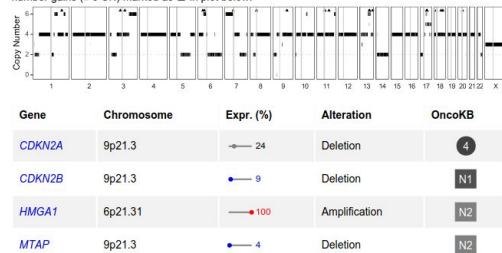
SNVS AND IN/DELS

247 somatic mutation(s) were detected in exonic or splice regions, of which **187** impacted a coding sequence, and **2** corresponded to an oncogenic mutation, as defined by OncoKB.



COPY NUMBER VARIATION

The percent genome altered (PGA) was **30%**, **9** cancer gene(s) were subject to copy number variation, of which **4** corresponded to an oncogenic alteration, as defined by OncoKB. Regions with large copy number gains (≥ 6 CN) marked as ▲ in plot below.



Expr. (%): Expression Percentile for gene mRNA, or NA if comparison data is not available

... and even more!

- Fusions
- Purity & ploidy
- Coverage & callability
- Glossary of terms

Coming soon:

- Immune activity
- Virus infiltration
- Tissue of origin inference

Clinical Reporting: Continued Example

GENOMIC LANDSCAPE

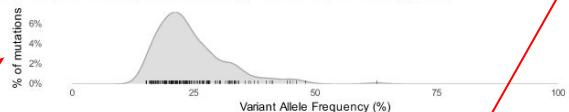
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Biomarker Call Score & Confidence



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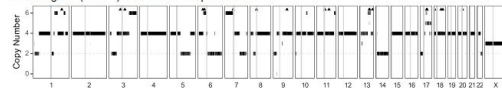
Gene	Chr.	Protein	Type	VAF	Depth	Expr. (%)	Copy State	OncoKB
IDH2	15q26.1	p.R172M	Missense Mutation	21	40/188	89	Neutral	3B
ZFXH3	16q22.2-q22.3	p.G1319Kfs*28	Frame Shift Ins	23	14/60	5	Neutral	N2

Chr.: Chromosome and cytoband

Expr. (%): Expression Percentile for gene mRNA, or NA if comparison data is not available

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Gene	Chromosome	Expr. (%)	Alteration	OncoKB
CDKN2A	9p21.3	24	Deletion	4
CDKN2B	9p21.3	9	Deletion	N1
HMGAI	6p21.31	100	Amplification	N2
MTAP	9p21.3	4	Deletion	N2

Expr. (%): Expression Percentile for gene mRNA, or NA if comparison data is not available

... and even more!

- Fusions
- Purity & ploidy
- Coverage & callability
- Glossary of terms

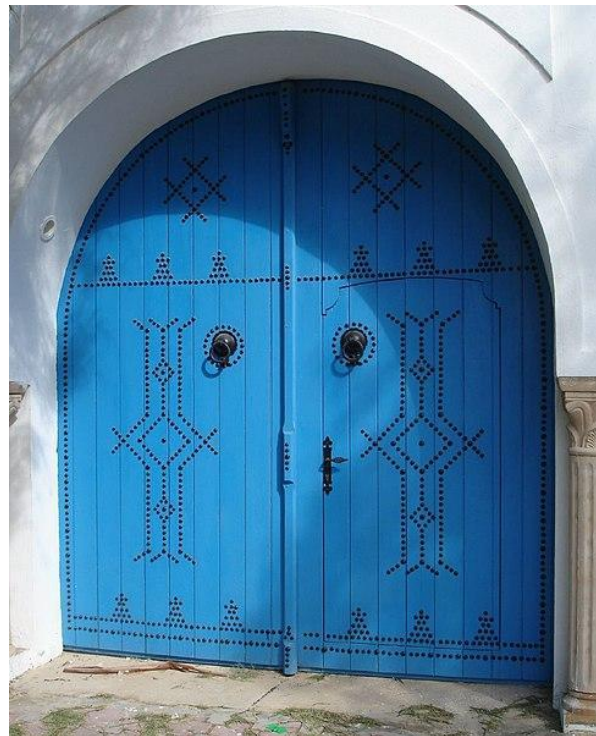
Coming soon:

- Immune activity
- Virus infiltration
- Tissue of origin inference

2. How Djerba works

Introducing Djerba

- github.com/oicr-gsi/djerba
- Developed from scratch
- No existing application filled its niche
- Open source
- GPL 3.0 licence
- 100+ reports since January 2022



Doorway on the island of Djerba

Photo by Alain Feulvarch, Wikimedia Commons

How Djerba works

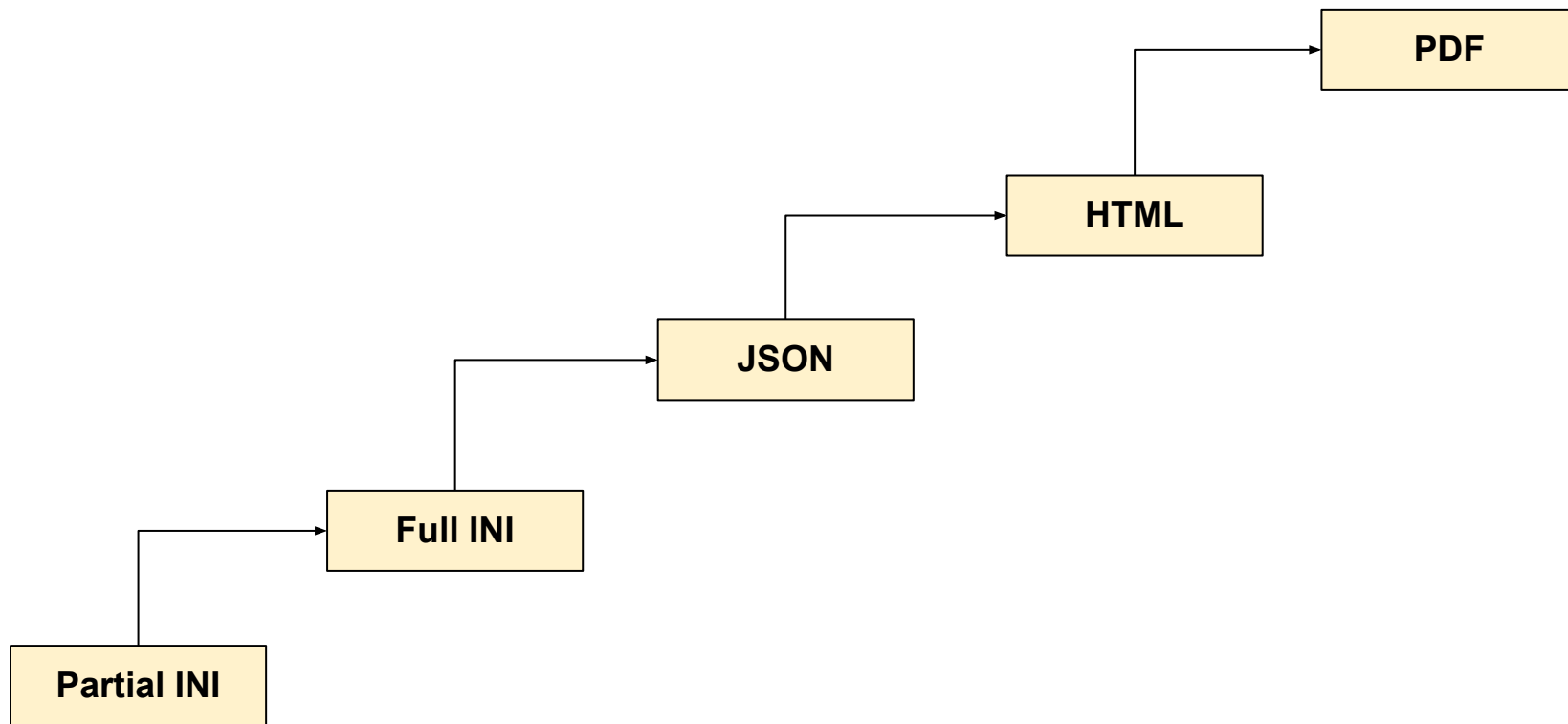
Step	Format	Read by
Configure	INI	Human 😊
Extract	JSON	Machine 🤖
Render	HTML	Human 😊
Publish	PDF	Human 😊

How Djerba works

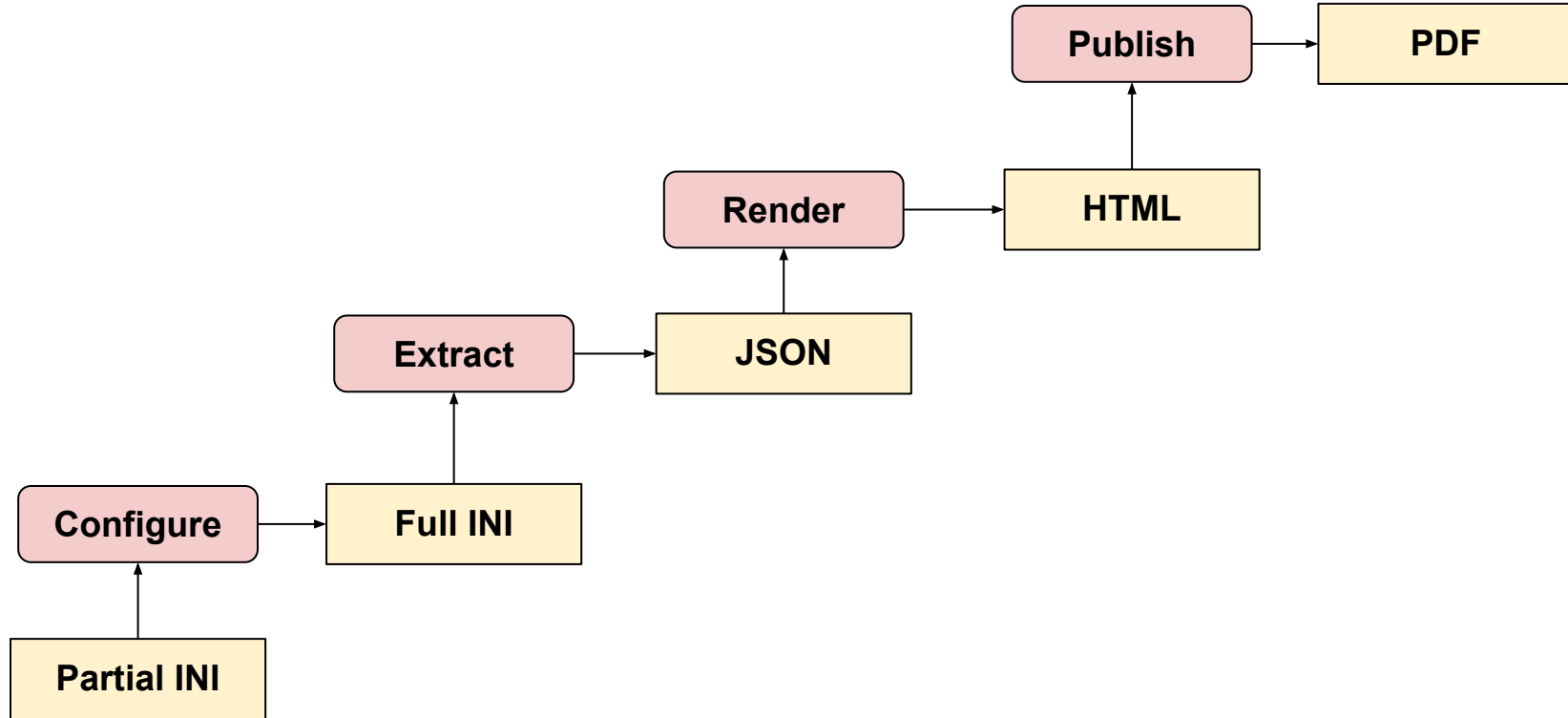
Step	Format	Read by
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Explained in one table!

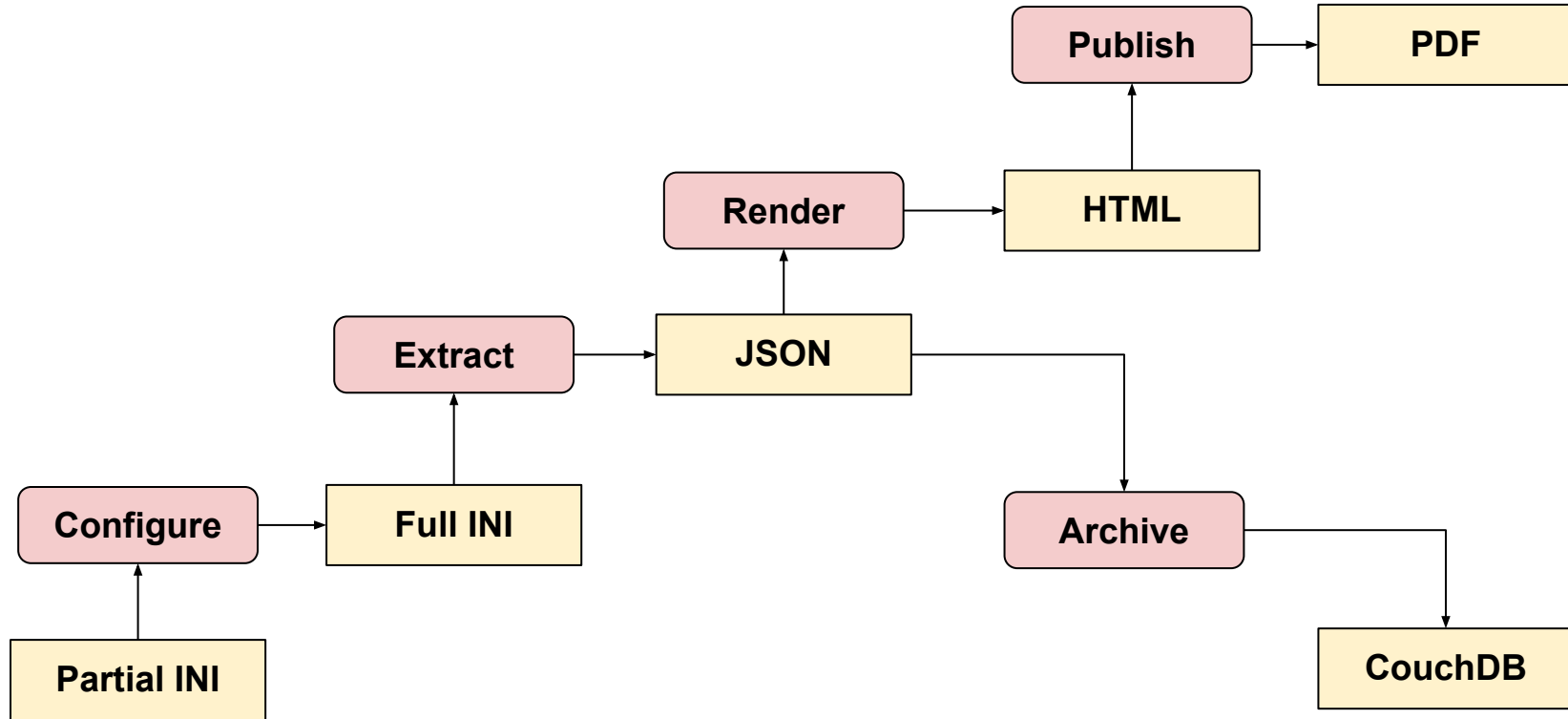
Djerba steps: File types



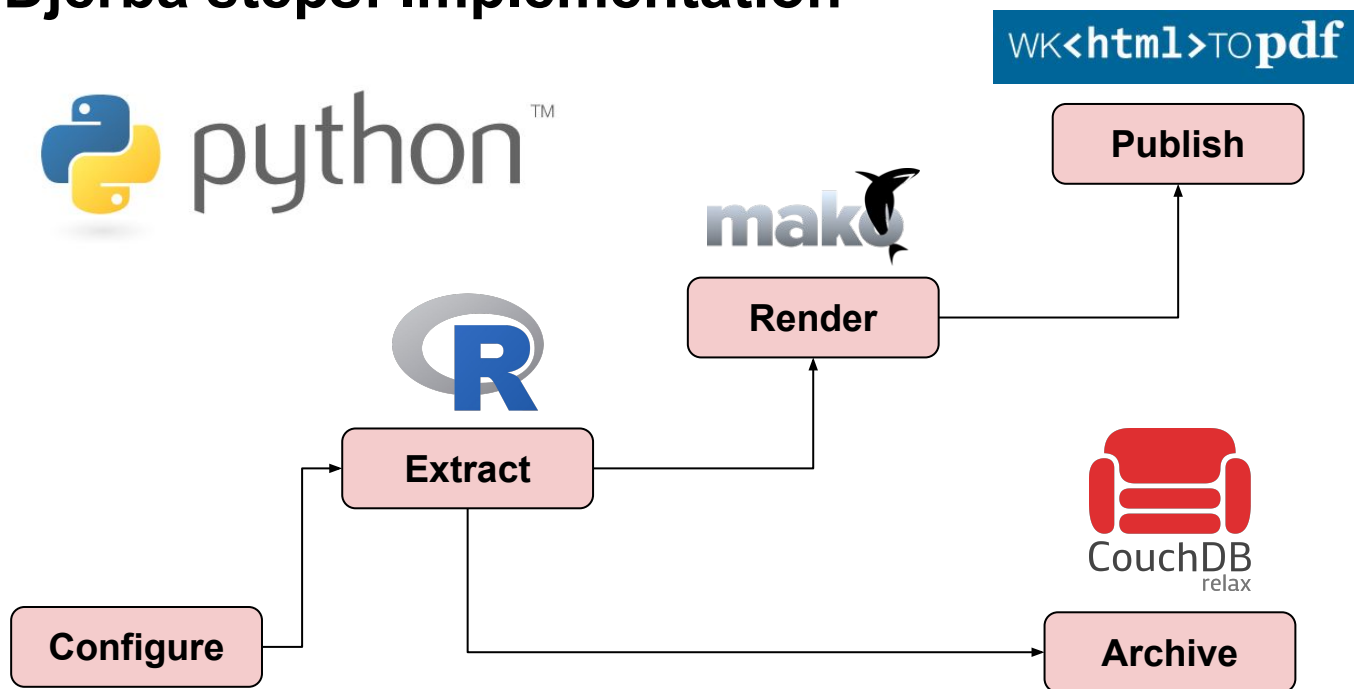
Djerba steps: File types and actions



Djerba steps: File types and actions and more!



Djerba steps: Implementation



Running Djerba

```
djerba.py report --ini config.ini --out ./output
```



3. Going modular

Plugins for Djerba

- Djerba is growing
- Make it modular!
- **Core** manages the plugins
- **Plugins** are easy to:
 - Write
 - Test
 - Update
 - Share

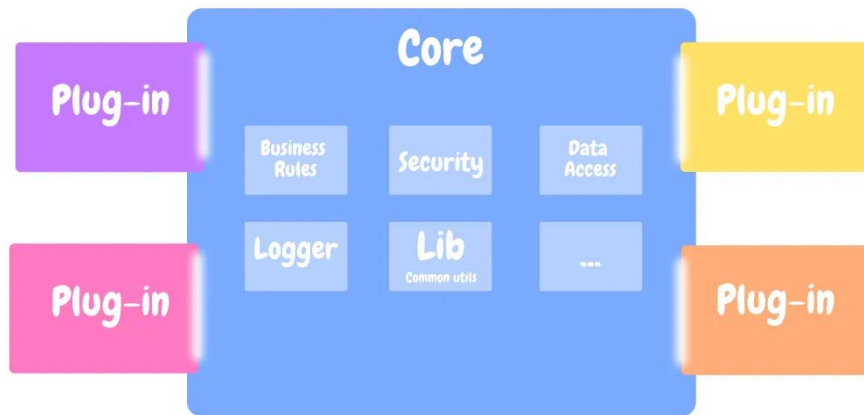


Image via <https://medium.com/omarelgabrys-blog>



Complex
interconnected
system



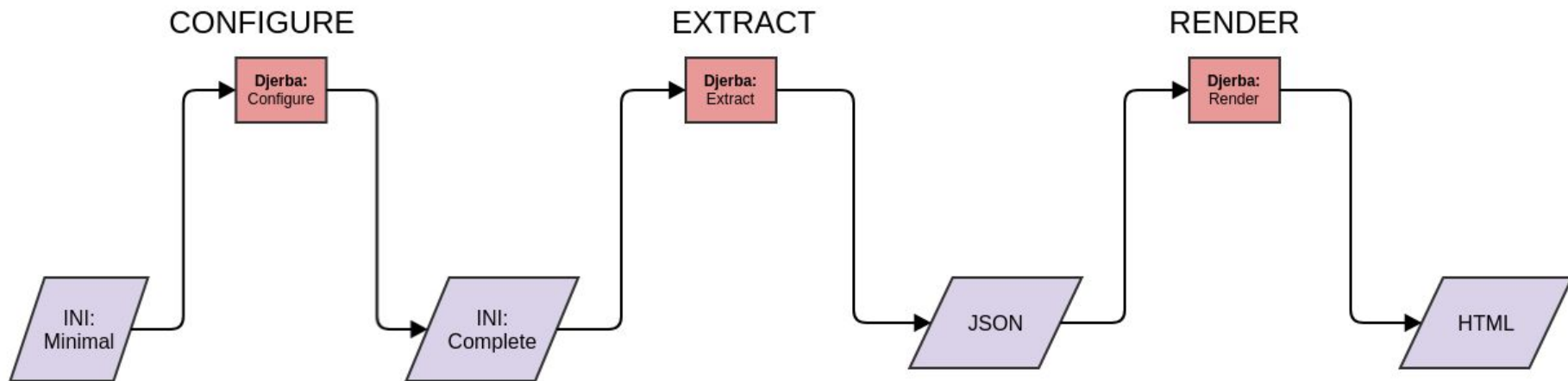
Simple
plugins in
a well-defined
framework

Plugins are Miniature Djerbas

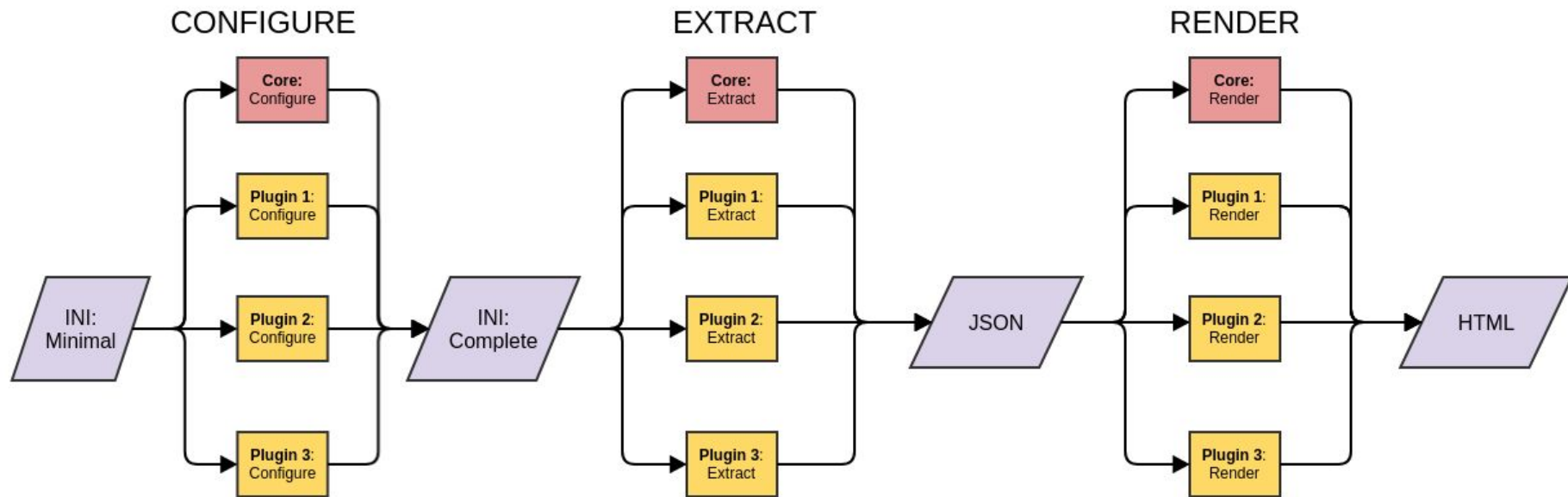
- Generate a **section** of the report
 - Configure INI
 - Extract JSON
 - Render HTML
- The Djerba **core**:
 - Runs multiple plugins
 - Makes the completed report
- Launch September 2023



Reminder: Djerba without plugins



New and improved: Djerba with plugins



Plugin capabilities

- Generate example INI files
- Required and default parameters
- Runtime priorities
- Shared workspace
- Merge outputs
- ... and more!



Conclusion

Summary

- Djerba is a system for clinical reports
- 4 steps:
 - Configure INI
 - Extract JSON
 - Render HTML
 - Publish PDF
- JSON archived to CouchDB database
- Modular structure enables extension and collaboration
- Github: [oicr-gsi/djerba](https://github.com/oicr-gsi/djerba)



Acknowledgements

- Alex Fortuna
- Felix Beaudry
- Aqsa Alam



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is provided by the Government of Ontario

