# An AI-derived Tool to Pre-screen Lung Cancer Candidates for Clinical Trials

**Mihaela Aldea[1], Pierre Rolland[2], Lodovica Zullo[1], Aliette Poplu[2], Solenne Simon[1], Azeddine Djarallah[2], Muriel Wartelle[3], Lisa Chuttoo[2], Benjamin Vignal[2], Jean-Charles Louis[2], François Lion[3], Sandra Platano[2], Anas Gazzah[4], Caroline Robert[1], Fabrice Andre[1], Fabrice Barlesi[1], Stefan Michiels[5], Capucine Baldini[4], Christophe Massard[4], Franck Le Ouay[2], Benjamin Besse[1]**

1 Department of Medical Oncology, Gustave Roussy Cancer Center, Villejuif, France
2 Lifen, Paris, France
3 Informatic Team (DTNSI), Gustave Roussy, Villejuif, France
4 Drug Development Department, Gustave Roussy, Villejuif, France
5 Biostatistics & Epidemiology, Gustave Roussy, Villejuif, France

## BACKGROUND

- Patient selection in clinical trials is crucial but challenging, traditionally dependent on clinician-led identification that might overlook potential participants.
- This study's objective was to assess an artificial intelligence (AI)-enhanced approach for institutional patient screening to improve trial enrolment.

## METHOD

**POPULATION**
Patients with thoracic cancer seen at Gustave Roussy between Feb 2021 and June 2024.

**MANUAL DATA ENTRY (MDE)**
Manual retrospective collection of data in a secured RedCap database.

**AUTOMATED DATA ENTRY (ADE) – INPUT**
- Unstructured patient medical letters between February 2021 - July 2024.
- A schematic description of each variable.

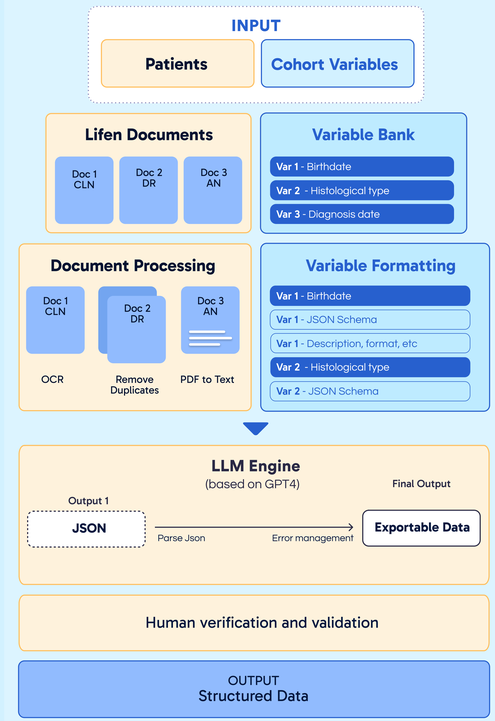
**METHOD**
- Generative AI to find, quote and process variables into a structured form.
- Large language model (LLM) actions with prompt engineering and tailored few-shots examples.
- Mortality data were auto-extracted from the French public registry, INSEE.

**OUTPUT**
Demographics, disease characteristics, comorbidities, treatment history and life status.

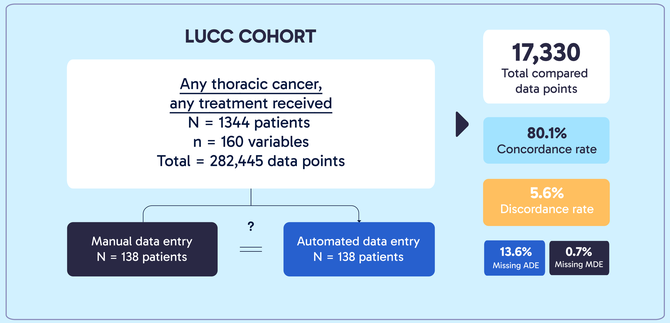
**METRICS**
Concordance between comparable dates from MDE and ADE, secondary manual review for mismatches (senior physician), correctness (accuracy after checking), time per patient.

## RESULTS

### Algorithm




### Concordance ADE vs MDE




### Correctness

Correctness was calculated after checking for discordances and excluding missing data on both sides.

**83.6%**
Overall correctness

| CORRECTNESS 95% - 100% | 85% - 94% | < 85% |
|---|---|---|
| Gender & Birthdate | Histology | Date first diagnosis/metastasis |
| Life status & date of death | Smoking status | Systemic treatment lines and details |
| Comorbidities (Cardiac disease, autoimmune disease, HIV, hepatitis B and C, thromboembolic events etc.) | PDL1 expression | Pack years |
| | Metastatic from diagnosis | TMB value |
| Molecular alterations (EGFR, BRAF, ROS1, RET, MET, HER2, PIK3CA, SMARCA4, KEAP1, NRG1, NTRK) | Metastatic anytime | Latest performance status |

### Discordances check

- 32.8% MDE errors
- 29.1% ADE errors due to limited access to data
- 17.6% ADE errors
- 14.4% False errors
- 6.1% MDE & ADE common errors

ADE errors were mostly from data gaps in medical notes.
Also, detailed information was often accessible to MDE in imaging or pathology reports, yet inaccessible to ADE.

### Accuracy

Taking as an example a clinical trial with the following criteria (Life status, SMARCA4 alterations, metastatic disease, treated in advanced settings, type of 1st line, progression)

| Criteria | ADE | MDE |
|---|---|---|
| Life Status | 100% | 96% |
| SMARCA 4 alterations | 100% | 88% |
| Metastatic disease | 93% | 95% |
| 1st line type & progression | 75% | 94% |
| **Total** | **70%** | **74%** |

### Time per Patient

**ADE**
**3 min**
WITH QUALITY CHECK

**MDE**
**>20 min**
PER PATIENT

## CONCLUSION

- Generative AI can identify eligible clinical trial candidates with over 70% accuracy between ADE and MDE depending on selected criteria.
- High performance of ADE is seen with demographics, life status, histology, molecular alterations and comorbidities.
- ADE errors or missing data are often due to a lack of information in medical notes.
- ADE has the potential to enhance the efficiency, accuracy, and scalability of clinical trial pre-screening.