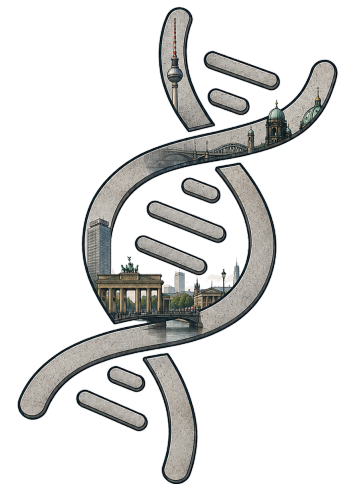


# LLMs for personal genomics?

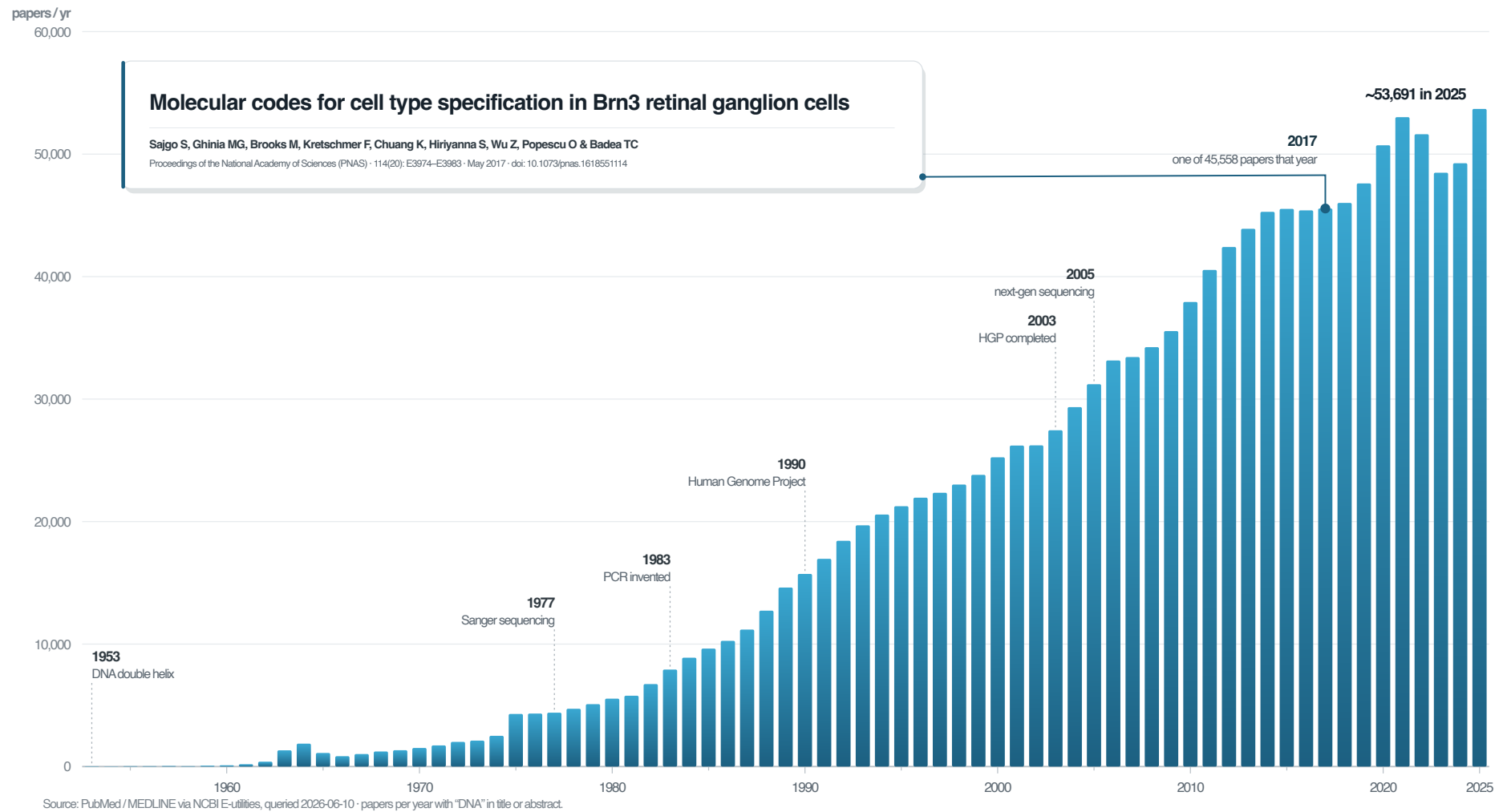
## Bridging promise and reality

16 June 2026  
Futura Camp, Berlin

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Dark Bio Founder



# Exploding breadth and depth



## The promise

*"Hey Claude, write a genetic analysis for alcohol tolerance!"* ~Me, ETHPrague hackathon

### Tolerance:

- **rs671** – how fast you metabolize acetaldehyde (alcohol gunk)
- **rs1229984** – how fast you turn alcohol into acetaldehyde (Asia)
- **rs2066702** – how fast you turn alcohol into acetaldehyde (Africa)

### Pleasure:

- **rs1799971** – higher endorphin sensitivity
- **rs1800497** – lower dopamine sensitivity
- **rs279858** – elevated calming effect

## The reality

- Bug #1 – Mixed up the two DNA strands (dataset vs. literature)
- Bug #2 – One marker's position was off by 25K bases
- Bug #3 – Interpreted the mutation as the issue, not what it was
- Bug #4 – Missing data interpreted as all is good
- Bug #5 – Uncertain data interpreted as all is good
- Bug #6 – Multiple-data points collapsed into first
- Bug #7 – Loaded multi-letter sequence, computed on first

I only caught these because results "looked" weird...

# Problem: Complex inputs, no feedback loop

```
10 102638119 . TAAA TAAA 119 PASS INDEL;IDV=9;IMF=0.409091;DP=22;
VDB=0.197059;SGB=-0.670168;MQSB=0.734889;MQOF=0;ICB=1;HOB=0.5;AC=1;AN=2;DP4=8,4,
6,4;MQ=44 GT:PL:DP:AD:GQ 0/1:152,0,182:22:12,10:127
10 102638120 . A . . PASS END=102638178;MinDP=12 GT:DP 0/0:12
10 102638179 . TAAAA TAAA 31.0542 PASS INDEL;IDV=5;IMF=0.357143;
DP=14;VDB=0.120429;SGB=-0.590765;MQSB=0.612626;MQOF=0;ICB=1;HOB=0.5;AC=1;AN=2;
DP4=7,2,3,2;MQ=54 GT:PL:DP:AD:GQ 0/1:64,0,100:14:9,5:64
10 102638180 . A . 228 PASS END=102638181;MinDP=9;AN=2 GT:DP 0/0:9
10 102638182 . AATATAAATATATATATAATATATAT AATATAAATATATAT 92 PASS
INDEL;IDV=3;IMF=0.2;DP=15;VDB=0.262608;SGB=-0.511536;MQSB=0.76338;MQOF=0;
ICB=1;HOB=0.5;AC=1;AN=2;DP4=8,4,2,1;MQ=55 GT:PL:DP:AD:GQ 0/1:126,0,255:15:12,
3:124
10 102638183 . A . 257 PASS END=102638220;MinDP=9;AN=2 GT:DP 0/0:9
10 102638221 . G . . PASS END=102638530;MinDP=16 GT:DP 0/0:16
10 102638531 rs11593061 A G 222 PASS DP=32;VDB=0.0772975;SGB=-0
.690438;RPB=0.217575;MQB=1;MQSB=1;BQB=0.972037;MQOF=0;ICB=1;HOB=0.5;AC=1;AN=2;
DP4=8,6,6,11;MQ=60 GT:PL:DP:AD:GQ 0/1:255,0,240:31:14,17:127
10 102638532 . A . . PASS END=102638824;MinDP=31 GT:DP 0/0:31
10 102638825 rs3977756 G A 166 PASS DP=37;VDB=0.677053;SGB=-0.680642;
RPB=0.31171;MQB=1;MQSB=1;BQB=0.996487;MQOF=0;ICB=1;HOB=0.5;AC=1;AN=2;DP4=15,9,8,
4;MQ=60 GT:PL:DP:AD:GQ 0/1:199,0,255:36:24,12:127
```

Your genome variants • 1.45GB

```
NC_000006.12 Gnomon CDS 121317495 121317672 . - 1
ID=cds-XP_047274270.1;Parent=rna-XM_047418314.1;Dbxref=GeneID:221322,
GenBank:XP_047274270.1,HGNC:HGNC:21485,MIM:615867;Name=XP_047274270.1;gbkey=CDS;
gene=TBC1D32;product=protein broad-minded isoform X9;protein_id=XP_047274270.1
NC_000006.12 Gnomon CDS 121310779 121310847 . - 0
ID=cds-XP_047274270.1;Parent=rna-XM_047418314.1;Dbxref=GeneID:221322,
GenBank:XP_047274270.1,HGNC:HGNC:21485,MIM:615867;Name=XP_047274270.1;gbkey=CDS;
gene=TBC1D32;product=protein broad-minded isoform X9;protein_id=XP_047274270.1
NC_000006.12 Gnomon CDS 121307976 121308101 . - 0
ID=cds-XP_047274270.1;Parent=rna-XM_047418314.1;Dbxref=GeneID:221322,
GenBank:XP_047274270.1,HGNC:HGNC:21485,MIM:615867;Name=XP_047274270.1;gbkey=CDS;
gene=TBC1D32;product=protein broad-minded isoform X9;protein_id=XP_047274270.1
NC_000006.12 Gnomon CDS 121304755 121304833 . - 0
ID=cds-XP_047274270.1;Parent=rna-XM_047418314.1;Dbxref=GeneID:221322,
GenBank:XP_047274270.1,HGNC:HGNC:21485,MIM:615867;Name=XP_047274270.1;gbkey=CDS;
gene=TBC1D32;product=protein broad-minded isoform X9;protein_id=XP_047274270.1
NC_000006.12 Gnomon CDS 121304522 121304625 . - 2
ID=cds-XP_047274270.1;Parent=rna-XM_047418314.1;Dbxref=GeneID:221322,
GenBank:XP_047274270.1,HGNC:HGNC:21485,MIM:615867;Name=XP_047274270.1;gbkey=CDS;
gene=TBC1D32;product=protein broad-minded isoform X9;protein_id=XP_047274270.1
NC_000006.12 Gnomon CDS 121304365 121304426 . - 0
```

Gene annotations • 1.6GB

```
GGGAGGTGGCTTCTCTATGGAGGATGGGTTGGAATAAGTCGCAAGCAAGAAGGGTGTGAGCAGACACACGGGAAGAAGCT
ATTGCAGTCCCAAGTGAAGAGGGGGCTGCAGCAGGAAGCTGAGGCAGCAAGTGGAGCTGGAGAGAAGTAACTCCTGTGGGACA
TGCTTGGAGATGGAGGCACAGGACCTGAGGGTGCATTGAGTGTGGGATGAGAAAAAGAGAGAAGCAAGGATTTCTTTTT
GACTTGGCAACTGGGTGGATGGGACCTGAGGATGCATTGAGTGTGGGATGAGAAAAAGAGAGAAGCAAGGATTTCTTTT
TTGACTTGGGAACTGGGTGGATGGGACCTGAGGATGCATTGAGTGTGGGATGAGAAAAAGAGAGAAGCAAGGATTTCTT
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AAGAGCTCCTTTTGCATGTGTAGGTTGAGATGCCATCAGACATCCAGGTAGGTGGCTGAGTGCAGACTTGGATACG
TGGCTCCAGAAATTCAGGAAGAGCCAGACAGGAGACTCCACTTGGGAGTCATCAACCTATAGGTGGTATTTAAAGCC
GAGGATGAGGTCACTTGGGATGGTGTGATGctagaagaagaatggcCAAAGATGGGGCTCTAGGGCACTACACTCG
AACATTCGGAGGTCAAGCAGGGGAGAGGGCAGCAAGAGGTAGAGAAGATGCAGTGGTTGAAGGGCATTGAGGAGAGA
GGAGGACCATGAAGCCAGGGAGGGGGCTTGTCACTGATAGGAAATGTGGAGGGATCTGGTCCGGTAAAGACAGAGAA
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ATCCAATTAAGTATAGTTCAGGAAGACTGTGAGGCAAGGACAGAAATGATgaaatagaaaaatggaacagTAGCTGTA
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AGGTGGTGGGGTGGCTTTGGCTTGCACAGGTGGAGGGGGGGCTTGGCTTGGGGCAGGACAGTTCAGCCATAGAAAT
GGGGGAAAGTGGGGAGTGGTGGTCCAGATGGAGGTGCCAGTGGTGGGAAAGCCCTTGTGTTTGGCTGCTTCAATTTGAT
GAAGAATGAGACAGTTGCATGCCAAAAGAGAGAAGGTGAAGGGGAGTGGCTTGGAAAGTgagagggagggagggagggg
agcAGATAGGCTGGGGAGTGGAGATTGCTGCGATGTGTCTGATGCTTGTAGAGATGTGTGACCATAGAGGCTCAGTGA
TCCCATCTTGTCTGTTGTGATCTTCTCTTACCACCTCAGGAGCTCGAGTGGGATGGAGTGAAGGTTGCCGGGAT
```

Reference genome • 3.34GB

```
NC_000001.11 216490399 rs1254721246 T C . . RS=1254721246;
dbSNPBuildID=157;SSR=0;GENEINFO=LOC107985596:107985596;VC=SNV;INT;GNO;
FREQ=GnomAD_genomes:1,7.056e-06|db6aP_PopFreq:1,0
NC_000001.11 216490401 rs2102827570 T G . . RS=2102827570;
dbSNPBuildID=157;SSR=0;GENEINFO=LOC107985596:107985596;VC=SNV;INT;GNO;
FREQ=GnomAD_genomes:1,7.038e-06
NC_000001.11 216490402 rs2040384890 A C . . RS=2040384890;
dbSNPBuildID=155;SSR=0;GENEINFO=LOC107985596:107985596;VC=SNV;INT;GNO;
FREQ=TOPMED:1,7.556e-06|db6aP_PopFreq:1,0
NC_000001.11 216490404 rs988072233 A G . . RS=988072233;
dbSNPBuildID=151;SSR=0;GENEINFO=LOC107985596:107985596;VC=SNV;INT;GNO;
FREQ=1000Genomes_30X:0.9994,0.0006246|GnomAD_genomes:0.9998,0.0002037|TOPMED:0
.9997,0.0003476|db6aP_PopFreq:0.9997,0.0002529
NC_000001.11 216490406 rs1483853010 A C,G . . RS=1483853010;
dbSNPBuildID=155;SSR=0;GENEINFO=LOC107985596:107985596;VC=SNV;INT;GNO;
FREQ=TOPMED:1,,3.778e-06|db6aP_PopFreq:1,,0
NC_000001.11 216490414 rs1390552343 C A,T . . RS=1390552343;
dbSNPBuildID=151;SSR=0;GENEINFO=LOC107985596:107985596;VC=SNV;INT;GNO;
FREQ=GnomAD_genomes:1,,7.12e-06|TOPMED:1,,3.778e-06|db6aP_PopFreq:1,,0
NC_000001.11 216490416 rs2040384939 G A,T . . RS=2040384939;
dbSNPBuildID=157;SSR=0;GENEINFO=LOC107985596:107985596;VC=SNV;INT;GNO;
```

Known variant database • 213.78GB

## Solution: Deterministic foundations, expert feedback loops

LLMs are a *last-mile* technology

- Good at combining horizontals, bad at cross-cutting verticals
- Any layer can be built, if everything below is deterministic

LLMs are hallucinating slop-machines

- Extremely capable, but always slightly inaccurate
- Error correction needs *some* feedback loop

Thank you

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Dark Bio Founder  
<https://dark.bio/whitepaper>

