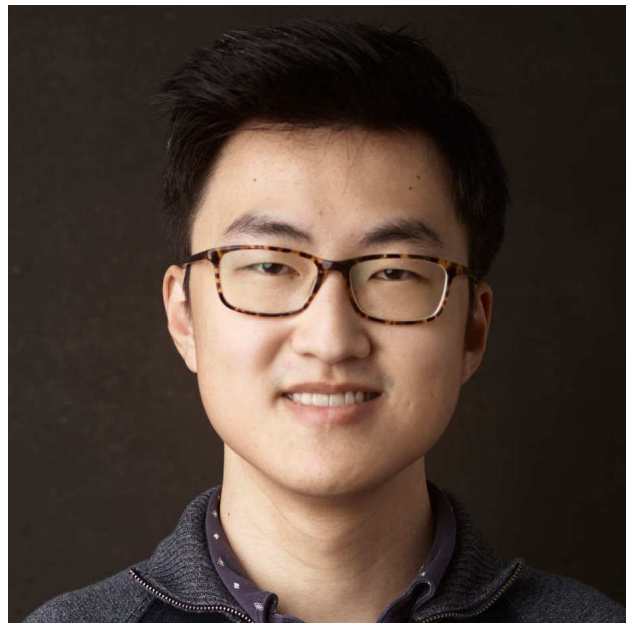


Standardizing and unifying unstructured instrument data with LLMs

Andrew Chen



Andrew Chen

Stanford  **Combinator**

Stanford MS Computer Science at age 20



Florence Pham

 **airbnb**  **YouTube**

Tech lead for highest-traffic page at Airbnb
>100M visitors

The Problem

Analogy: Translation

English

Analogy: Translation

Mandarin

English

Analogy: Translation

Mandarin

Catalan

English

Analogy: Translation

Mandarin

Catalan

Swahili

... 100s of languages

English

Analogy: Translation

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Catalan

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Analogy: Translation

Mandarin

Catalan

Swahili

... 100s of languages

Native speaker

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Writer

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Analogy: Translation

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create

Dictionary

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create

Dictionary

2-6 weeks
per language

**And repeat
100x!**

English



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Catalan

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Native speaker

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Takes long time, resource-intensive

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ASM

Takes long time, resource-intensive

Our vision with LLMs

Proprietary

Instrument

Formats

... 1000s of formats

SME*

+

Dev

+

LLM

create

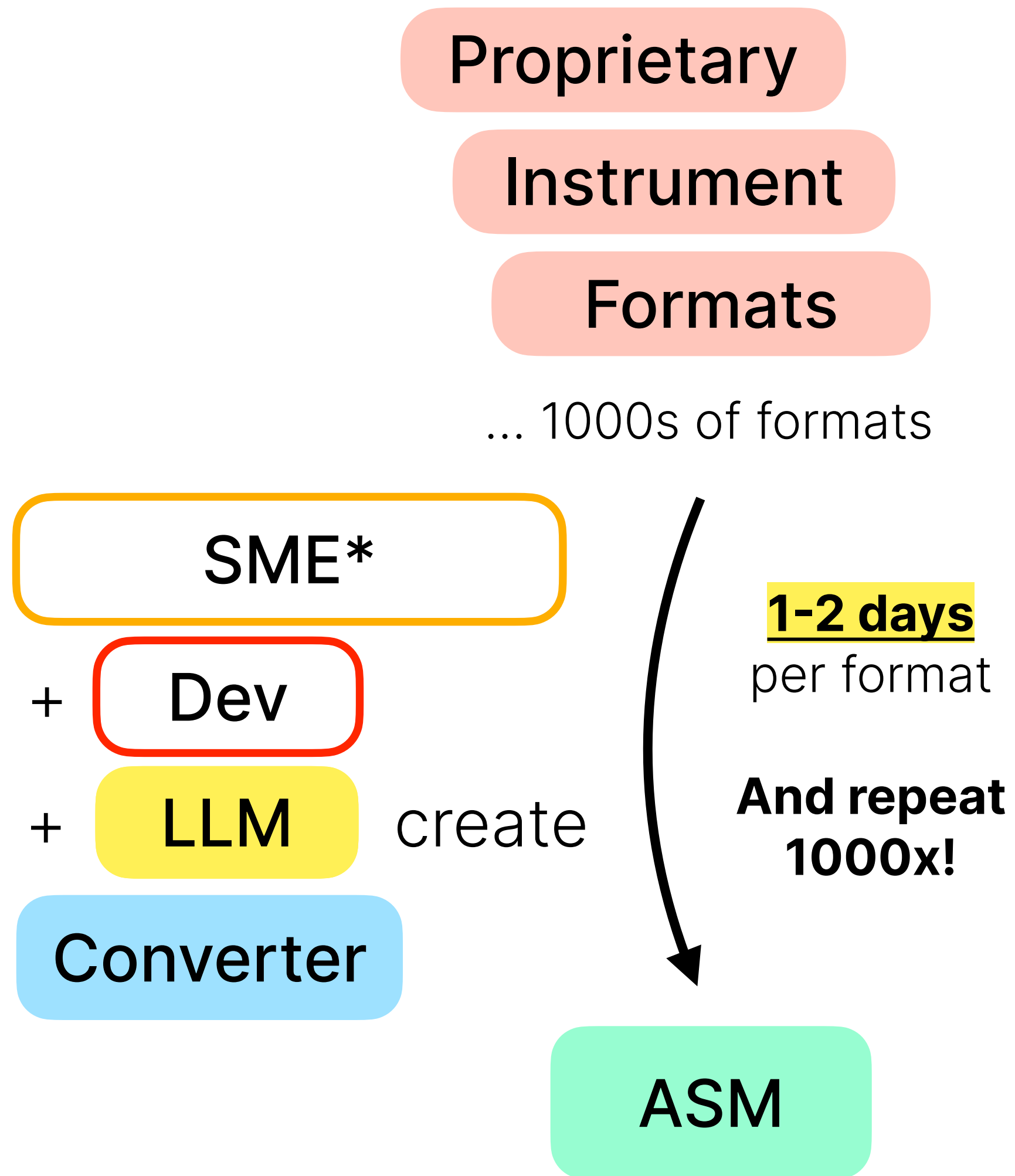
Converter

1-2 days
per format

**And repeat
1000x!**

ASM

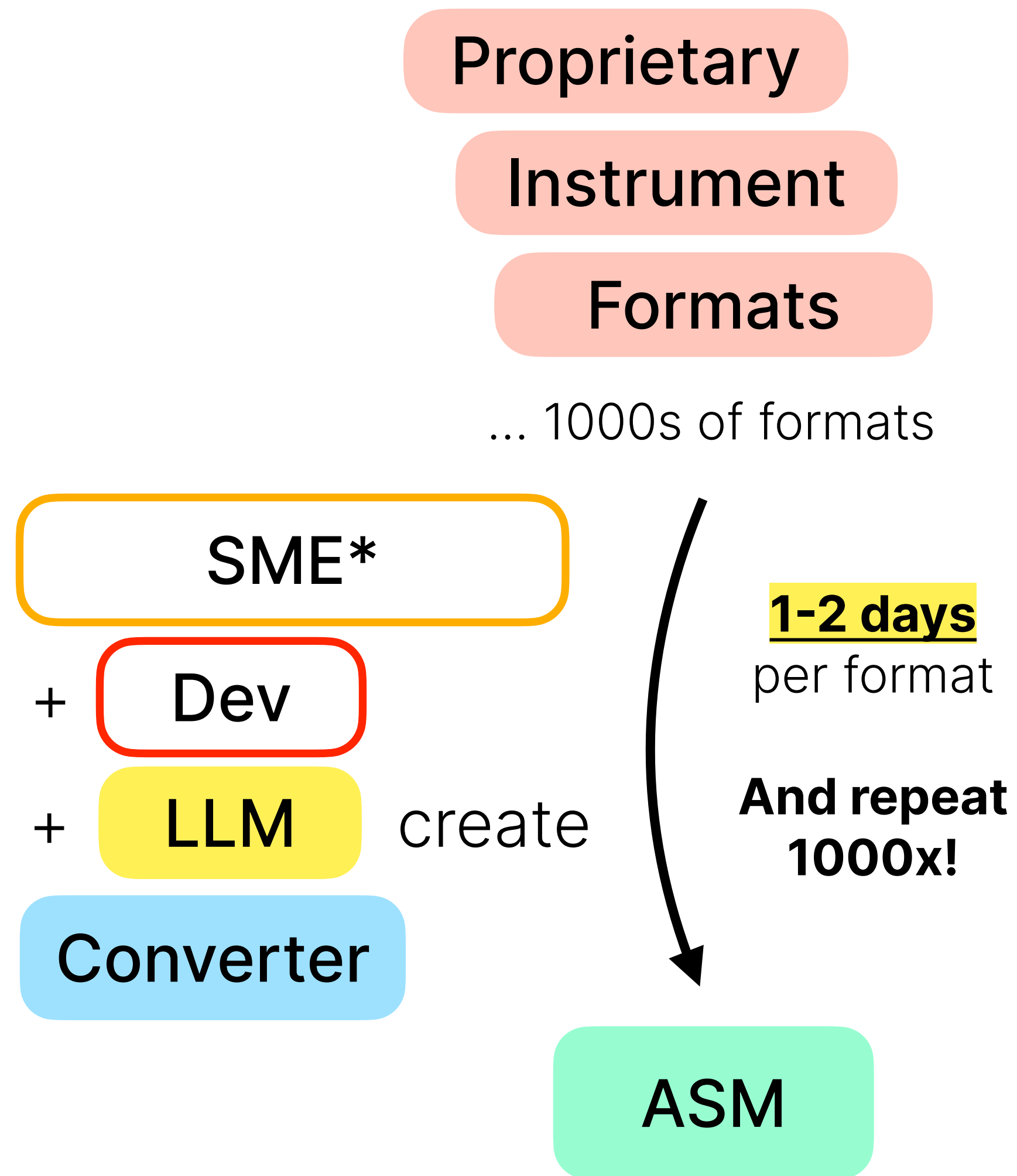
Our vision with LLMs



We used LLMs to build
converters for 19 instruments

Open-source test set from Benching

Our vision with LLMs



We used LLMs to build
converters for 19 instruments

Open-source test set from Benching

Findings:

- 1-2 day turnaround end-to-end
- * SME involvement minimized
Only needed for validation, which is
accelerated through LLM-specific tooling

Get familiar with the raw data
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40 2023-09-15 16:59:16 SMPL3 SAM LAC2B g/L < TEST RNG < 0.00 0.00329 R
40 2023-09-15 16:59:38 SMPL3 SAM TP2D g/L < TEST RNG < 40.0 0.02702 R
40 2023-09-15 17:00:52 SMPL3 SAM TP2LB g/L 4.8 0.15436 R
40 2023-09-16 10:12:10 SMPL4 SAM GLN2B mmol/L 2.07 0.14503 R
40 2023-09-16 10:12:12 SMPL4 SAM GLC3B g/L 4.09 0.68160 R
40 2023-09-16 10:13:29 SMPL4 SAM LDH2B U/L 334.84 0.02665 R
40 2023-09-16 10:13:37 SMPL4 SAM NH3B mmol/L 3.788 0.11415 R
40 2023-09-16 10:22:55 SMPL4 SAM LAC2B g/L v 1.89 0.15187 R
```


Get familiar with the raw data
from this cell culture analyzer...



```
0 2023-09-17 13:04:06 #ARC-FILE# 1.1a 2021-05-01 2023-09-17 CEDEX BIO HT 123456 6.0.0.1905 (1905) ADMIN
40 2023-09-15 16:55:51 SMPL1 SAM GLN2B mmol/L 2.43 0.17138 R
40 2023-09-15 16:55:53 SMPL1 SAM GLC3B g/L 6.32 1.05394 R
40 2023-09-15 16:56:18 SMPL1 SAM LDH2B U/L 88.09 0.00728 R
40 2023-09-15 16:56:26 SMPL1 SAM NH3B mmol/L 1.846 0.05333 R
40 2023-09-15 16:56:37 SMPL1 SAM LAC2B g/L 0.02 0.01567 R
40 2023-09-15 16:56:48 SMPL1 SAM TP2LB g/L 4.6 0.14883 R
40 2023-09-15 16:56:58 SMPL2 SAM GLN2B mmol/L 2.40 0.16787 R
40 2023-09-15 16:57:09 SMPL2 SAM GLC3B g/L 6.71 1.11766 R
40 2023-09-15 16:57:19 SMPL2 SAM LDH2B U/L < TEST RNG < 20.00 0.00060 R
40 2023-09-15 16:57:30 SMPL2 SAM NH3B mmol/L 1.870 0.05408 R
40 2023-09-15 16:57:41 SMPL2 SAM LAC2B g/L < TEST RNG < 0.00 0.00310 R
40 2023-09-15 16:57:51 SMPL2 SAM TP2B g/L < TEST RNG < 4.0 0.03322 R
40 2023-09-15 16:58:02 SMPL2 SAM TP2D g/L < TEST RNG < 40.0 0.02653 R
40 2023-09-15 16:58:23 SMPL2 SAM TP2LB g/L 4.7 0.15217 R
40 2023-09-15 16:58:34 SMPL3 SAM GLN2B mmol/L 2.43 0.17049 R
40 2023-09-15 16:58:45 SMPL3 SAM GLC3B g/L 6.71 1.11813 R
40 2023-09-15 16:58:55 SMPL3 SAM LDH2B U/L < TEST RNG < 20.00 0.00076 R
40 2023-09-15 16:59:06 SMPL3 SAM NH3B mmol/L 1.817 0.05242 R
40 2023-09-15 16:59:16 SMPL3 SAM LAC2B g/L < TEST RNG < 0.00 0.00329 R
40 2023-09-15 16:59:38 SMPL3 SAM TP2D g/L < TEST RNG < 40.0 0.02702 R
40 2023-09-15 17:00:52 SMPL3 SAM TP2LB g/L 4.8 0.15436 R
40 2023-09-16 10:12:10 SMPL4 SAM GLN2B mmol/L 2.07 0.14503 R
40 2023-09-16 10:12:12 SMPL4 SAM GLC3B g/L 4.09 0.68160 R
40 2023-09-16 10:13:29 SMPL4 SAM LDH2B U/L 334.84 0.02665 R
40 2023-09-16 10:13:37 SMPL4 SAM NH3B mmol/L 3.788 0.11415 R
40 2023-09-16 10:22:55 SMPL4 SAM LAC2B g/L v 1.89 0.15187 R
```


Get familiar with the raw data
from this cell culture analyzer...



```
0 2023-09-17 13:04:06 #ARC-FILE# 1.1a 2021-05-01 2023-09-17 CEDEX BIO HT 123456 6.0.0.1905 (1905) ADMIN
40 2023-09-15 16:55:51 SMPL1 SAM GLN2B mmol/L 2.45 0.17138 R
40 2023-09-15 16:55:53 SMPL1 SAM GLC3B g/L 6.32 1.05394 R
40 2023-09-15 16:56:18 SMPL1 SAM LDH2B U/L 88.09 0.00728 R
40 2023-09-15 16:56:26 SMPL1 SAM NH3B mmol/L 1.846 0.05333 R
40 2023-09-15 16:56:37 SMPL1 SAM LAC2B g/L 0.02 0.01567 R
40 2023-09-15 16:56:48 SMPL1 SAM TP2LB g/L 4.6 0.14883 R
40 2023-09-15 16:56:58 SMPL2 SAM GLN2B mmol/L 2.40 0.16787 R
40 2023-09-15 16:57:09 SMPL2 SAM GLC3B g/L 6.71 1.11766 R
40 2023-09-15 16:57:19 SMPL2 SAM LDH2B U/L < TEST RNG < 20.00 0.00060 R
40 2023-09-15 16:57:30 SMPL2 SAM NH3B mmol/L 1.870 0.05408 R
40 2023-09-15 16:57:41 SMPL2 SAM LAC2B g/L < TEST RNG < 0.00 0.00310 R
40 2023-09-15 16:57:51 SMPL2 SAM TP2B g/L < TEST RNG < 4.0 0.03322 R
40 2023-09-15 16:58:02 SMPL2 SAM TP2D g/L < TEST RNG < 40.0 0.02653 R
40 2023-09-15 16:58:23 SMPL2 SAM TP2LB g/L 4.7 0.15217 R
40 2023-09-15 16:58:34 SMPL3 SAM GLN2B mmol/L 2.43 0.17049 R
40 2023-09-15 16:58:45 SMPL3 SAM GLC3B g/L 6.71 1.11813 R
40 2023-09-15 16:58:55 SMPL3 SAM LDH2B U/L < TEST RNG < 20.00 0.00076 R
40 2023-09-15 16:59:06 SMPL3 SAM NH3B mmol/L 1.817 0.05242 R
40 2023-09-15 16:59:16 SMPL3 SAM LAC2B g/L < TEST RNG < 0.00 0.00329 R
40 2023-09-15 16:59:38 SMPL3 SAM TP2D g/L < TEST RNG < 40.0 0.02702 R
40 2023-09-15 17:00:52 SMPL3 SAM TP2LB g/L 4.8 0.15436 R
40 2023-09-16 10:12:10 SMPL4 SAM GLN2B mmol/L 2.07 0.14503 R
40 2023-09-16 10:12:12 SMPL4 SAM GLC3B g/L 4.09 0.68160 R
40 2023-09-16 10:13:29 SMPL4 SAM LDH2B U/L 334.84 0.02665 R
40 2023-09-16 10:13:37 SMPL4 SAM NH3B mmol/L 3.788 0.11415 R
40 2023-09-16 10:22:55 SMPL4 SAM LAC2B g/L v 1.89 0.15187 R
```


Our findings: what is an LLM good at?

Domain knowledge

0	2023-09-17 13:04:06	#ARC-FILE#	1.1a	2021-05-01	2023-09-17	CEDEX	BIO	HT	123456	6.0.0.1905	(1905)	ADMIN
40	2023-09-15 16:55:51	SMPL1	SAM	GLN2B	mmol/L	2.45	0.17138	R				
40	2023-09-15 16:55:53	SMPL1	SAM	GLC3B	g/L	6.32	1.05394	R				
40	2023-09-15 16:56:18	SMPL1	SAM	LDH2B	U/L	88.09	0.00728	R				
40	2023-09-15 16:56:26	SMPL1	SAM	NH3B	mmol/L	1.846	0.05333	R				
40	2023-09-15 16:56:37	SMPL1	SAM	LAC2B	g/L	0.02	0.01567	R				
40	2023-09-15 16:56:48	SMPL1	SAM	TP2LB	g/L	4.6	0.14883	R				
40	2023-09-15 16:56:58	SMPL2	SAM	GLN2B	mmol/L	2.40	0.16787	R				
40	2023-09-15 16:57:09	SMPL2	SAM	GLC3B	g/L	6.71	1.11766	R				
40	2023-09-15 16:57:19	SMPL2	SAM	LDH2B	U/L < TEST RNG	< 20.00	0.00060	R				
40	2023-09-15 16:57:30	SMPL2	SAM	NH3B	mmol/L	1.870	0.05408	R				
40	2023-09-15 16:57:41	SMPL2	SAM	LAC2B	g/L < TEST RNG	< 0.00	0.00310	R				
40	2023-09-15 16:57:51	SMPL2	SAM	TP2B	g/L < TEST RNG	< 4.0	0.03322	R				
40	2023-09-15 16:58:02	SMPL2	SAM	TP2D	g/L < TEST RNG	< 40.0	0.02653	R				
40	2023-09-15 16:58:23	SMPL2	SAM	TP2LB	g/L	4.7	0.15217	R				
40	2023-09-15 16:58:34	SMPL3	SAM	GLN2B	mmol/L	2.43	0.17049	R				
40	2023-09-15 16:58:45	SMPL3	SAM	GLC3B	g/L	6.71	1.11813	R				
40	2023-09-15 16:58:55	SMPL3	SAM	LDH2B	U/L < TEST RNG	< 20.00	0.00076	R				
40	2023-09-15 16:59:06	SMPL3	SAM	NH3B	mmol/L	1.817	0.05242	R				
40	2023-09-15 16:59:16	SMPL3	SAM	LAC2B	g/L < TEST RNG	< 0.00	0.00329	R				
40	2023-09-15 16:59:38	SMPL3	SAM	TP2D	g/L < TEST RNG	< 40.0	0.02702	R				
40	2023-09-15 17:00:52	SMPL3	SAM	TP2LB	g/L	4.8	0.15436	R				
40	2023-09-16 10:12:10	SMPL4	SAM	GLN2B	mmol/L	2.07	0.14503	R				
40	2023-09-16 10:12:12	SMPL4	SAM	GLC3B	g/L	4.09	0.68160	R				
40	2023-09-16 10:13:29	SMPL4	SAM	LDH2B	U/L	334.84	0.02665	R				
40	2023-09-16 10:13:37	SMPL4	SAM	NH3B	mmol/L	3.788	0.11415	R				
40	2023-09-16 10:22:55	SMPL4	SAM	LAC2B	g/L v	1.89	0.15187	R				

GLN2B
GLC3B
LDH2B
NH3B
LAC2B

Raw instrument data

```
"glutamine analysis": { ...
},
"glucose analysis": { ...
},
"lactate dehydrogenase analysis": { ...
},
"ammonia analysis": { ...
},
"lactate analysis": { ...
},
```

An LLM extraction result (collapsed for readability)

Test, Analyte	Test kit	Cat. no.	Content [tests]	On-board stability	Calibrator, interval	Test code
Glutamate	Glutamate V2 Bio	07395582001	4 x 50	28 days	A, lot, 56 days	GLU2B 812 v4 GLU2D 813 v4
	Glutamate V2 Bio HT	07395566001	200	56 days	A, lot, 56 days	GLU2B 0-894 v1 GLU2D 0-978 v1
Glutamine	Glutamine V2 Bio	07395655001	4 x 50	28 days	B, lot, 84 days	GLN2B 015 v7 GLN2D 016 v7
	Glutamine V2 Bio HT	07395612001	200	84 days	B, lot, 84 days	GLN2B 0-737 v3 GLN2D 0-674 v3

Unlike an engineer, doesn't need back-and-forth with SMEs for domain knowledge

Our findings: what is an LLM good at?

Extracting and Structuring Data

0	2023-09-17	13:04:06	#ARC-FILE#	1.1a	2021-05-01	2023-09-17	CEDEX	BIO	HT	123456	6.0.0.1905
	(1905)	ADMIN									
40	2023-09-15	16:55:51	SMPL1	SAM	GLN2B	mmol/L	2.45	0.17138	R		
40	2023-09-15	16:55:53	SMPL1	SAM	GLC3B	g/L	6.32	1.05394	R		
40	2023-09-15	16:56:18	SMPL1	SAM	LDH2B	U/L	88.09	0.00728	R		
40	2023-09-15	16:56:26	SMPL1	SAM	NH3B	mmol/L	1.846	0.05333	R		
40	2023-09-15	16:56:37	SMPL1	SAM	LAC2B	g/L	0.02	0.01567	R		

Our findings: what is an LLM good at?

Extracting and Structuring Data

```
0 2023-09-17 13:04:06 #AF
(1905) ADMIN
40 2023-09-15 16:55:51 S
40 2023-09-15 16:55:53 S
40 2023-09-15 16:56:18 S
40 2023-09-15 16:56:26 S
40 2023-09-15 16:56:37 S
```

```
- metadata:
  measurement id: NOT_PRESENT
  measurement time: "2023-09-15T16:55:51Z"
  analyst: ADMIN
  sample identifier: SMPL1
  equipment serial number: "123456"
  results data:
    glutamine analysis:
      molar concentration: 2.45
      molar concentration unit: mmol/L
    glucose analysis:
      mass concentration: 6.32
      mass concentration unit: g/L
    lactate dehydrogenase analysis:
      molar concentration: 88.09
      molar concentration unit: U/L
    ammonia analysis:
      molar concentration: 1.846
      molar concentration unit: mmol/L
    lactate analysis:
      mass concentration: 0.02
      mass concentration unit: g/L
  data processing time: "2023-09-17T13:04:06Z"
```

```
) HT 123456 6.0.0.1905
2.45 0.17138 R
32 1.05394 R
09 0.00728 R
1.846 0.05333 R
02 0.01567 R
```


Our findings: what is an LLM good at?

Generalization

Raw instrument data

```
TP2LB          g/L      4.7
```

Successful extraction of
field not in ASM schema

```
total protein analysis:  
  mass concentration: 4.7  
  mass concentration unit: g/L
```

Our findings: what is an LLM good at?

Generalization

Raw instrument data

```
TP2LB          g/L      4.7
```

Successful extraction of
field not in ASM schema

```
total protein analysis:  
  mass concentration: 4.7  
  mass concentration unit: g/L
```


Our findings: what is an LLM bad at?

Consistency

```
metadata:  
  measurement id: NOT_PRESENT  
  measurement time: "2023-09-15T16:55:51Z"  
  analyst: ADMIN  
  sample identifier: SMPL1  
  equipment serial number: "123456"
```



```
metadata:  
  measurement id: "NOT_PRESENT"  
  measurement time: "2023-03-16 08:07:30"  
  analyst: ADMIN  
  sample identifier: Plate1_1  
  equipment serial number: "620139"  
  batch identifier: PATCH_29
```



```
metadata:  
  measurement id: NOT_PRESENT  
  measurement time: 2022-10-20 09:44:05  
  analyst: ADMIN  
  sample identifier: "Plate1_1"  
  equipment serial number: "555555"  
  batch identifier: P_391
```



```
metadata:  
  measurement id: NOT_PRESENT  
  measurement time: "2022-10-17T08:12:47"  
  analyst: SAM  
  sample identifier: Sample_1  
  equipment serial number: "112233"  
  batch identifier: IBATCH_111
```



Needs validation!

Our findings: what is an LLM bad at?

Explainability

```
metadata:  
  measurement id: "NOT_PRESENT"  
  measurement time: "2023-03-16 08:07:30"  
  analyst: ADMIN  
  sample identifier: Plate1_1  
  equipment serial number: "620139"  
  batch identifier: PATCH_29
```



```
metadata:  
  measurement id: NOT_PRESENT  
  measurement time: "2022-10-17T08:12:47"  
  analyst: SAM  
  sample identifier: Sample_1  
  equipment serial number: "112233"  
  batch identifier: IBATCH_111
```



How do you explain this to an auditor?

Our findings: what is an LLM bad at?

Expensive to run at high volumes

Moderately-sized raw data file (~50k tokens) **~\$5 per day**

If you're a lab with 10k instruments **10s of millions annually (\$)**

Many caveats — just for illustration

Our findings: what is an LLM bad at?

Expensive to run at high volumes

Moderately-sized raw data file (~50k tokens) **~\$5 per day**

If you're a lab with 10k instruments **10s of millions annually (\$)**



All three LLM negatives (**consistency**, **explainability**, **cost**) can be solved through code

Our approach

Take advantage of the good and mitigate the bad



converter.py

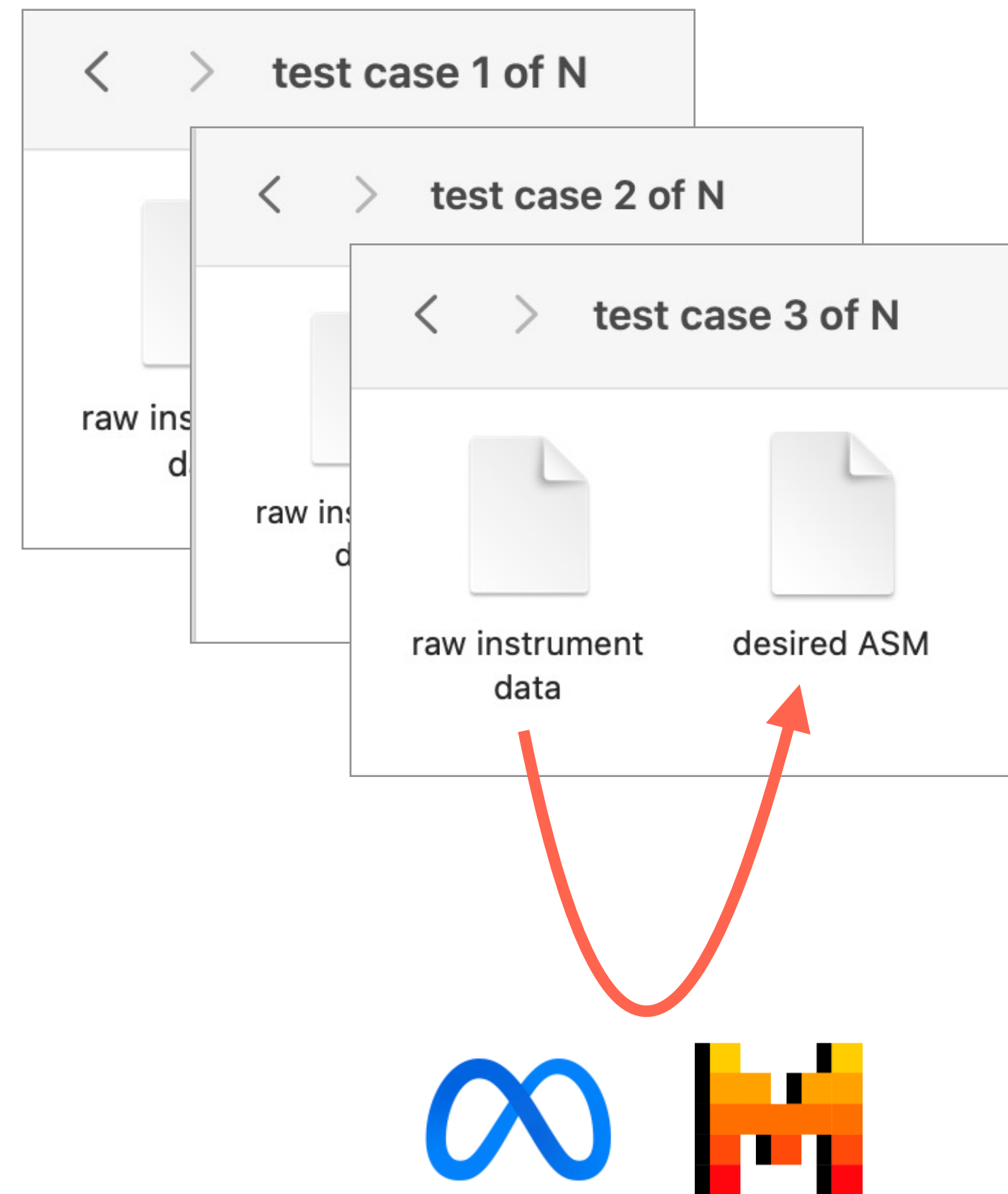
Our approach

Take advantage of the good and mitigate the bad



Our approach

Take advantage of the good and mitigate the bad

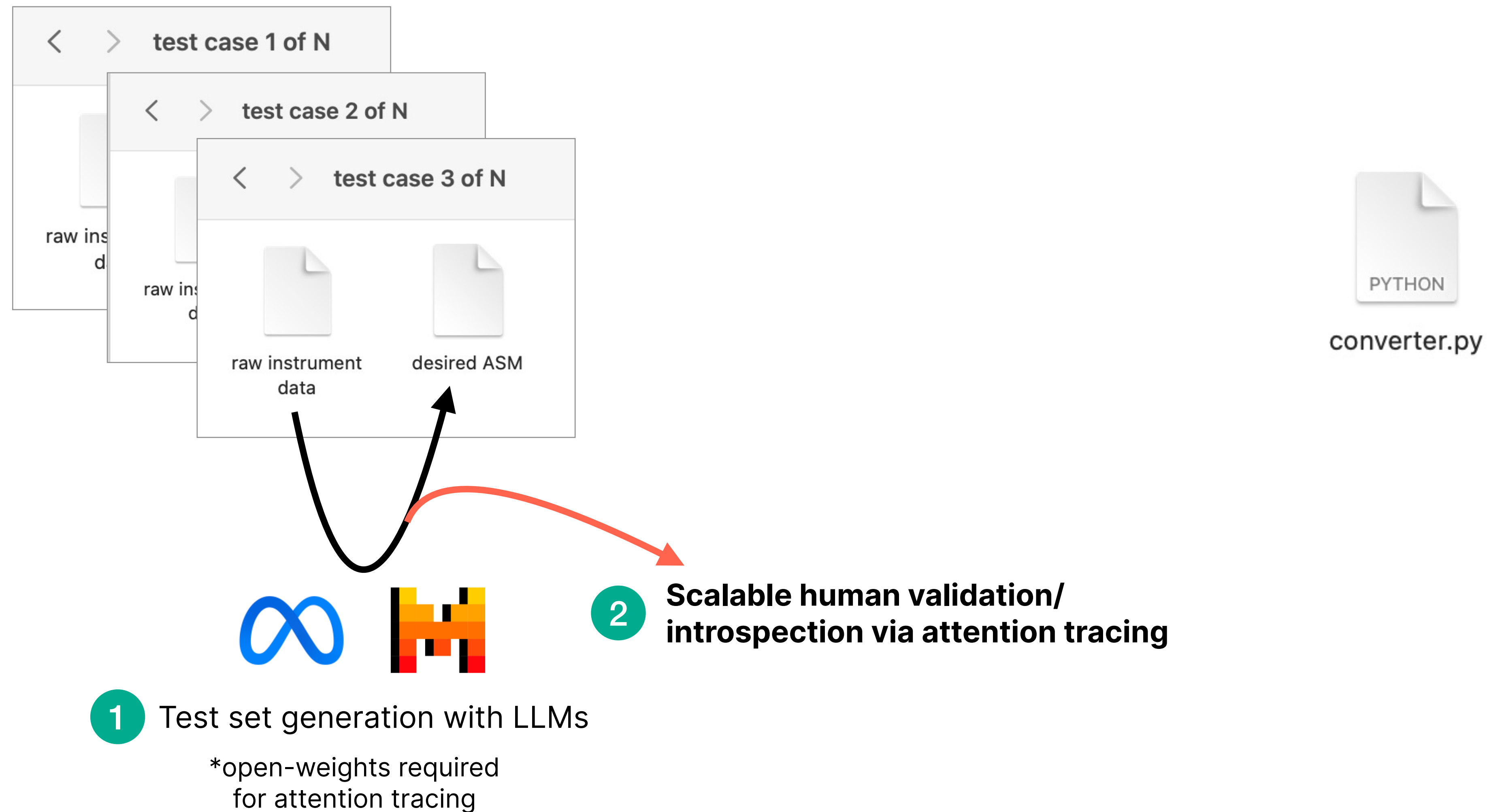


1 Test set generation with LLMs

*open-weights required
for attention tracing

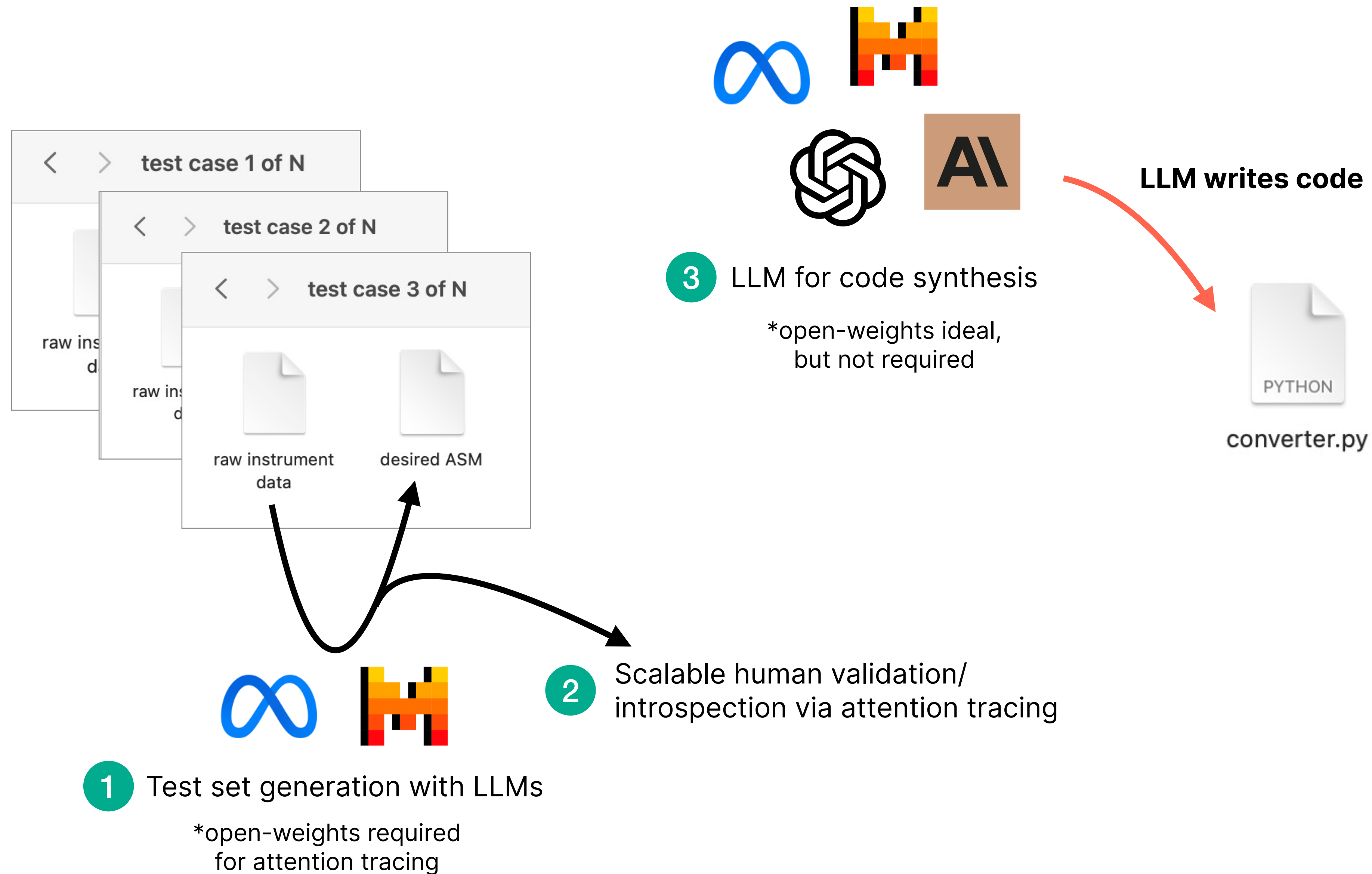
Our approach

Take advantage of the good and mitigate the bad



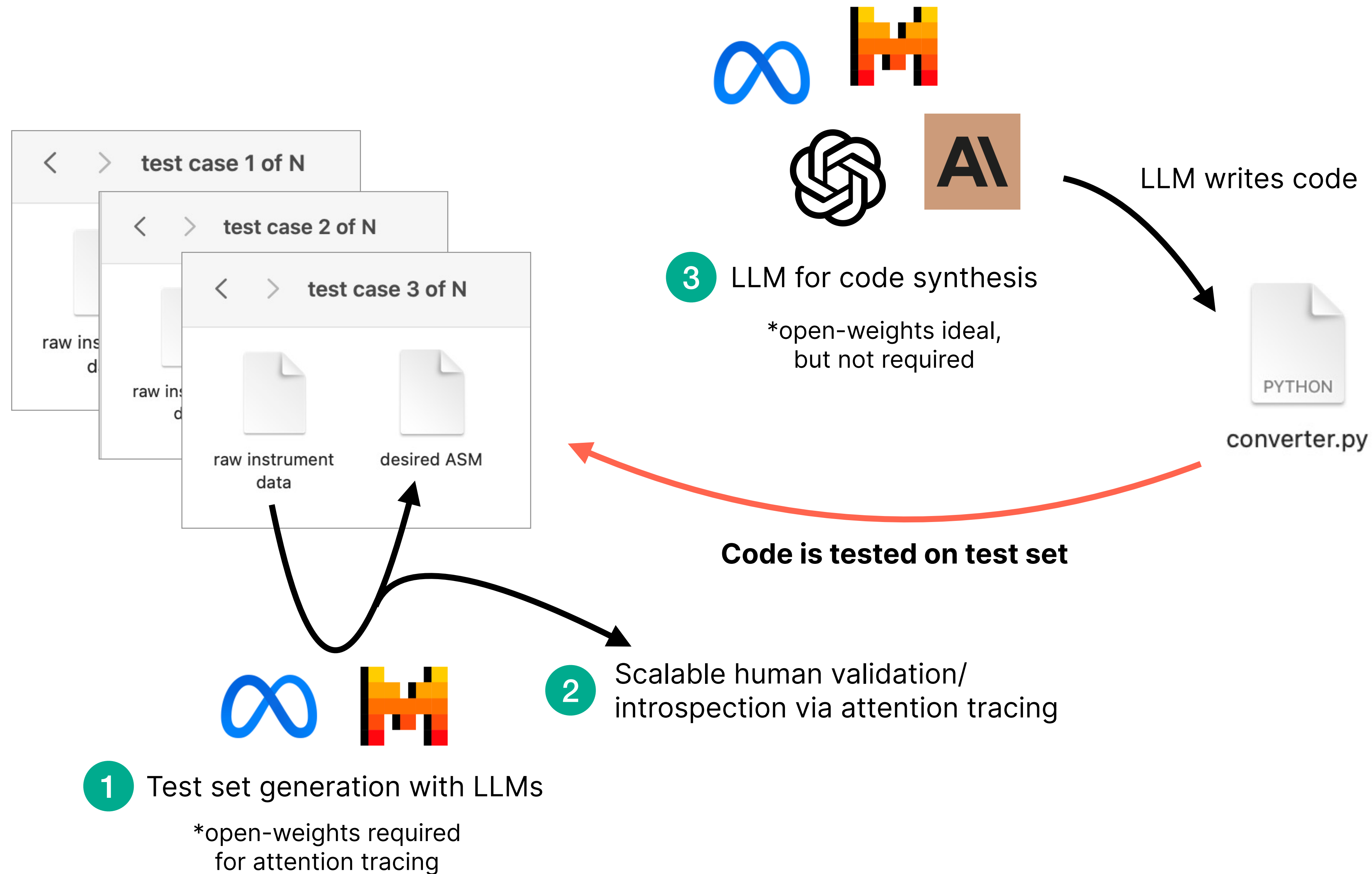
Our approach

Take advantage of the good and mitigate the bad



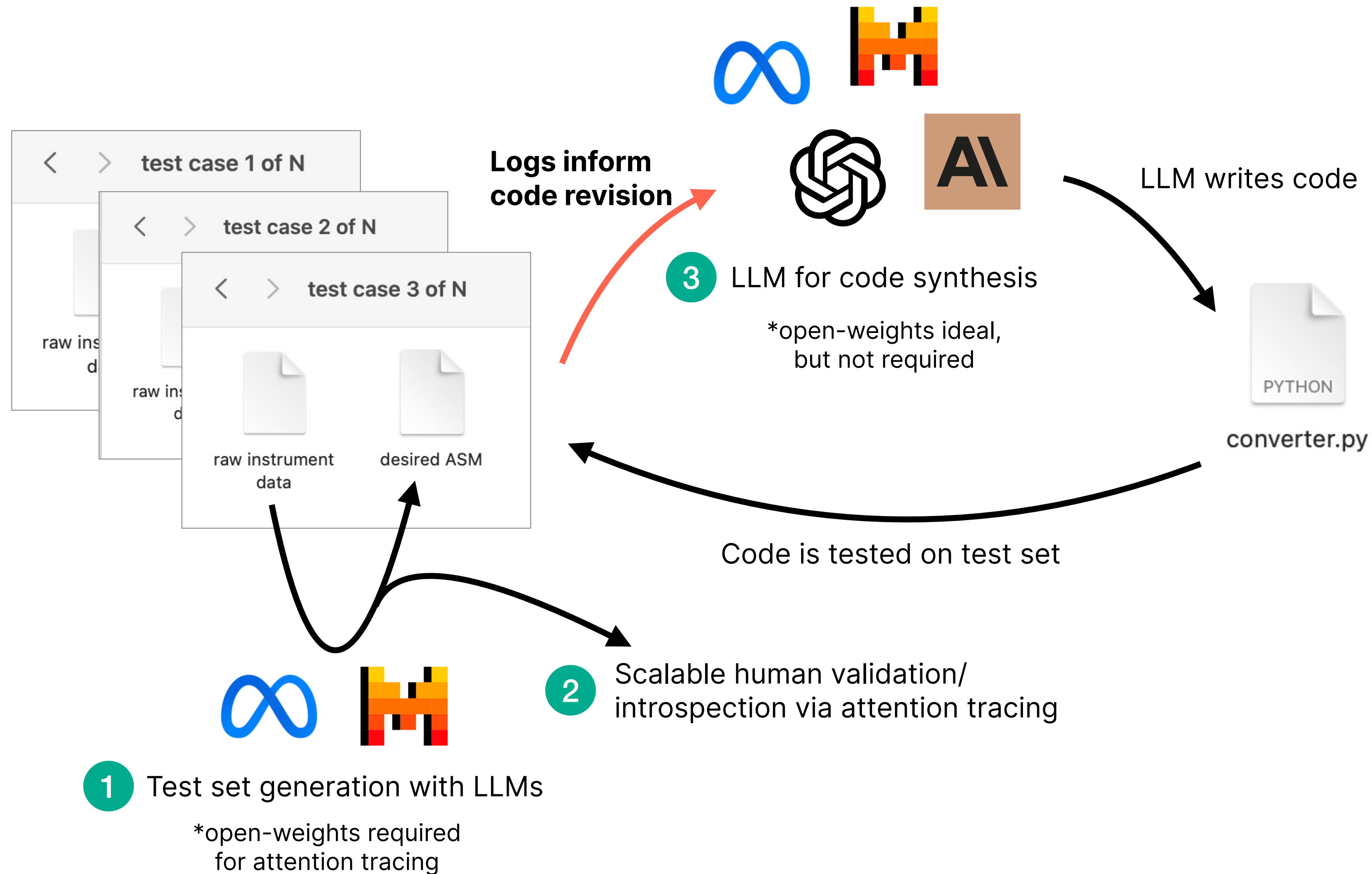
Our approach

Take advantage of the good and mitigate the bad



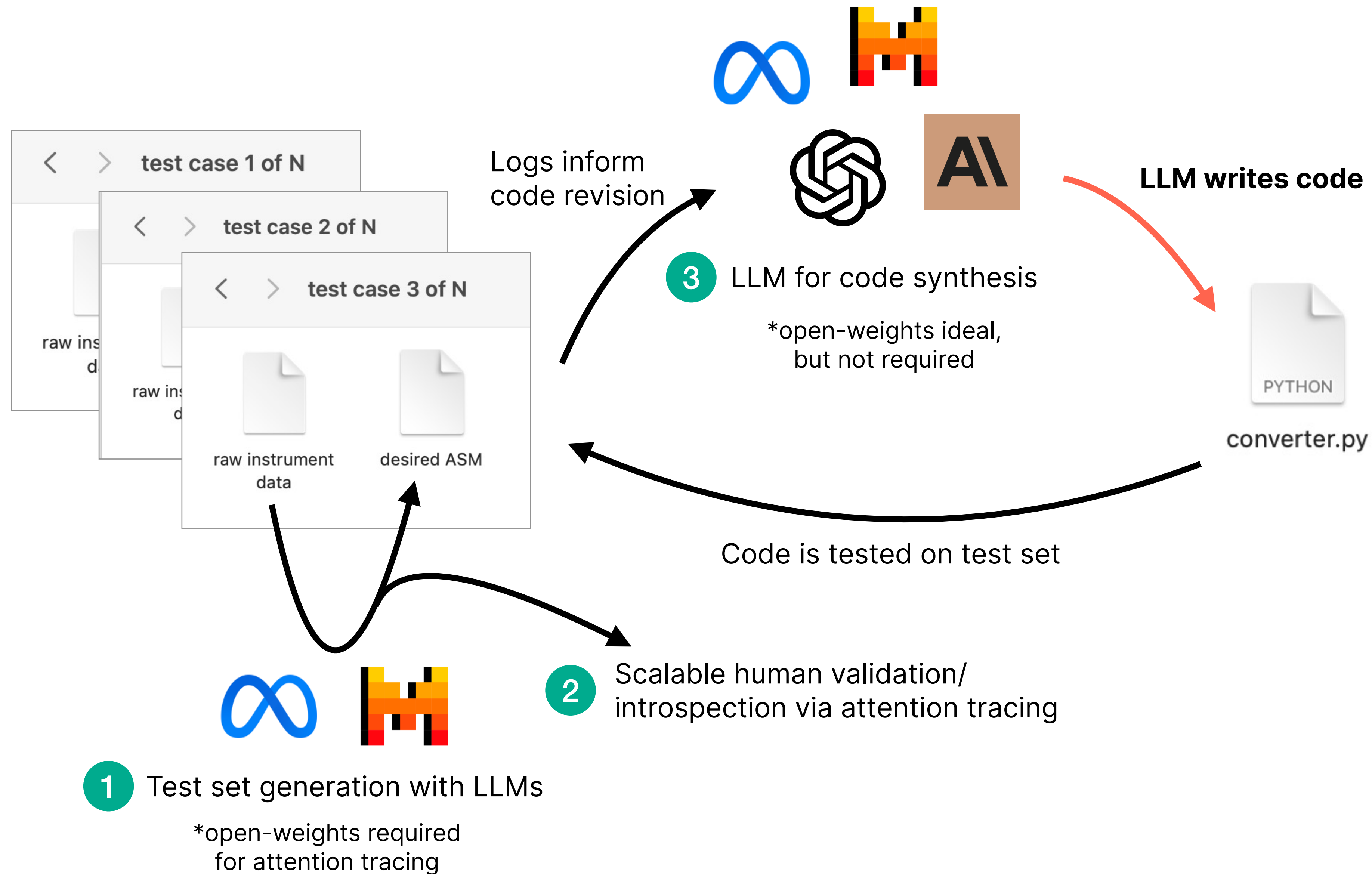
Our approach

Take advantage of the good and mitigate the bad



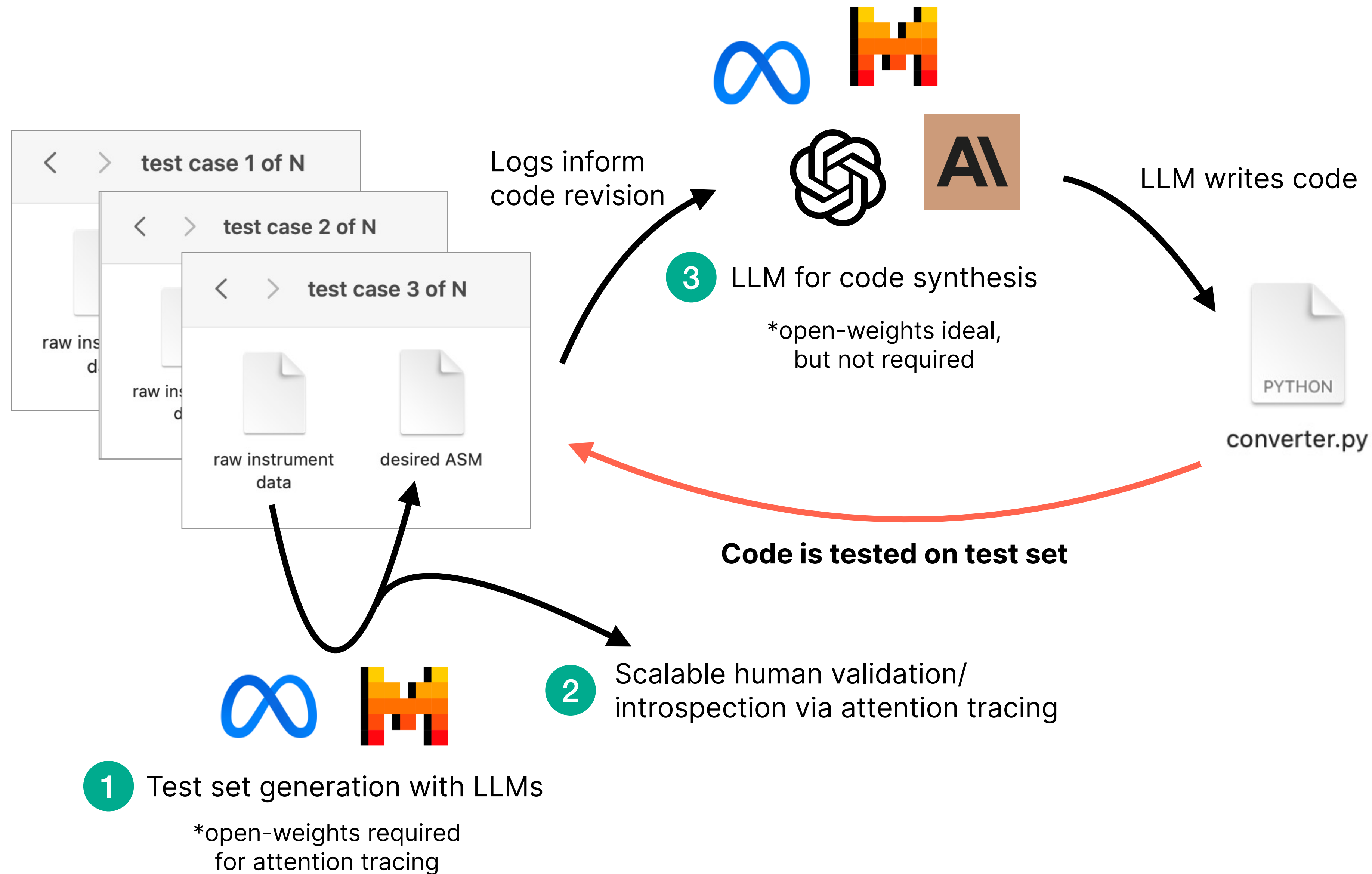
Our approach

Take advantage of the good and mitigate the bad



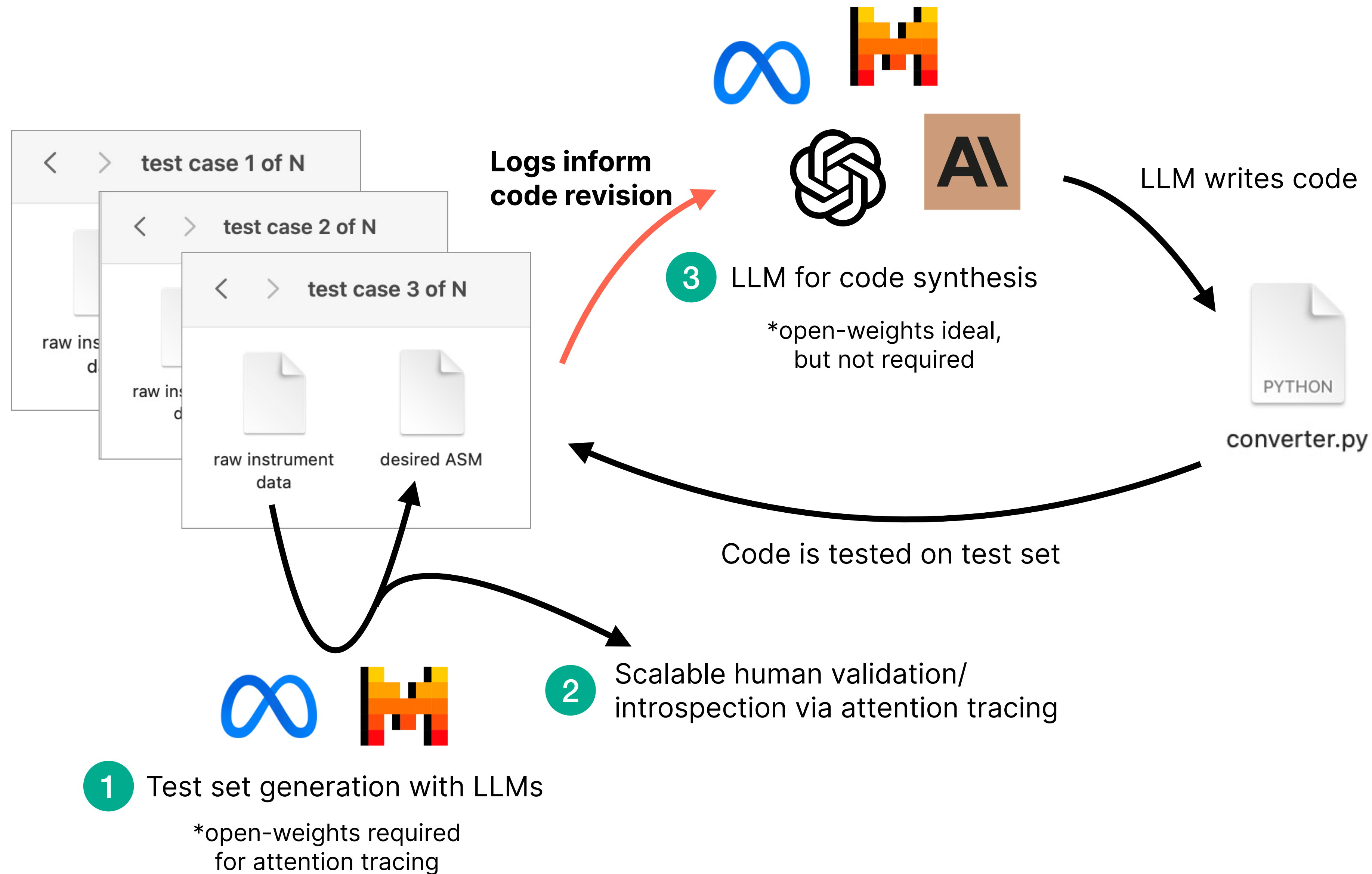
Our approach

Take advantage of the good and mitigate the bad



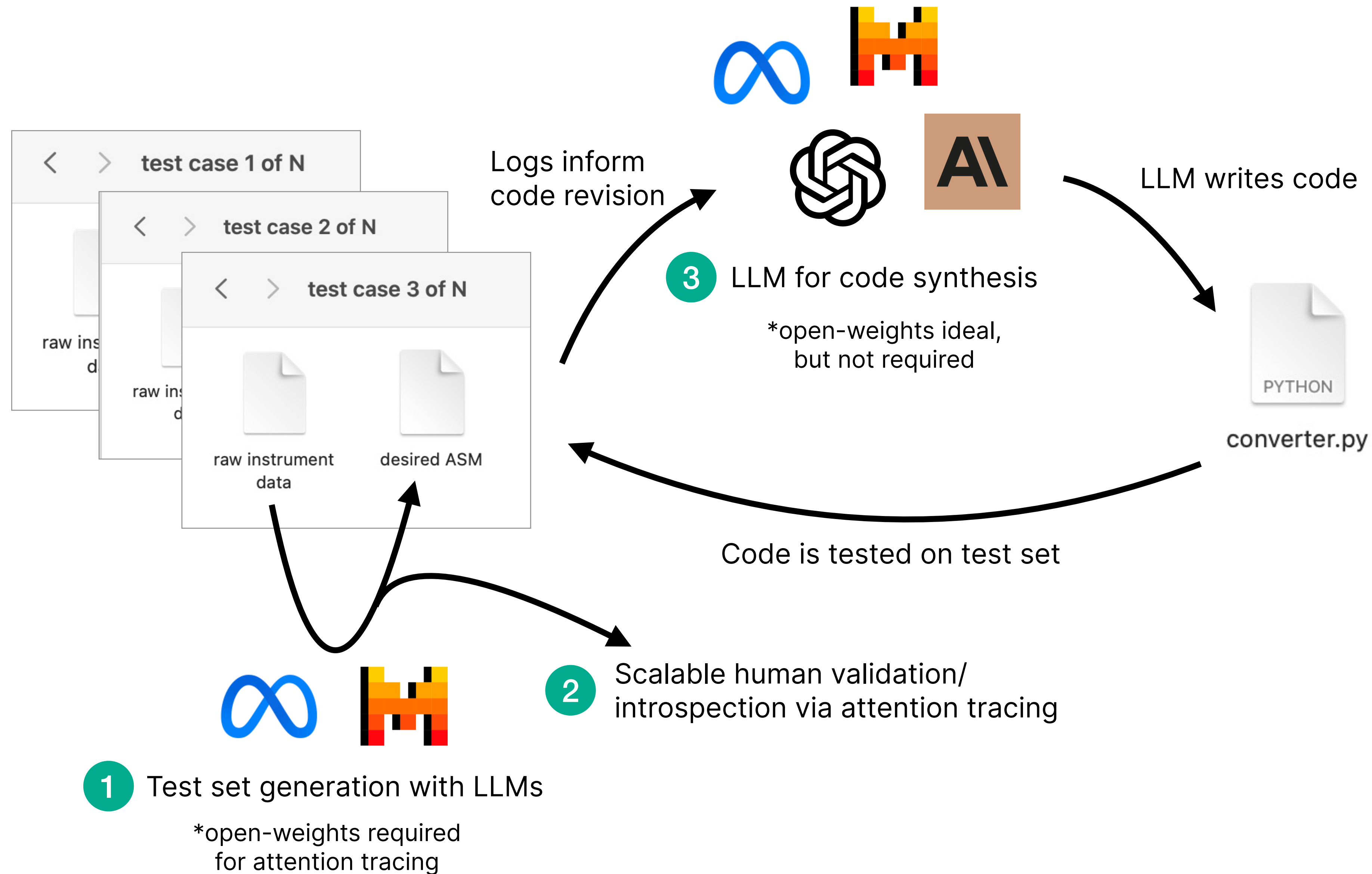
Our approach

Take advantage of the good and mitigate the bad



Our approach

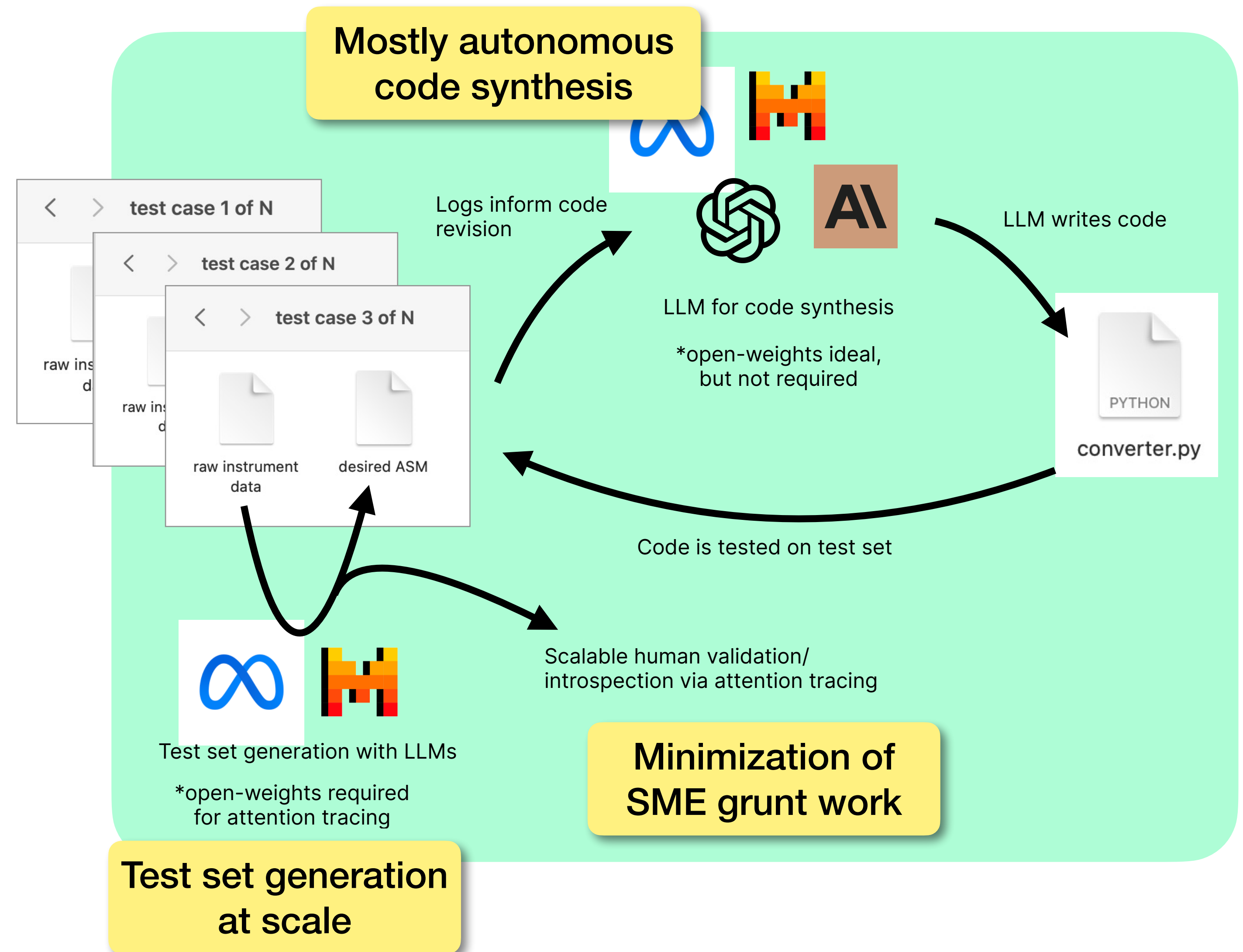
Take advantage of the good and mitigate the bad



Why is this better and faster?

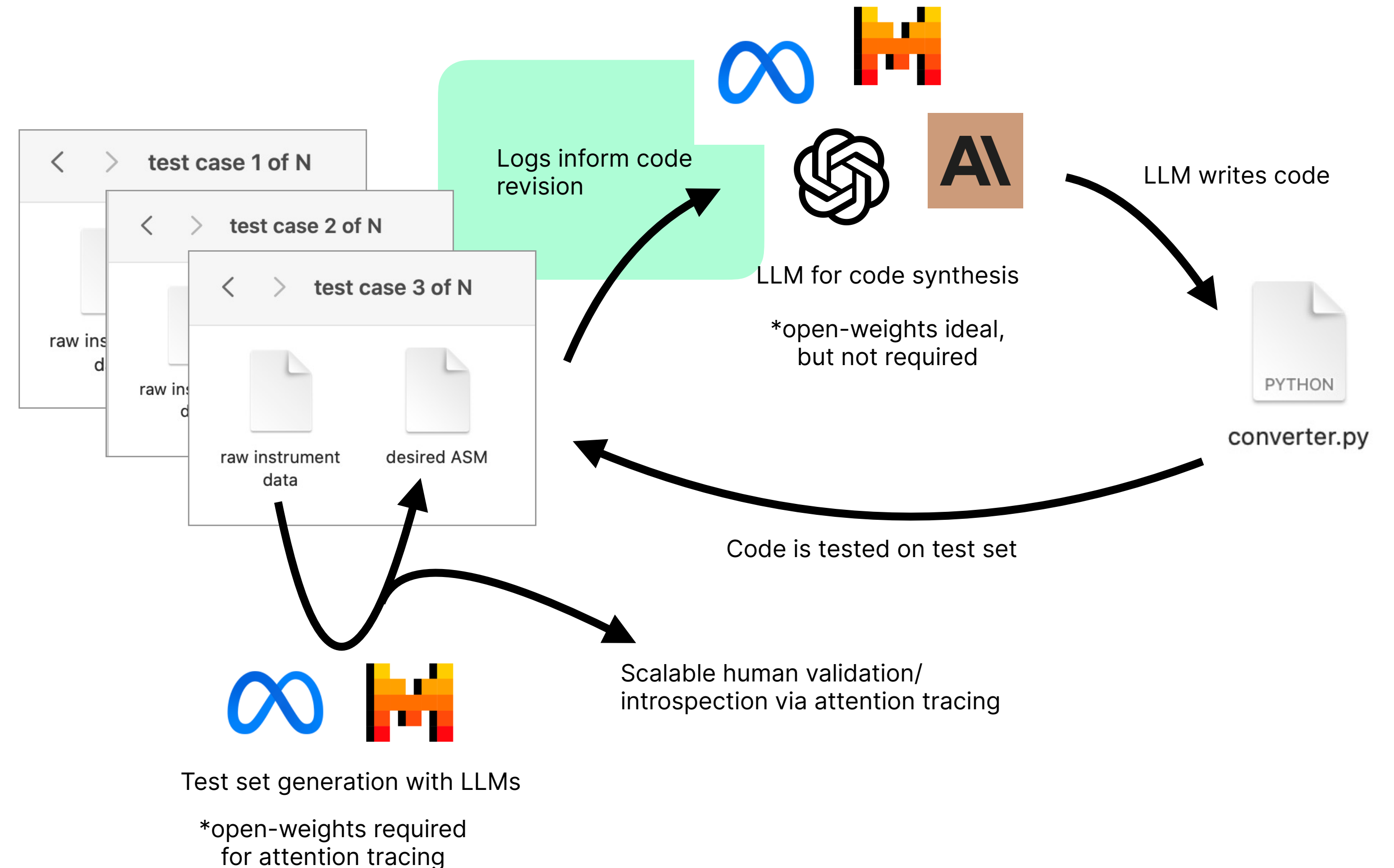
Why is this better and faster?

- LLM-based workflow enables 1-2 day turnaround



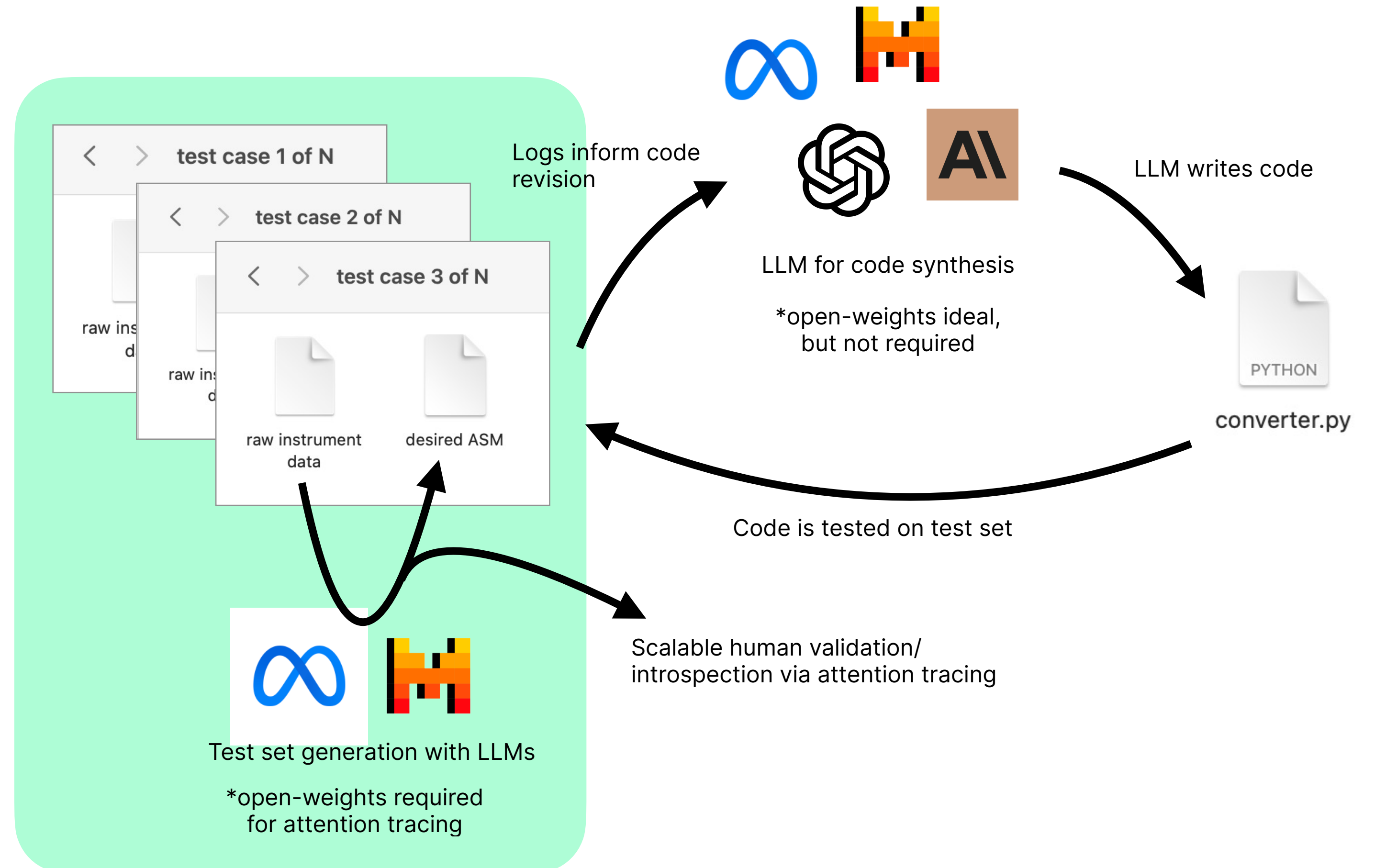
Why is this better and faster?

- LLM-based workflow enables 1-2 day turnaround
- **LLMs can generate 100x the tests vs software engineers**



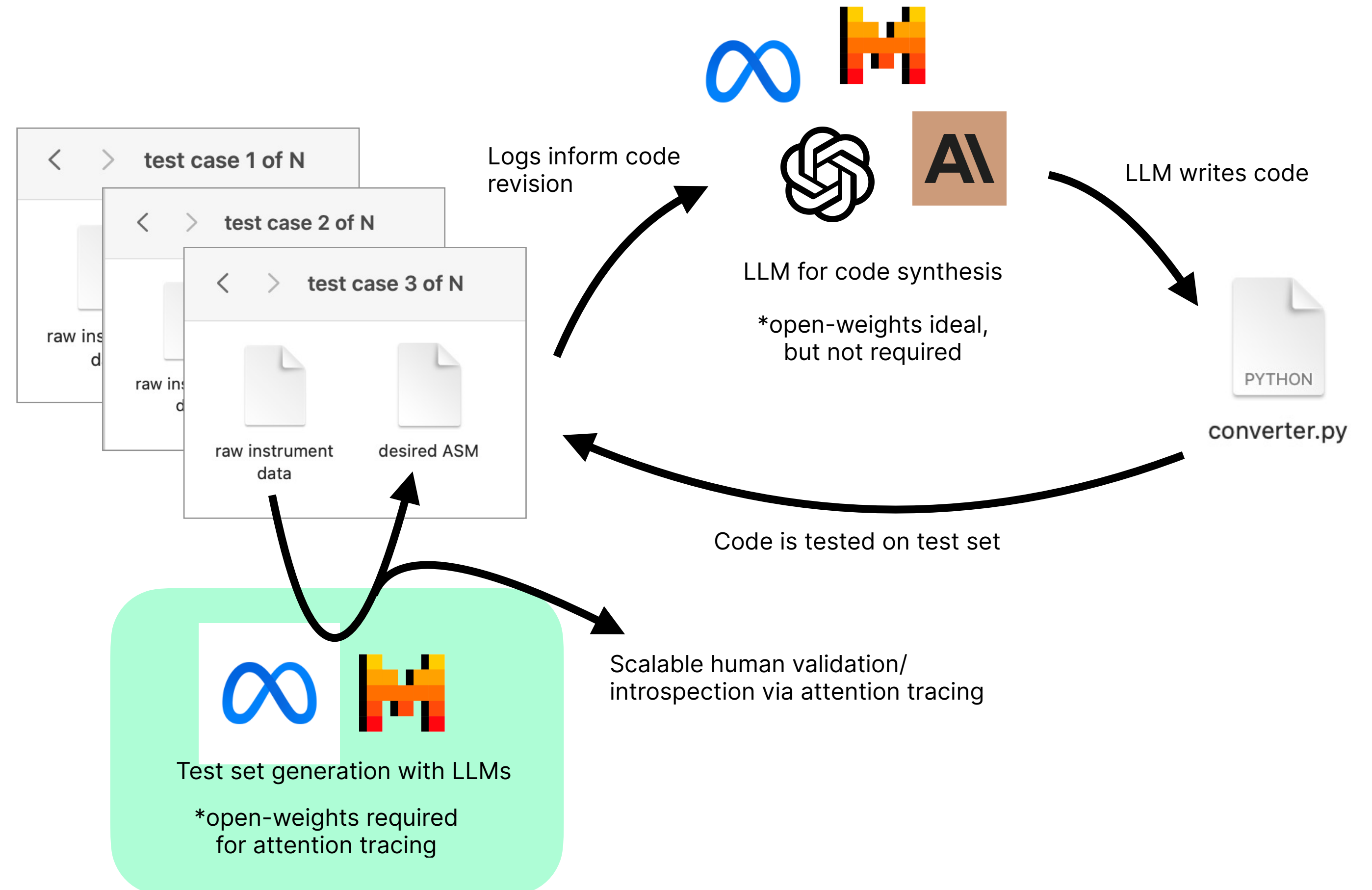
Why is this better and faster?

- LLM-based workflow enables 1-2 day turnaround
- LLMs can generate 100x the tests vs software engineers
- **Take advantage of existing data for highly comprehensive testing**



Why is this better and faster?

- LLM-based workflow enables 1-2 day turnaround
- LLMs can generate 100x the tests vs software engineers
- Take advantage of existing data for highly comprehensive testing
- **LLM domain knowledge eliminates SME and engineer back-and-forth**



Why is this better and faster?

Another benefit of the domain knowledge...

TP2LB

g/L

4.7

Raw instrument data

total protein analysis:

mass concentration: 4.7

mass concentration unit: g/L

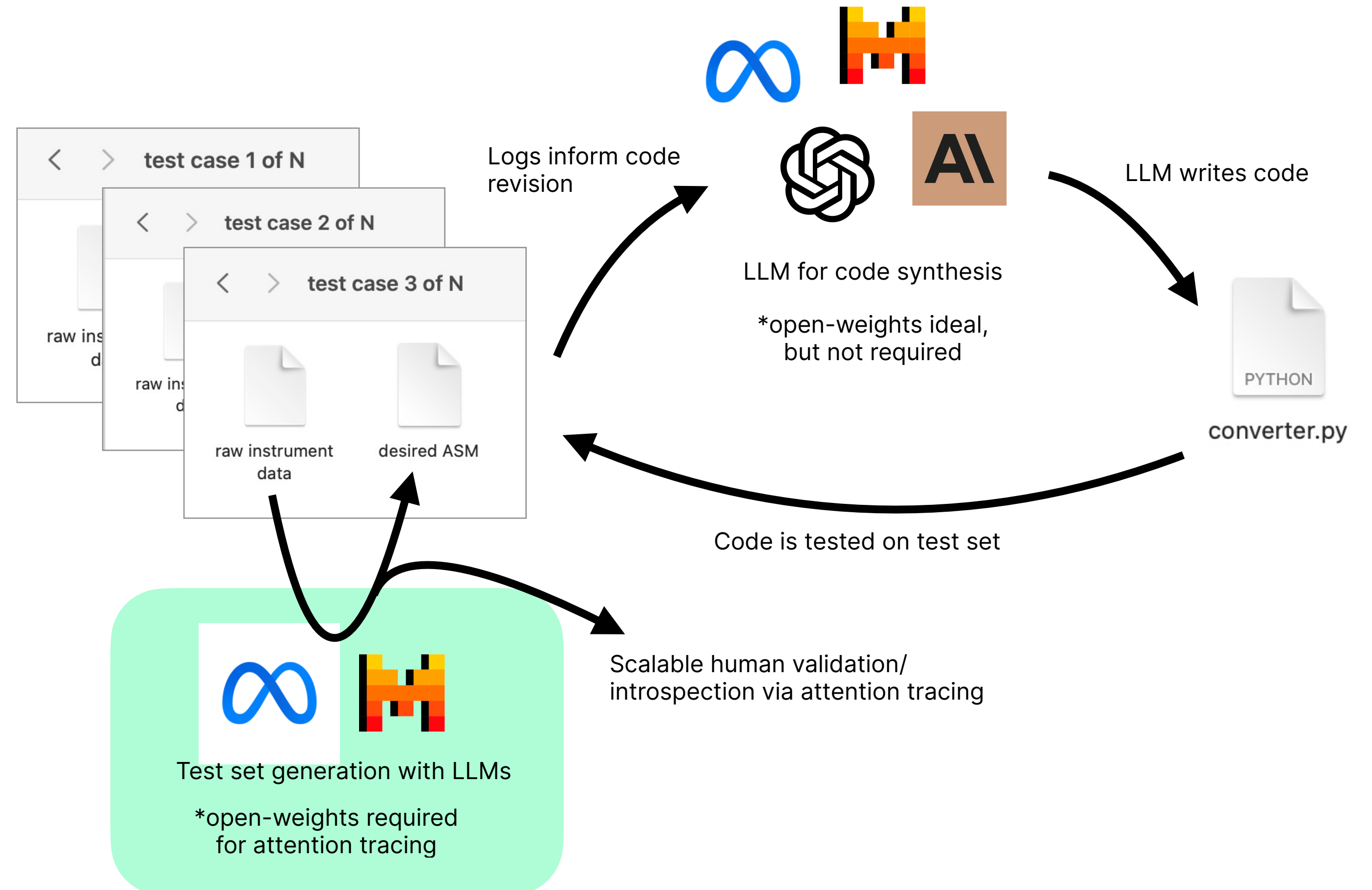
Successful extraction of field not in ASM schema

Opportunity to identify additions
to Allotrope standards!

- LLM-based workflow enables 1-2 day turnaround
- LLMs can generate 100x the tests vs software engineers
- Take advantage of existing data for highly comprehensive testing
- **LLM domain knowledge eliminates SME and engineering back-and-forth**

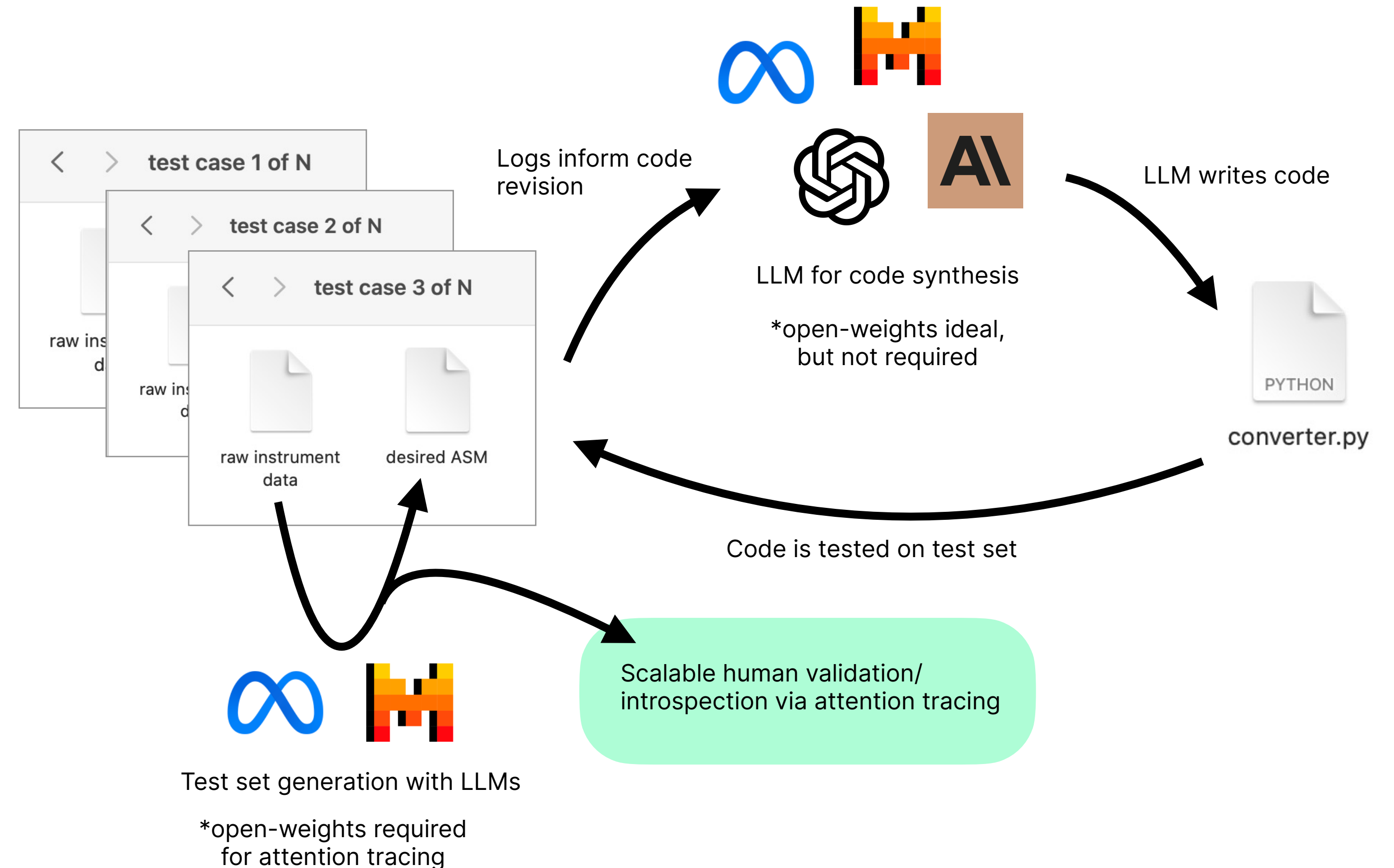
Why is this better and faster?

- LLM-based workflow enables 1-2 day turnaround
- LLMs can generate 100x the tests vs software engineers
- Take advantage of existing data for highly comprehensive testing
- **LLM domain knowledge eliminates SME and engineer back-and-forth**



Why is this better and faster?

- LLM-based workflow enables 1-2 day turnaround
- LLMs can generate 100x the tests vs software engineers
- Take advantage of existing data for highly comprehensive testing
- LLM domain knowledge eliminates SME and engineer back-and-forth
- **Tooling built around LLM attention greatly speeds up manual SME validation work**



Scalable human validation/introspection via attention tracing

Snapshots from our attention tracing tool

```
- metadata:
  measurement id: NOT_PRESENT
  measurement time: "2023-09-15T16:58:34Z"
  analyst: ADMIN
  sample identifier: SMPL3
  equipment serial number: "123456"
results data:
  glutamine analysis:
    molar concentration: 2.43
    molar concentration unit: mmol/L
  glucose analysis:
    mass concentration: 6.71
    mass concentration unit: g/L
```

09	SMPL2	SAM	GLC3B	g/L	6.71
19	SMPL2	SAM	LDH2B	U/L	< TEST RNG
30	SMPL2	SAM	NH3B	mmol/L	1.870
41	SMPL2	SAM	LAC2B	g/L	< TEST RNG
51	SMPL2	SAM	TP2B	g/L	< TEST RNG
02	SMPL2	SAM	TP2D	g/L	< TEST RNG
23	SMPL2	SAM	TP2LB	g/L	4.7
34	SMPL3	SAM	GLN2B	mmol/L	2.43
45	SMPL3	SAM	GLC3B	g/L	6.71
55	SMPL3	SAM	LDH2B	U/L	< TEST RNG

Raw instrument data

Highlighting LLM interpretation
in our attention tracing tool

Scalable human validation/introspection via attention tracing

Snapshots from our attention tracing tool

This glucose result is from SMPL3

```
- metadata:
  measurement id: NOT_PRESENT
  measurement time: "2023-09-15T16:58:34Z"
  analyst: ADMIN
  sample identifier: SMPL3
  equipment serial number: "123456"
results data:
  glutamine analysis:
    molar concentration: 2.43
    molar concentration unit: mmol/L
  glucose analysis:
    mass concentration: 6.71
    mass concentration unit: g/L
```

Highlighting LLM interpretation
in our attention tracing tool

09	SMPL2	SAM	GLC3B	g/L	6.71
19	SMPL2	SAM	LDH2B	U/L	< TEST RNG
30	SMPL2	SAM	NH3B	mmol/L	1.870
41	SMPL2	SAM	LAC2B	g/L	< TEST RNG
51	SMPL2	SAM	TP2B	g/L	< TEST RNG
02	SMPL2	SAM	TP2D	g/L	< TEST RNG
23	SMPL2	SAM	TP2LB	g/L	4.7
34	SMPL3	SAM	GLN2B	mmol/L	2.43
45	SMPL3	SAM	GLC3B	g/L	6.71
55	SMPL3	SAM	LDH2B	U/L	< TEST RNG

Raw instrument data

Attention is only directed at the correct 6.71 from SMPL3

Scalable human validation/introspection via attention tracing

Snapshots from our attention tracing tool

This glucose result is from SMPL3

Also Glucose, also 6.71, but from a different sample (SMPL2)

```
- metadata:
  measurement id: NOT_PRESENT
  measurement time: "2023-09-15T16:58:34Z"
  analyst: ADMIN
  sample identifier: SMPL3
  equipment serial number: "123456"
results data:
  glutamine analysis:
    molar concentration: 2.43
    molar concentration unit: mmol/L
  glucose analysis:
    mass concentration: 6.71
    mass concentration unit: g/L
```

09	SMPL2	SAM	GLC3B	g/L	6.71
19	SMPL2	SAM	LDH2B	U/L	< TEST RNG
30	SMPL2	SAM	NH3B	mmol/L	1.870
41	SMPL2	SAM	LAC2B	g/L	< TEST RNG
51	SMPL2	SAM	TP2B	g/L	< TEST RNG
02	SMPL2	SAM	TP2D	g/L	< TEST RNG
23	SMPL2	SAM	TP2LB	g/L	4.7
34	SMPL3	SAM	GLN2B	mmol/L	2.43
45	SMPL3	SAM	GLC3B	g/L	6.71
55	SMPL3	SAM	LDH2B	U/L	< TEST RNG

Raw instrument data

Highlighting LLM interpretation
in our attention tracing tool

Attention is only directed at the correct 6.71 from SMPL3

Scalable human validation/introspection via attention tracing

Snapshots from our attention tracing tool

```
- metadata:
  measurement id: NOT_PRESENT
  measurement time: "2023-09-15T16:56:58Z"
  analyst: ADMIN
  sample identifier: SMPL2
  equipment serial number: "123456"
results data:
  glutamine analysis:
    molar concentration: 2.4
    molar concentration unit: mmol/L
  glucose analysis:
    mass concentration: 6.71
    mass concentration unit: g/L
  lactate dehydrogenase analysis:
    molar concentration: BELOW_RANGE
    molar concentration unit: U/L
  ammonia analysis:
    molar concentration: 1.87
    molar concentration unit: mmol/L
  lactate analysis:
    mass concentration: BELOW_RANGE
    mass concentration unit: g/L
```

0	2023-09-17 13:04:06	#ARC-FILE#	1.1a	2021-05-01	2023-09-17	CEDEX BIO HT	123456	6.0.0.1905 (1905)	ADMIN
40	2023-09-15 16:55:51	SMPL1	SAM		GLN2B	mmol/L	2.45	0.17138	R
40	2023-09-15 16:55:53	SMPL1	SAM		GLC3B	g/L	6.32	1.05394	R
40	2023-09-15 16:56:18	SMPL1	SAM		LDH2B	U/L	88.09	0.00728	R
40	2023-09-15 16:56:26	SMPL1	SAM		NH3B	mmol/L	1.846	0.05333	R
40	2023-09-15 16:56:37	SMPL1	SAM		LAC2B	g/L	0.02	0.01567	R
40	2023-09-15 16:56:48	SMPL1	SAM		TP2LB	g/L	4.6	0.14883	R
40	2023-09-15 16:56:58	SMPL2	SAM		GLN2B	mmol/L	2.40	0.16787	R
40	2023-09-15 16:57:09	SMPL2	SAM		GLC3B	g/L	6.71	1.11766	R
40	2023-09-15 16:57:19	SMPL2	SAM		LDH2B	U/L	< TEST RNG	< 20.00	0.00060 R
40	2023-09-15 16:57:30	SMPL2	SAM		NH3B	mmol/L	1.870	0.05408	R
40	2023-09-15 16:57:41	SMPL2	SAM		LAC2B	g/L	< TEST RNG	< 0.00	0.00310 R
40	2023-09-15 16:57:51	SMPL2	SAM		TP2B	g/L	< TEST RNG	< 4.0	0.03322 R
40	2023-09-15 16:58:02	SMPL2	SAM		TP2D	g/L	< TEST RNG	< 40.0	0.02653 R
40	2023-09-15 16:58:23	SMPL2	SAM		TP2LB	g/L	4.7	0.15217	R
40	2023-09-15 16:58:34	SMPL3	SAM		GLN2B	mmol/L	2.43	0.17049	R
40	2023-09-15 16:58:45	SMPL3	SAM		GLC3B	g/L	6.71	1.11813	R
40	2023-09-15 16:58:55	SMPL3	SAM		LDH2B	U/L	< TEST RNG	< 20.00	0.00076 R

Raw instrument data

Highlighting LLM interpretation
in our attention tracing tool

Scalable human validation/introspection via attention tracing

Snapshots from our attention tracing tool

```
- metadata:
  measurement id: NOT_PRESENT
  measurement time: "2023-09-15T16:56:58Z"
  analyst: ADMIN
  sample identifier: SMPL2
  equipment serial number: "123456"
results data:
  glutamine analysis:
    molar concentration: 2.4
    molar concentration unit: mmol/L
  glucose analysis:
    mass concentration: 6.71
    mass concentration unit: g/L
  lactate dehydrogenase analysis:
    molar concentration: BELOW_RANGE
    molar concentration unit: U/L
  ammonia analysis:
    molar concentration: 1.87
    molar concentration unit: mmol/L
  lactate analysis:
    mass concentration: BELOW_RANGE
    mass concentration unit: g/L
```

0	2023-09-17 13:04:06	#ARC-FILE#	1.1a	2021-05-01	2023-09-17	CEDEX BIO HT	123456	6.0.0.1905 (1905)	ADMIN
40	2023-09-15 16:55:51	SMPL1	SAM		GLN2B	mmol/L	2.45	0.17138	R
40	2023-09-15 16:55:53	SMPL1	SAM		GLC3B	g/L	6.32	1.05394	R
40	2023-09-15 16:56:18	SMPL1	SAM		LDH2B	U/L	88.09	0.00728	R
40	2023-09-15 16:56:26	SMPL1	SAM		NH3B	mmol/L	1.846	0.05333	R
40	2023-09-15 16:56:37	SMPL1	SAM		LAC2B	g/L	0.02	0.01567	R
40	2023-09-15 16:56:48	SMPL1	SAM		TP2LB	g/L	4.6	0.14883	R
40	2023-09-15 16:56:58	SMPL2	SAM		GLN2B	mmol/L	2.40	0.16787	R
40	2023-09-15 16:57:09	SMPL2	SAM		GLC3B	g/L	6.71	1.11766	R
40	2023-09-15 16:57:19	SMPL2	SAM		LDH2B	U/L	< TEST RNG	< 20.00	0.00060 R
40	2023-09-15 16:57:30	SMPL2	SAM		NH3B	mmol/L	1.870	0.05408	R
40	2023-09-15 16:57:41	SMPL2	SAM		LAC2B	g/L	< TEST RNG	< 0.00	0.00310 R
40	2023-09-15 16:57:51	SMPL2	SAM		TP2B	g/L	< TEST RNG	< 4.0	0.03322 R
40	2023-09-15 16:58:02	SMPL2	SAM		TP2D	g/L	< TEST RNG	< 40.0	0.02653 R
40	2023-09-15 16:58:23	SMPL2	SAM		TP2LB	g/L	4.7	0.15217	R
40	2023-09-15 16:58:34	SMPL3	SAM		GLN2B	mmol/L	2.43	0.17049	R
40	2023-09-15 16:58:45	SMPL3	SAM		GLC3B	g/L	6.71	1.11813	R
40	2023-09-15 16:58:55	SMPL3	SAM		LDH2B	U/L	< TEST RNG	< 20.00	0.00076 R

Raw instrument data

Correctly interprets < TEST RNG value as below measurement range

Highlighting LLM interpretation in our attention tracing tool

Scalable human validation/introspection via attention tracing

Snapshots from our attention tracing tool

```
- metadata:
  measurement id: NOT_PRESENT
  measurement time: "2023-09-15T16:56:58Z"
  analyst: ADMIN
  sample identifier: SMPL2
  equipment serial number: "123456"
results data:
  glutamine analysis:
    molar concentration: 2.4
    molar concentration unit: mmol/L
  glucose analysis:
    mass concentration: 6.71
    mass concentration unit: g/L
  lactate dehydrogenase analysis:
    molar concentration: BELOW_RANGE
    molar concentration unit: U/L
  ammonia analysis:
    molar concentration: 1.87
    molar concentration unit: mmol/L
  lactate analysis:
    mass concentration: BELOW_RANGE
    mass concentration unit: g/L
```

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40	2023-09-15 16:56:58	SMPL2	SAM		GLN2B	mmol/L	2.40	0.16787	R
40	2023-09-15 16:57:09	SMPL2	SAM		GLC3B	g/L	6.71	1.11766	R
40	2023-09-15 16:57:19	SMPL2	SAM		LDH2B	U/L	< TEST RNG	< 20.00	0.00060 R
40	2023-09-15 16:57:30	SMPL2	SAM		NH3B	mmol/L	1.870	0.05408	R
40	2023-09-15 16:57:41	SMPL2	SAM		LAC2B	g/L	< TEST RNG	< 0.00	0.00310 R
40	2023-09-15 16:57:51	SMPL2	SAM		TP2B	g/L	< TEST RNG	< 4.0	0.03322 R
40	2023-09-15 16:58:02	SMPL2	SAM		TP2D	g/L	< TEST RNG	< 40.0	0.02653 R
40	2023-09-15 16:58:23	SMPL2	SAM		TP2LB	g/L	4.7	0.15217	R
40	2023-09-15 16:58:34	SMPL3	SAM		GLN2B	mmol/L	2.43	0.17049	R
40	2023-09-15 16:58:45	SMPL3	SAM		GLC3B	g/L	6.71	1.11813	R
40	2023-09-15 16:58:55	SMPL3	SAM		LDH2B	U/L	< TEST RNG	< 20.00	0.00076 R

Raw instrument data

Correctly interprets < TEST RNG value as below measurement range

Highlighting LLM interpretation in our attention tracing tool

Scalable human validation/introspection via attention tracing

Snapshots from our attention tracing tool

```
- metadata:
  measurement id: NOT_PRESENT
  measurement time: "2023-09-15T16:56:58Z"
  analyst: ADMIN
  sample identifier: SMPL2
  equipment serial number: "123456"
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  glutamine analysis:
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    mass concentration unit: g/L
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    molar concentration: BELOW_RANGE
    molar concentration unit: U/L
  ammonia analysis:
    molar concentration: 1.87
    molar concentration unit: mmol/L
  lactate analysis:
    mass concentration: BELOW_RANGE
    mass concentration unit: g/L
```

Highlighting LLM interpretation in our attention tracing tool

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40	2023-09-15 16:56:18	SMPL1	SAM		LDH2B	U/L	88.09	0.00728	R
40	2023-09-15 16:56:26	SMPL1	SAM		NH3B	mmol/L	1.846	0.05333	R
40	2023-09-15 16:56:37	SMPL1	SAM		LAC2B	g/L	0.02	0.01567	R
40	2023-09-15 16:56:48	SMPL1	SAM		TP2LB	g/L	4.6	0.14883	R
40	2023-09-15 16:56:58	SMPL2	SAM		GLN2B	mmol/L	2.40	0.16787	R
40	2023-09-15 16:57:09	SMPL2	SAM		GLC3B	g/L	6.71	1.11766	R
40	2023-09-15 16:57:19	SMPL2	SAM		LDH2B	U/L	< TEST RNG	< 20.00	0.00060 R
40	2023-09-15 16:57:30	SMPL2	SAM		NH3B	mmol/L	1.870	0.05408	R
40	2023-09-15 16:57:41	SMPL2	SAM		LAC2B	g/L	< TEST RNG	< 0.00	0.00310 R
40	2023-09-15 16:57:51	SMPL2	SAM		TP2B	g/L	< TEST RNG	< 4.0	0.03322 R
40	2023-09-15 16:58:02	SMPL2	SAM		TP2D	g/L	< TEST RNG	< 40.0	0.02653 R
40	2023-09-15 16:58:23	SMPL2	SAM		TP2LB	g/L	4.7	0.15217	R
40	2023-09-15 16:58:34	SMPL3	SAM		GLN2B	mmol/L	2.43	0.17049	R
40	2023-09-15 16:58:45	SMPL3	SAM		GLC3B	g/L	6.71	1.11813	R
40	2023-09-15 16:58:55	SMPL3	SAM		LDH2B	U/L	< TEST RNG	< 20.00	0.00076 R

Raw instrument data

Directs attention to the correct < TEST RNG value only

Correctly interprets < TEST RNG value as below measurement range

We can build converters fast

What else can we do with LLMs to further FAIR data and Allotrope adoption?

We can build converters fast

What else can we do with LLMs to further FAIR data and Allotrope adoption?



We can build converters fast

What else can we do with LLMs to further FAIR data and Allotrope adoption?

Identify extensions to
Allotrope standards



Low-Hanging Fruit

High-Effort but Transformative

We can build converters fast

What else can we do with LLMs to further FAIR data and Allotrope adoption?

Identify extensions to
Allotrope standards

Automate drafting of
Allotrope models



Low-Hanging Fruit

High-Effort but Transformative

We can build converters fast

What else can we do with LLMs to further FAIR data and Allotrope adoption?

Identify extensions to
Allotrope standards

Automate drafting of
Allotrope models

Extract and structure experiments,
methods, and materials



Low-Hanging Fruit

High-Effort but Transformative

Thank you!

Questions? Feedback? Comments?

a@awchen.com