# Integrating Next Generation Sequencing, EHR, and Claims Data to Extend Follow-Up in a Real-World Advanced Lung Adenocarcinoma Biomarker-Treatment Landscape

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## INTRODUCTION

Comprehensive genomic profiling (CGP) datasets linked with systemic anticancer treatments are key tools in precision oncology, but clinical follow-up may be limited if derived from a single data modality. When supplementing electronic health records (EHRs), administrative claims data may improve the completeness of treatment journeys. In this study, we extended abstracted treatment histories using closed claims data and used the integrated data to characterize real-world biomarker-treatment relationships.

## METHODS

We extracted CGP results and abstracted EHRs from the Tempus multimodal database for 6487 stage 4 lung adenocarcinoma patients diagnosed between 2020 and 2023. Closed claims data were joined using deterministic patient linkages. Patient biomarker status was determined from Tempus sequencing results in combination with NCCN guidelines.
Ongoing abstracted lines of therapy (LOTs) were extended using claims until: i) a treatment gap of at least 90 days, ii) a new class of persistent treatment (at least 2 claims), or iii) end of follow-up. New LOTs from claims began at the next persistent treatment, included all unique persistent medications within 30 days, and were extended similarly. Our study assessed the subset of patients with an integrated LOT1 beginning 0-60 days after CGP testing.

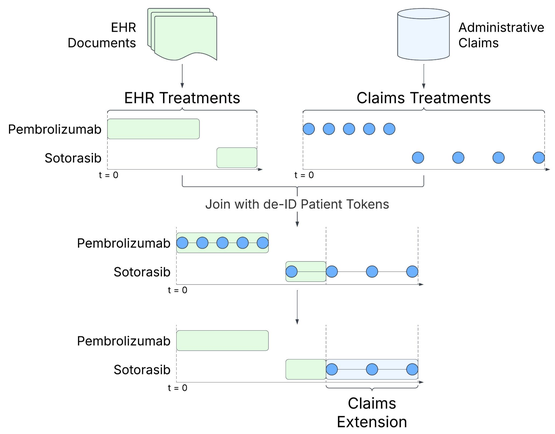


**Figure 1.** Treatment data from abstracted EHRs and administrative claims were combined at the patient level using deterministic patient linkages. Claims after a patient's last abstracted treatment date were eligible for integration into lines of therapy (LOTs).

## CONCLUSIONS

- Integrating claims and EHR data increases the number of patients with known lines of therapy and associated end dates, and can extend end dates for patients lost to follow-up.
- This study highlights the use of closed claims to extend EHR-abstracted cancer treatment data, demonstrating utility for real-world treatment patterns and outcome analyses.

## RESULTS

### Schematic for iterative algorithm to extend LOTs using claims data

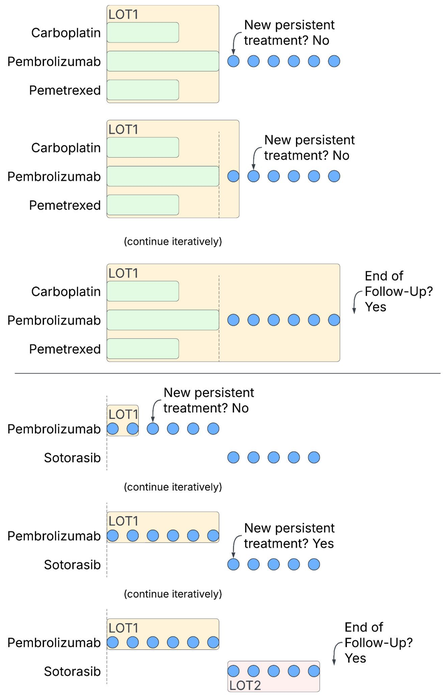


**Figure 2.** LOTs are extended by iterating through each subsequent claim with a series of stopping rules (listed in Methods). Top: An abstracted LOT is iteratively extended through the end of follow-up because there are no treatment gaps nor new classes of persistent treatment. Bottom: LOT1 is identified from claims and extended until a new class of persistent treatment. That new treatment ends LOT1 and begins LOT2, which is similarly extended until the end of follow-up.

### Impact of integrating claims into abstracted LOTs

| | LOT Therapies Are Known | | | LOT End Date is Known | | | LOT Extension | | |
|---|---|---|---|---|---|---|---|---|---|
| Line of Therapy | Abstracted Only | Integrated | % Lift | Abstracted Only | Integrated | % Lift | Abstracted as Lost to Follow-Up | Integration Extends ≥ 30 Days | % Extended ≥ 30 Days |
| LOT1 | 1597 | 1774 | 11.1 | 746 | 932 | 24.9 | 851 | 72 | 8.5 |
| LOT2 | 380 | 456 | 20.0 | 196 | 275 | 40.3 | 184 | 16 | 8.7 |
| LOT3 | 108 | 139 | 28.7 | 50 | 75 | 50.0 | 58 | 2 | 3.4 |

| | LOT1 Therapies Are Known | | | LOT1 End Date is Known | | | LOT1 Extension | | |
|---|---|---|---|---|---|---|---|---|---|
| Biomarker Status | Abstracted Only | Integrated | % Lift | Abstracted Only | Integrated | % Lift | Abstracted as Lost to Follow-Up | Integration Extends ≥ 30 Days | % Extended ≥ 30 Days |
| EGFR | 269 | 293 | 8.9 | 89 | 117 | 31.5 | 180 | 21 | 11.7 |
| KRAS | 217 | 244 | 12.4 | 105 | 136 | 29.5 | 112 | 11 | 9.8 |
| ALK | 71 | 83 | 16.9 | 22 | 28 | 27.3 | 49 | 5 | 10.2 |
| ERBB2 | 37 | 46 | 24.3 | 20 | 27 | 35.0 | 17 | 1 | 5.9 |
| BRAF | 31 | 34 | 9.7 | 16 | 18 | 12.5 | 15 | 0 | 0.0 |
| RET | 20 | 23 | 15.0 | 11 | 13 | 18.2 | 9 | 0 | 0.0 |
| ROS1 | 17 | 17 | 0.0 | 11 | 12 | 9.1 | 6 | 0 | 0.0 |
| MET | 16 | 17 | 6.3 | 8 | 9 | 12.5 | 8 | 0 | 0.0 |
| NTRK | 1 | 1 | 0.0 | 0 | 0 | - | 1 | 0 | 0.0 |
| No Targetable Genes | 918 | 1016 | 10.7 | 464 | 572 | 23.3 | 454 | 34 | 7.5 |

**Tables 1 & 2.** The impact of LOT integration was determined by comparison against abstracted LOTs. Impacts included i) identification of an integrated LOT when no LOT was abstracted , ii) identification of an integrated end date when no end date was abstracted, and iii) extension by at least 30 days of an LOT abstracted as lost to follow-up. Top: Impacts across all patients by LOT number. Bottom: Impacts for LOT1, by biomarker status.

### Integrated LOT1s for patients with targetable alterations

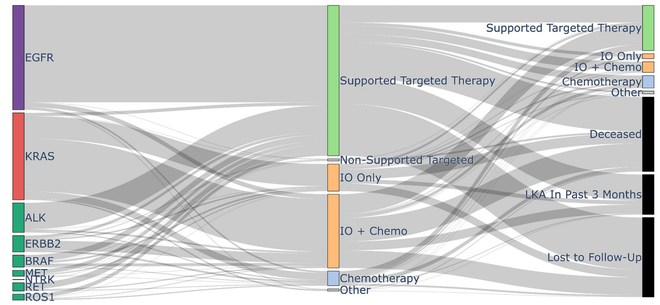


**Figure 3.** Using integrated LOT, we tracked patient treatment journeys from biomarker testing results (left) to LOT1 (center) and onto LOT2 or study exit (right). Most patients with a targetable alteration received a supported targeted therapy in LOT1. Inflows to LOT1 immunotherapy are primarily driven by KRAS patients, for whom targeted therapy is approved in second line. Targeted therapies for certain indications, like ERBB2, were added to guidelines after the start of our study look back window, which may contribute to inflows to LOT1s other than Supported Targeted Therapy. About 31% of patients (209 of 668) are known to have died prior to initiation of LOT2.

### Integrated LOT journeys for EGFR-mutated and KRAS-mutated patients

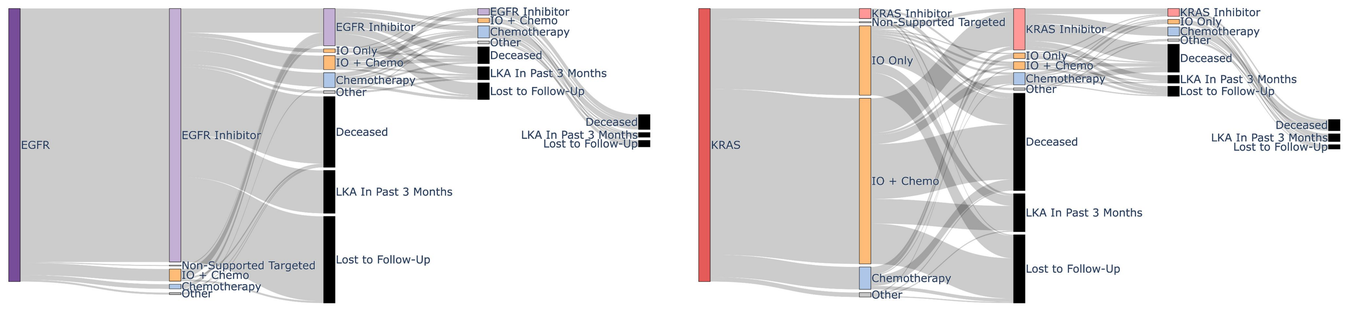


**Figure 4.** Using integrated LOT, we tracked patient treatment journeys for EGFR (left) and KRAS (right) through LOT3. 93% of LOT1s for EGFR-mutated patients included an EGFR inhibitor. For KRAS p.G12C, where targeted therapies are currently approved in second-line, 86% of LOT1s included immunotherapy and 60% of LOT2s included a KRAS inhibitor.

**Looking for more?**
See our companion poster SA56 (Thurs. 4 - 7 PM): "Assessing the Completeness of Oncology Treatment Data from Administrative Claims: A Benchmarking Study Against Abstracted EHRs Using Patient-Level Linkages" (Abstract number: 4306)

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