# Hypercap CC NLP Analysis

## Table of contents

# 1 Workbook for MIMIC Hypercapnia Presenting Chief Concern Analysis

This notebook is a deterministic analysis workflow for the NLP-augmented hypercapnia cohort workbook.

## 1.1 Environment Gate

Fail fast if required packages are missing. Use `uv sync` to repair the environment.

```python
import importlib.util

required_packages = [
    "numpy",
    "pandas",
    "matplotlib",
    "seaborn",
    "statsmodels",
    "upsetplot",
    "openpyxl",
]
missing = [pkg for pkg in required_packages if importlib.util.find_spec(pkg)
 ↪  is None]
if missing:
    raise ModuleNotFoundError(
        "Missing required packages: "
        + ", ".join(missing)
        + ". Run `uv sync` from the repository root and rerun the notebook."
    )
print("Environment check passed.")
```

```
Environment check passed.
```

## 1.2 Load Data

Use a single canonical workbook path under `MIMIC tabular data`.

```python
import json
import os
import sys
from pathlib import Path

import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import statsmodels.api as sm
from statsmodels.stats.proportion import proportion_confint
from upsetplot import UpSet, from_indicators

WORK_DIR = Path(os.getenv("WORK_DIR", Path.cwd())).expanduser().resolve()
SRC_DIR = WORK_DIR / "src"
if SRC_DIR.exists() and str(SRC_DIR) not in sys.path:
    sys.path.insert(0, str(SRC_DIR))
```

```python
CANONICAL_NLP_FILENAME = "MIMICIV all with CC_with_NLP.xlsx"


def resolve_analysis_input_path(work_dir: Path, input_filename: str | None =
↪  None) -> Path:
    filename = input_filename or CANONICAL_NLP_FILENAME
    input_path = (work_dir / "MIMIC tabular data" /
↪   filename).expanduser().resolve()
    if not input_path.exists():
        raise FileNotFoundError(
            "Expected analysis input workbook was not found at "
            f"{input_path}. Run the classifier notebook first or set "
            "ANALYSIS_INPUT_FILENAME."
        )
    return input_path


def ensure_required_columns(df: pd.DataFrame, required: list[str]) -> None:
    missing = sorted(set(required).difference(df.columns))
    if missing:
        raise KeyError(f"Missing required columns: {missing}")


def to_binary_flag(series: pd.Series) -> pd.Series:
    numeric = pd.to_numeric(series, errors="coerce").fillna(0)
    return (numeric > 0).astype(int)


def _binary_or_zero(df: pd.DataFrame, column: str) -> pd.Series:
    if column in df.columns:
        return to_binary_flag(df[column])
    return pd.Series(0, index=df.index, dtype="int64")


def classify_icd_category_vectorized(df: pd.DataFrame) -> pd.Series:
    j9602 = _binary_or_zero(df, "ICD10_J9602")
    j9612 = _binary_or_zero(df, "ICD10_J9612")
    j9622 = _binary_or_zero(df, "ICD10_J9622")
    j9692 = _binary_or_zero(df, "ICD10_J9692")
    e662 = _binary_or_zero(df, "ICD10_E662")
    icd9_27803 = _binary_or_zero(df, "ICD9_27803")

    category = np.select(
        [
            j9602.eq(1),
            j9612.eq(1),
            j9622.eq(1),
            j9692.eq(1),
            e662.eq(1) | icd9_27803.eq(1),
        ],
        [
            "Acute RF with hypoxia",
            "Acute RF with hypercapnia",
            "Acute RF with hypoxia & hypercapnia",
            "Respiratory failure, unspecified",
            "Obesity hypoventilation syndrome",
        ],
        default="Other / None",
    )
    return pd.Series(category, index=df.index, name="icd_category")


def classify_inclusion_type_vectorized(any_icd: pd.Series, gas_any:
↪   pd.Series) -> pd.Series:
    any_icd_bin = to_binary_flag(any_icd)
    gas_any_bin = to_binary_flag(gas_any)
    labels = np.select(
        [
            any_icd_bin.eq(1) & gas_any_bin.eq(1),
            any_icd_bin.eq(1) & gas_any_bin.eq(0),
            any_icd_bin.eq(0) & gas_any_bin.eq(1),
        ],
        ["Both", "ICD_only", "Gas_only"],
        default="Neither",
    )
    return pd.Series(labels, index=any_icd.index, name="inclusion_type")


def binary_crosstab_yes_no(df: pd.DataFrame, row_col: str, flag_col: str) ->
↪   pd.DataFrame:
    ensure_required_columns(df, [row_col, flag_col])
    tab = pd.crosstab(df[row_col], to_binary_flag(df[flag_col]),
↪   margins=False, dropna=False)
    tab = tab.reindex(columns=[0, 1], fill_value=0)
    tab.columns = ["No", "Yes"]
    row_totals = tab.sum(axis=1).replace(0, np.nan)
    tab["Percent_yes"] = (tab["Yes"] / row_totals * 100).round(1).fillna(0)
    return tab


def symptom_distribution_by_overlap(
    df: pd.DataFrame,
    group_col: str,
    symptom_col: str,
    top_k: int = 10,
) -> tuple[pd.DataFrame, pd.DataFrame]:
    ensure_required_columns(df, [group_col, symptom_col])
    tmp = df.dropna(subset=[group_col, symptom_col]).copy()
    if tmp.empty:
        return pd.DataFrame(columns=[group_col, "symptom_group", "N",
         ↪  "Percent"]), pd.DataFrame()
    top_symptoms =
 ↪  tmp[symptom_col].value_counts(dropna=False).head(top_k).index
    tmp["symptom_group"] =
 ↪  tmp[symptom_col].where(tmp[symptom_col].isin(top_symptoms), "Other")
    counts = (
        tmp.groupby([group_col, "symptom_group"], dropna=False)
        .size()
        .reset_index(name="N")
    )
    counts["Percent"] = (
        counts.groupby(group_col)["N"].transform(lambda x: x / x.sum() *
 ↪  100).round(1)
    )
    pivot = counts.pivot_table(
        index="symptom_group",
        columns=group_col,
        values="Percent",
        fill_value=0,
    ).round(1)
    return counts, pivot


def classify_gas_source_overlap(
    abg_series: pd.Series,
    vbg_series: pd.Series,
    other_series: pd.Series,
) -> pd.Series:
    abg = to_binary_flag(abg_series)
    vbg = to_binary_flag(vbg_series)
    other = to_binary_flag(other_series)
    labels = np.select(
        [
            abg.eq(1) & vbg.eq(1) & other.eq(1),
            abg.eq(1) & vbg.eq(1) & other.eq(0),
            abg.eq(1) & vbg.eq(0) & other.eq(1),
            abg.eq(0) & vbg.eq(1) & other.eq(1),
            abg.eq(1) & vbg.eq(0) & other.eq(0),
            abg.eq(0) & vbg.eq(1) & other.eq(0),
            abg.eq(0) & vbg.eq(0) & other.eq(1),
        ],
        [
            "ABG+VBG+OTHER",
            "ABG+VBG",
            "ABG+OTHER",
            "VBG+OTHER",
            "ABG-only",
            "VBG-only",
            "OTHER-only",
        ],
        default="No-gas",
    )
    return pd.Series(labels, index=abg_series.index,
     ↪  name="gas_source_overlap")


def select_preferred_vital_column(
    df: pd.DataFrame,
    *,
    clean_column: str,
    fallback_model_column: str,
) -> str | None:
    """Select cleaned vital column when available, otherwise fall back to
     ↪  model alias."""
    if clean_column in df.columns:
        return clean_column
    if fallback_model_column in df.columns:
        return fallback_model_column
    return None


def render_latex_longtable(
    table_df: pd.DataFrame,
    *,
    caption: str,
    label: str,
    landscape: bool = False,
    index: bool = True,
) -> str:
    latex_text = table_df.to_latex(
        index=index,
        escape=False,
        longtable=True,
        caption=caption,
        label=label,
    )
    if landscape:
        latex_text = "\\begin{landscape}\\n" + latex_text +
 ↪  "\\n\\end{landscape}\\n"
    return latex_text


from hypercap_cc_nlp.pipeline_audit import collect_run_manifest

ANALYSIS_INPUT_FILENAME = os.getenv("ANALYSIS_INPUT_FILENAME")
ANALYSIS_INPUT_PATH = resolve_analysis_input_path(
    WORK_DIR,
    ANALYSIS_INPUT_FILENAME if ANALYSIS_INPUT_FILENAME else None,
)
OUTPUT_DIR = WORK_DIR

HYPERCAP_CRITERIA = [
    "any_hypercap_icd",
    "abg_hypercap_threshold",
    "vbg_hypercap_threshold",
    "other_hypercap_threshold",
    "pco2_threshold_any",
]

SYMPTOM_COL = "RFV1_name"

df = pd.read_excel(ANALYSIS_INPUT_PATH, engine="openpyxl")
required_analysis_cols = sorted({SYMPTOM_COL, *HYPERCAP_CRITERIA})
try:
    ensure_required_columns(df, required_analysis_cols)
```

```
except KeyError as exc:
    raise KeyError(
        "Analysis input schema mismatch. Run 'Hypercap CC NLP Classifier.qmd'
         ↪  "
        f"to regenerate '{CANONICAL_NLP_FILENAME}' before running analysis."
    ) from exc

for column in HYPERCAP_CRITERIA:
    df[column] = to_binary_flag(df[column])

print(
    f"Loaded {ANALYSIS_INPUT_PATH.name}: {df.shape[0]:,} rows x
     ↪  {df.shape[1]:,} columns"
)
print(f"Analysis input path: {ANALYSIS_INPUT_PATH}")
```

```
Loaded MIMICIV all with CC_with_NLP.xlsx: 11,769 rows x 331 columns
Analysis input path: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Res
CC-NLP/MIMIC tabular data/MIMICIV all with CC_with_NLP.xlsx
```

## 1.3 Descriptive Checks

Compute core cohort summaries with guarded column checks.

```
gender_candidates = [col for col in df.columns if
 ↪  col.lower().startswith("gender")]
if not gender_candidates:
    raise KeyError("No gender-like column found. Expected a column starting
     ↪  with 'gender'.")
gender_col = gender_candidates[0]

gender_summary = (
    df[gender_col]
    .value_counts(dropna=False)
    .rename_axis(gender_col)
    .to_frame("Count")
)
gender_summary["Percent"] = (gender_summary["Count"] / len(df) *
 ↪  100).round(1)

age_summary = pd.Series(
    {
        "Mean": round(float(df["age"].mean()), 2),
        "SD": round(float(df["age"].std()), 2),
        "Q1": round(float(df["age"].quantile(0.25)), 2),
        "Q3": round(float(df["age"].quantile(0.75)), 2),
    },
    name="Age (years)",
)

prevalence_label_map = {
    "any_hypercap_icd": "Hypercapnic RF ICD (any)",
    "abg_hypercap_threshold": "ABG hypercapnia threshold",
    "vbg_hypercap_threshold": "VBG hypercapnia threshold",
    "other_hypercap_threshold": "PCO2 OTHER threshold",
    "pco2_threshold_any": "PCO2 threshold any source",
}
cohort_n = int(len(df))
hypercap_prevalence = (
    pd.DataFrame(
        {
            "Definition": [prevalence_label_map[col] for col in
             ↪  HYPERCAP_CRITERIA],
            "Column": HYPERCAP_CRITERIA,
            "Count": [int(df[col].sum()) for col in HYPERCAP_CRITERIA],
            "Denominator_N": [cohort_n for _ in HYPERCAP_CRITERIA],
            "Percent": [round(float(df[col].mean() * 100), 1) for col in
             ↪  HYPERCAP_CRITERIA],
        }
    )
    .set_index("Definition")
    .sort_values("Count", ascending=False)
)

display(gender_summary)
display(age_summary.to_frame())
display(hypercap_prevalence)
```

| | Count | Percent |
|---|---|---|
| gender | | |
| M | 6314 | 53.6 |
| F | 5455 | 46.4 |

|  | Age (years) |
|---|---|
| Mean | 66.11 |
| SD | 16.54 |
| Q1 | 56.00 |
| Q3 | 78.00 |

| Definition | Column | Count | Denominator_N | Percent |
|---|---|---|---|---|
| PCO2 threshold any source | pco2_threshold_any | 11309 | 11769 | 96.1 |
| ABG hypercapnia threshold | abg_hypercap_threshold | 7270 | 11769 | 61.8 |
| VBG hypercapnia threshold | vbg_hypercap_threshold | 6244 | 11769 | 53.1 |
| Hypercapnic RF ICD (any) | any_hypercap_icd | 1983 | 11769 | 16.8 |
| PCO2 OTHER threshold | other_hypercap_threshold | 1350 | 11769 | 11.5 |

### 1.4 ED Vitals Data Quality (cleaned-column preference)

Use cleaned ED-vitals columns when available (`*_clean`), falling back to `*_model` aliases only when needed.

```python
vital_preference_specs = {
    "triage_temp_f": ("ed_triage_temp_f_clean", "ed_triage_temp_model"),
    "first_temp_f": ("ed_first_temp_f_clean", "ed_first_temp_model"),
    "triage_pain": ("ed_triage_pain_clean", "ed_triage_pain_model"),
    "first_pain": ("ed_first_pain_clean", "ed_first_pain_model"),
    "triage_sbp": ("ed_triage_sbp_clean", "ed_triage_sbp_model"),
    "first_sbp": ("ed_first_sbp_clean", "ed_first_sbp_model"),
    "triage_dbp": ("ed_triage_dbp_clean", "ed_triage_dbp_model"),
    "first_dbp": ("ed_first_dbp_clean", "ed_first_dbp_model"),
    "triage_o2sat": ("ed_triage_o2sat_clean", "ed_triage_o2sat_model"),
    "first_o2sat": ("ed_first_o2sat_clean", "ed_first_o2sat_model"),
}

selected_vital_columns: dict[str, str | None] = {}
vitals_quality_rows: list[dict[str, object]] = []
for vital_name, (clean_col, fallback_col) in vital_preference_specs.items():
    selected_column = select_preferred_vital_column(
        df,
        clean_column=clean_col,
        fallback_model_column=fallback_col,
    )
    selected_vital_columns[vital_name] = selected_column
    if selected_column is None:
        vitals_quality_rows.append(
            {
                "vital_name": vital_name,
                "selected_column": None,
                "n_non_missing": 0,
                "median": np.nan,
                "mean": np.nan,
            }
        )
        continue
    numeric = pd.to_numeric(df[selected_column], errors="coerce")
    vitals_quality_rows.append(
        {
            "vital_name": vital_name,
            "selected_column": selected_column,
            "n_non_missing": int(numeric.notna().sum()),
            "median": float(numeric.median()) if numeric.notna().any() else
             ↪  np.nan,
            "mean": float(numeric.mean()) if numeric.notna().any() else
             ↪  np.nan,
        }
    )

vitals_quality_summary =
 ↪  pd.DataFrame(vitals_quality_rows).sort_values("vital_name")
display(vitals_quality_summary)

print(
    "Cohort-run ED vitals audits are written under "
    "'MIMIC tabular data/prior runs/YYYY-MM-DD ed_vitals_*.csv'."
)
```

| | vital_name | selected_column | n_non_missing | median | mean |
|---|---|---|---|---|---|
| 7 | first_dbp | ed_first_dbp_clean | 9139 | 71.0 | 72.116862 |
| 9 | first_o2sat | ed_first_o2sat_clean | 8906 | 97.0 | 96.232877 |
| 3 | first_pain | ed_first_pain_clean | 7067 | 0.0 | 2.681831 |
| 5 | first_sbp | ed_first_sbp_clean | 9142 | 127.0 | 128.856705 |
| 1 | first_temp_f | ed_first_temp_f_clean | 6901 | 98.0 | 98.153582 |
| 6 | triage_dbp | ed_triage_dbp_clean | 8715 | 72.0 | 73.017212 |
| 8 | triage_o2sat | ed_triage_o2sat_clean | 8667 | 97.0 | 96.195916 |

|   | vital_name | selected_column | n_non_missing | median | mean |
|---|---|---|---|---|---|
| 2 | triage_pain | ed_triage_pain_clean | 7586 | 0.0 | 2.944569 |
| 4 | triage_sbp | ed_triage_sbp_clean | 8759 | 128.0 | 130.047037 |
| 0 | triage_temp_f | ed_triage_temp_f_clean | 8330 | 98.0 | 98.091937 |

```
Cohort-run ED vitals audits are written under 'MIMIC tabular data/prior runs/YYYY-
MM-DD ed_vitals_*.csv'.
```

### 1.5 Cohort Blood-Gas QC Snapshot

Summarize gas-source quarantine and anchor diagnostics emitted by cohort generation.

```
qa_summary_path = WORK_DIR / "qa_summary.json"
if qa_summary_path.exists():
    qa_summary_payload = json.loads(qa_summary_path.read_text())
    blood_gas_audit_paths = qa_summary_payload.get("blood_gas_audit_paths",
 ↪  {})
    timing_integrity_audit = qa_summary_payload.get("timing_integrity_audit",
 ↪  [{}])
    ventilation_timing_audit =
 ↪  qa_summary_payload.get("ventilation_timing_audit", [{}])
    timing_row = timing_integrity_audit[0] if timing_integrity_audit else {}
    vent_row = ventilation_timing_audit[0] if ventilation_timing_audit else
 ↪  {}
    qualifying_gas_observed_rate = (
        float(pd.to_numeric(df["qualifying_gas_observed"],
         ↪  errors="coerce").fillna(0).mean())
        if "qualifying_gas_observed" in df.columns
        else None
    )
    qc_rows = [
        {
            "metric": "OTHER semantics",
            "value": "LAB blood-gas unknown specimen only (POC OTHER
             ↪  quarantined).",
        },
        {
            "metric": "gas_source_other_rate",
            "value": qa_summary_payload.get("gas_source_other_rate"),
        },
        {
            "metric": "POC OTHER quarantined hadm count",
            "value": (
                qa_summary_payload.get("other_route_quarantine_audit",
↪   [{}])[0].get(
                    "poc_other_quarantined_hadm_n"
                )
                if qa_summary_payload.get("other_route_quarantine_audit")
                else None
            ),
        },
        {
            "metric": "POC OTHER leakage into threshold",
            "value": (
                qa_summary_payload.get("other_route_quarantine_audit",
↪   [{}])[0].get(
                    "poc_other_leak_into_other_threshold_n"
                )
                if qa_summary_payload.get("other_route_quarantine_audit")
                else None
            ),
        },
        {
            "metric": "first_gas_without_pco2_anchor_n",
            "value": (
                qa_summary_payload.get("first_gas_anchor_audit",
↪   [{}])[0].get(
                    "first_gas_without_pco2_anchor_n"
                )
                if qa_summary_payload.get("first_gas_anchor_audit")
                else None
            ),
        },
        {
            "metric": "qualifying_gas_observed_rate",
            "value": qualifying_gas_observed_rate,
        },
        {
            "metric": "hospital_los_negative_n",
            "value": timing_row.get("hospital_los_negative_n"),
        },
        {
            "metric": "admittime_before_ed_intime_n",
            "value": timing_row.get("admittime_before_ed_intime_n"),
        },
        {
            "metric": "imv_time_outside_window_n",
            "value": vent_row.get("imv_time_outside_window_n"),
        },
        {
            "metric": "niv_time_outside_window_n",
            "value": vent_row.get("niv_time_outside_window_n"),
        },
        {
            "metric": "poc_inclusion_enabled",
            "value": qa_summary_payload.get("poc_inclusion_enabled"),
        },
        {
            "metric": "poc_inclusion_reason",
            "value": qa_summary_payload.get("poc_inclusion_reason"),
        },
        {
            "metric": "pco2_source_distribution_audit_path",
            "value": blood_gas_audit_paths.get("pco2_source_distribution"),
        },
    ]
    cohort_qc_summary = pd.DataFrame(qc_rows)
else:
    cohort_qc_summary = pd.DataFrame(
        [{"metric": "qa_summary", "value": f"Missing: {qa_summary_path}"}]
    )

display(cohort_qc_summary)
```

| | metric | value |
|---|---|---|
| 0 | OTHER semantics | LAB blood-gas unknown specimen only (POC OTHER... |
| 1 | gas_source_other_rate | 0.661752 |
| 2 | POC OTHER quarantined hadm count | 0 |
| 3 | POC OTHER leakage into threshold | 0 |
| 4 | first_gas_without_pco2_anchor_n | 0 |
| 5 | qualifying_gas_observed_rate | 0.645849 |
| 6 | hospital_los_negative_n | 17 |
| 7 | admittime_before_ed_intime_n | 15 |
| 8 | imv_time_outside_window_n | 28 |
| 9 | niv_time_outside_window_n | 13 |
| 10 | poc_inclusion_enabled | False |

|    | metric | value |
|---|---|---|
| 11 | poc_inclusion_reason | manifest_has_no_icu_pco2_itemids |
| 12 | pco2_source_distribution_audit_path | /Users/blocke/Box Sync/Residency Personal File... |

## 1.6 ICD And Inclusion Categories

Use vectorized helper functions to avoid row-wise `apply(axis=1)`.

```
df["icd_category"] = classify_icd_category_vectorized(df)
df["inclusion_type"] = classify_inclusion_type_vectorized(
    df["any_hypercap_icd"],
    df["pco2_threshold_any"],
)

icd_category_summary = (
    df["icd_category"]
    .value_counts(dropna=False)
    .rename_axis("ICD Category")
    .to_frame("Count")
)
icd_category_summary["Percent"] = (icd_category_summary["Count"] / len(df) *
 ↪  100).round(1)
icd_category_summary["Denominator_N"] = int(len(df))

inclusion_summary = (
    df["inclusion_type"]
    .value_counts(dropna=False)
    .rename_axis("Inclusion Type")
    .to_frame("Count")
)
inclusion_summary["Percent"] = (inclusion_summary["Count"] / len(df) *
 ↪  100).round(1)
inclusion_summary["Denominator_N"] = int(len(df))

icd_positive_df = df.loc[df["any_hypercap_icd"].eq(1)].copy()
icd_positive_n = int(len(icd_positive_df))
icd_positive_breakdown = pd.DataFrame(
    {
        "Definition": [
            "ABG threshold positive",
            "VBG threshold positive",
            "PCO2 OTHER threshold positive",
            "Any gas threshold positive",
        ],
        "Count": [
            int(icd_positive_df["abg_hypercap_threshold"].sum()),
            int(icd_positive_df["vbg_hypercap_threshold"].sum()),
            int(icd_positive_df["other_hypercap_threshold"].sum()),
            int(icd_positive_df["pco2_threshold_any"].sum()),
        ],
    }
)
if icd_positive_n > 0:
    icd_positive_breakdown["Percent"] = (
        icd_positive_breakdown["Count"] / icd_positive_n * 100
    ).round(1)
else:
    icd_positive_breakdown["Percent"] = 0.0
icd_positive_breakdown["Denominator_N"] = icd_positive_n

icd_positive_category_summary = (
    icd_positive_df["icd_category"]
    .value_counts(dropna=False)
    .rename_axis("ICD Category (ICD-positive subset)")
    .to_frame("Count")
)
if icd_positive_n > 0:
    icd_positive_category_summary["Percent"] = (
        icd_positive_category_summary["Count"] / icd_positive_n * 100
    ).round(1)
else:
    icd_positive_category_summary["Percent"] = 0.0
icd_positive_category_summary["Denominator_N"] = icd_positive_n

display(icd_category_summary)
display(inclusion_summary)
display(icd_positive_category_summary)
display(icd_positive_breakdown)
```

| | Count | Percent | Denominator_N |
|---|---|---|---|
| ICD Category | | | |
| Other / None | 9786 | 83.2 | 11769 |
| Acute RF with hypoxia | 793 | 6.7 | 11769 |
| Obesity hypoventilation syndrome | 524 | 4.5 | 11769 |

| ICD Category | Count | Percent | Denominator_N |
|---|---|---|---|
| Acute RF with hypoxia & hypercapnia | 386 | 3.3 | 11769 |
| Respiratory failure, unspecified | 187 | 1.6 | 11769 |
| Acute RF with hypercapnia | 93 | 0.8 | 11769 |

| Inclusion Type | Count | Percent | Denominator_N |
|---|---|---|---|
| Gas_only | 9786 | 83.2 | 11769 |
| Both | 1523 | 12.9 | 11769 |
| ICD_only | 460 | 3.9 | 11769 |

| ICD Category (ICD-positive subset) | Count | Percent | Denominator_N |
|---|---|---|---|
| Acute RF with hypoxia | 793 | 40.0 | 1983 |
| Obesity hypoventilation syndrome | 524 | 26.4 | 1983 |
| Acute RF with hypoxia & hypercapnia | 386 | 19.5 | 1983 |
| Respiratory failure, unspecified | 187 | 9.4 | 1983 |
| Acute RF with hypercapnia | 93 | 4.7 | 1983 |

| | Definition | Count | Percent | Denominator_N |
|---|---|---|---|---|
| 0 | ABG threshold positive | 971 | 49.0 | 1983 |
| 1 | VBG threshold positive | 1300 | 65.6 | 1983 |
| 2 | PCO2 OTHER threshold positive | 330 | 16.6 | 1983 |
| 3 | Any gas threshold positive | 1523 | 76.8 | 1983 |

```
symptom_work_df = df.copy()
symptom_text =
 ↪  symptom_work_df[SYMPTOM_COL].fillna("").astype(str).str.strip()
symptom_work_df["symptom_missing_flag"] = symptom_text.eq("")
top_symptom_labels = symptom_text.loc[~symptom_work_df[
 ↪  "symptom_missing_flag"]].value_counts().head(10).index
symptom_work_df["symptom_group"] = symptom_text.where(
    symptom_text.isin(top_symptom_labels),
    "Other",
)
symptom_work_df.loc[symptom_work_df["symptom_missing_flag"], "symptom_group"]
 ↪  = "No symptom recorded"
```

```
crosstab_tables = {}
for definition in HYPERCAP_CRITERIA:
    definition_table = binary_crosstab_yes_no(symptom_work_df,
 ↪  "symptom_group", definition)
    crosstab_tables[definition] = definition_table.sort_values("Percent_yes",
 ↪  ascending=False)

display(crosstab_tables["pco2_threshold_any"].head(10))

symptom_non_null =
 ↪  symptom_work_df.loc[~symptom_work_df["symptom_missing_flag"]].copy()
```

|  | No | Yes | Percent_yes |
|---|---|---|---|
| symptom_group |  |  |  |
| Injuries & adverse effects | 31 | 1581 | 98.1 |
| Symptom – Digestive | 29 | 1374 | 97.9 |
| Diseases (patient-stated) | 16 | 623 | 97.5 |
| Symptom – Circulatory | 36 | 1083 | 96.8 |
| Symptom – Nervous | 48 | 1254 | 96.3 |
| Uncodable/Unknown | 9 | 229 | 96.2 |
| Symptom – Musculoskeletal | 11 | 260 | 95.9 |
| Symptom – Skin/Hair/Nails | 13 | 288 | 95.7 |
| Other | 34 | 742 | 95.6 |
| Symptom – General | 27 | 521 | 95.1 |

## 1.7 Symptom Composition By Hypercapnia Definition

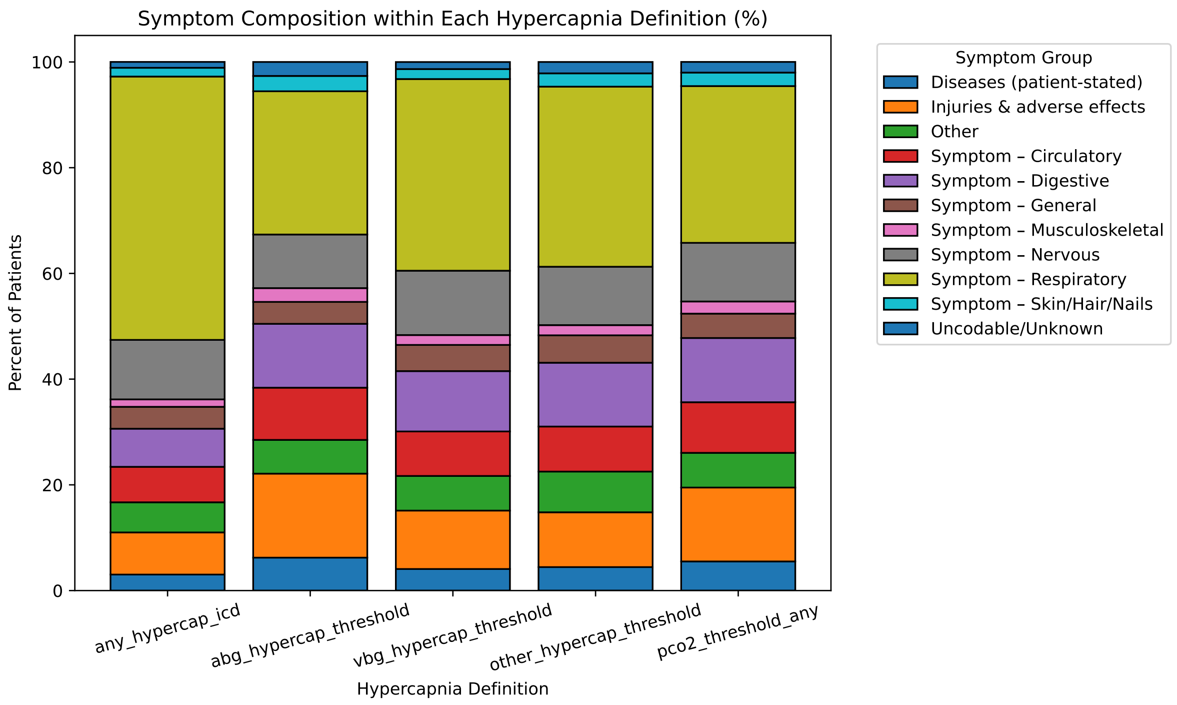
Generate counts, percentages, and clipped Wald 95% confidence intervals; export stable tables for downstream reporting.

```
definition_long_df = symptom_non_null.melt(
    id_vars=["symptom_group"],
    value_vars=HYPERCAP_CRITERIA,
    var_name="Hypercapnia_Definition",
    value_name="Positive",
)
definition_positive_df =
 ↪  definition_long_df.loc[definition_long_df["Positive"].eq(1)].copy()

definition_counts_df = (
    definition_positive_df.groupby(["Hypercapnia_Definition",
 ↪  "symptom_group"], dropna=False)
    .size()
    .reset_index(name="Count")
)
definition_counts_df["Total"] = definition_counts_df.groupby(⌋
 ↪  "Hypercapnia_Definition")["Count"].transform("sum")
definition_counts_df["Percent"] = definition_counts_df["Count"] /
 ↪  definition_counts_df["Total"] * 100

p_hat = (definition_counts_df["Percent"] / 100).clip(0, 1)
n_obs = definition_counts_df["Total"].replace(0, np.nan)
se = np.sqrt((p_hat * (1 - p_hat)) / n_obs).fillna(0)
definition_counts_df["CI_lower"] = ((p_hat - 1.96 * se).clip(0, 1) *
 ↪  100).round(2)
definition_counts_df["CI_upper"] = ((p_hat + 1.96 * se).clip(0, 1) *
 ↪  100).round(2)
definition_counts_df["Percent"] = definition_counts_df["Percent"].round(2)

definition_counts_df = definition_counts_df.sort_values(
    ["Hypercapnia_Definition", "Count"],
    ascending=[True, False],
)

definition_pivot_df = definition_counts_df.pivot_table(
    index="symptom_group",
    columns="Hypercapnia_Definition",
    values="Percent",
    fill_value=0,
).round(2)

definition_output_path = OUTPUT_DIR /
 ↪  "Symptom_Composition_by_Hypercapnia_Definition.xlsx"
pivot_output_path = OUTPUT_DIR / "Symptom_Composition_Pivot_ChartReady.xlsx"
definition_counts_df.to_excel(definition_output_path, index=False)
definition_pivot_df.to_excel(pivot_output_path)

display(definition_counts_df.head(12))
print(f"Exported: {definition_output_path}")
print(f"Exported: {pivot_output_path}")
```

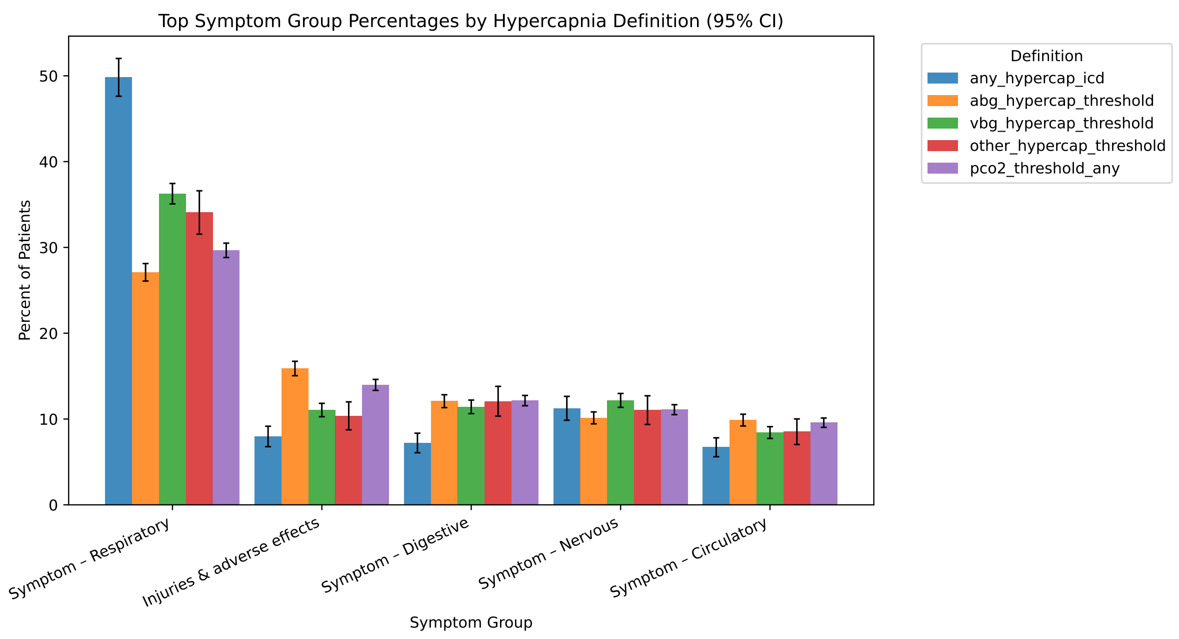
| | Hypercapnia_Definition | symptom_group | Count | Total | Percent | CI_lower | CI_uppe |
|---|---|---|---|---|---|---|---|
| 8 | abg_hypercap_threshold | Symptom – Respiratory | 1970 | 7270 | 27.10 | 26.08 | 28.12 |
| 1 | abg_hypercap_threshold | Injuries & adverse effects | 1155 | 7270 | 15.89 | 15.05 | 16.73 |
| 4 | abg_hypercap_threshold | Symptom – Digestive | 878 | 7270 | 12.08 | 11.33 | 12.83 |
| 7 | abg_hypercap_threshold | Symptom – Nervous | 737 | 7270 | 10.14 | 9.44 | 10.83 |
| 3 | abg_hypercap_threshold | Symptom – Circulatory | 718 | 7270 | 9.88 | 9.19 | 10.56 |
| 2 | abg_hypercap_threshold | Other | 464 | 7270 | 6.38 | 5.82 | 6.94 |
| 0 | abg_hypercap_threshold | Diseases (patient-stated) | 453 | 7270 | 6.23 | 5.68 | 6.79 |
| 5 | abg_hypercap_threshold | Symptom – General | 302 | 7270 | 4.15 | 3.70 | 4.61 |
| 9 | abg_hypercap_threshold | Symptom – Skin/Hair/Nails | 211 | 7270 | 2.90 | 2.52 | 3.29 |
| 10 | abg_hypercap_threshold | Uncodable/Unknown | 192 | 7270 | 2.64 | 2.27 | 3.01 |
| 6 | abg_hypercap_threshold | Symptom – Musculoskeletal | 190 | 7270 | 2.61 | 2.25 | 2.98 |
| 19 | any_hypercap_icd | Symptom – Respiratory | 988 | 1983 | 49.82 | 47.62 | 52.02 |

```
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Symptom_Composition_by_Hypercapnia_Definition.xlsx
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Symptom_Composition_Pivot_ChartReady.xlsx
```

```python
composition_plot_df = definition_pivot_df.T.loc[HYPERCAP_CRITERIA]

ax = composition_plot_df.plot(
    kind="bar",
    stacked=True,
    figsize=(10, 6),
    width=0.8,
    edgecolor="black",
)
ax.set_title("Symptom Composition within Each Hypercapnia Definition (%)")
ax.set_xlabel("Hypercapnia Definition")
ax.set_ylabel("Percent of Patients")
ax.tick_params(axis="x", labelrotation=15)
ax.legend(title="Symptom Group", bbox_to_anchor=(1.05, 1), loc="upper left")
plt.tight_layout()
plt.show()
```



```
top_for_ci = (
    definition_counts_df.groupby("symptom_group")["Count"]
    .sum()
    .sort_values(ascending=False)
    .head(5)
    .index
)
ci_plot_df = definition_counts_df.loc[definition_counts_df["symptom_group"
↪   ].isin(top_for_ci)].copy()
symptom_order = list(top_for_ci)
definition_order = HYPERCAP_CRITERIA

x = np.arange(len(symptom_order))
width = 0.18

fig, ax = plt.subplots(figsize=(11, 6))
for idx, definition in enumerate(definition_order):
    subset = (
        ci_plot_df.loc[ci_plot_df["Hypercapnia_Definition"].eq(definition)]
        .set_index("symptom_group")
        .reindex(symptom_order)
        .fillna(0)
    )
    x_pos = x + (idx - (len(definition_order) - 1) / 2) * width
    y = subset["Percent"].to_numpy()
    lower = subset["CI_lower"].to_numpy()
    upper = subset["CI_upper"].to_numpy()

    ax.bar(x_pos, y, width=width, label=definition, alpha=0.85)
    ax.errorbar(
        x_pos,
        y,
        yerr=[y - lower, upper - y],
        fmt="none",
        ecolor="black",
        elinewidth=1,
        capsize=2,
    )

ax.set_xticks(x)
ax.set_xticklabels(symptom_order, rotation=25, ha="right")
ax.set_ylabel("Percent of Patients")
ax.set_xlabel("Symptom Group")
ax.set_title("Top Symptom Group Percentages by Hypercapnia Definition (95%
 ↪  CI)")
ax.legend(title="Definition", bbox_to_anchor=(1.05, 1), loc="upper left")
plt.tight_layout()
plt.show()
```



## 1.8 Symptom Distribution By Ascertainment Overlap

```
overlap_required = [
    SYMPTOM_COL,
    "abg_hypercap_threshold",
    "vbg_hypercap_threshold",
    "other_hypercap_threshold",
    "any_hypercap_icd",
    "pco2_threshold_any",
]
ensure_required_columns(df, overlap_required)

abg_flag = to_binary_flag(df["abg_hypercap_threshold"])
vbg_flag = to_binary_flag(df["vbg_hypercap_threshold"])
other_flag = to_binary_flag(df["other_hypercap_threshold"])
icd_flag = to_binary_flag(df["any_hypercap_icd"])
gas_flag = to_binary_flag(df["pco2_threshold_any"])

gas_source_labels = classify_gas_source_overlap(abg_flag, vbg_flag,
 ↪ other_flag)
abg_vbg_labels = np.select(
    [
        abg_flag.eq(1) & vbg_flag.eq(1),
        abg_flag.eq(1) & vbg_flag.eq(0),
        abg_flag.eq(0) & vbg_flag.eq(1),
    ],
    ["ABG+VBG", "ABG-only", "VBG-only"],
    default="Neither",
)

icd_gas_labels = np.select(
    [
        icd_flag.eq(1) & gas_flag.eq(1),
        icd_flag.eq(1) & gas_flag.eq(0),
        icd_flag.eq(0) & gas_flag.eq(1),
    ],
    ["ICD+Gas", "ICD-only", "Gas-only"],
    default="Neither",
)

overlap_df = df.copy()
overlap_df["gas_source_overlap"] = gas_source_labels
overlap_df["abg_vbg_overlap"] = abg_vbg_labels
overlap_df["icd_gas_overlap"] = icd_gas_labels

gas_positive_df = overlap_df.loc[abg_flag.eq(1) | vbg_flag.eq(1) |
↪   other_flag.eq(1)].copy()
abg_vbg_positive_df = overlap_df.loc[abg_flag.eq(1) | vbg_flag.eq(1)].copy()
abg_vbg_counts_df, abg_vbg_pivot_df = symptom_distribution_by_overlap(
    abg_vbg_positive_df,
    group_col="abg_vbg_overlap",
    symptom_col=SYMPTOM_COL,
    top_k=10,
)
gas_source_counts_df, gas_source_pivot_df = symptom_distribution_by_overlap(
    gas_positive_df,
    group_col="gas_source_overlap",
    symptom_col=SYMPTOM_COL,
    top_k=10,
)
icd_gas_counts_df, icd_gas_pivot_df = symptom_distribution_by_overlap(
    overlap_df,
    group_col="icd_gas_overlap",
    symptom_col=SYMPTOM_COL,
    top_k=10,
)
```

```
gas_source_output_path = OUTPUT_DIR /
 ↪ "Symptom_Composition_by_ABG_VBG_Overlap.xlsx"
gas_source_expanded_output_path = OUTPUT_DIR /
 ↪ "Symptom_Composition_by_Gas_Source_Overlap.xlsx"
icd_gas_output_path = OUTPUT_DIR /
 ↪ "Symptom_Composition_by_ICD_Gas_Overlap.xlsx"
abg_vbg_pivot_df.to_excel(gas_source_output_path)
gas_source_pivot_df.to_excel(gas_source_expanded_output_path)
icd_gas_pivot_df.to_excel(icd_gas_output_path)

print("Symptom distribution by ABG/VBG overlap (legacy output):")
display(abg_vbg_pivot_df.head(15))
print("Symptom distribution by ABG/VBG/OTHER overlap (expanded output):")
display(gas_source_pivot_df.head(15))
print("Symptom distribution by ICD/Gas overlap:")
display(icd_gas_pivot_df.head(15))
print(f"Exported: {gas_source_output_path}")
print(f"Exported: {gas_source_expanded_output_path}")
print(f"Exported: {icd_gas_output_path}")
```

```
Symptom distribution by ABG/VBG overlap (legacy output):
```

| abg_vbg_overlap | ABG+VBG | ABG-only | VBG-only |
|---|---|---|---|
| symptom_group | | | |
| Diseases (patient-stated) | 4.1 | 7.3 | 4.1 |
| Injuries & adverse effects | 11.8 | 18.0 | 10.6 |
| Other | 6.1 | 6.5 | 6.9 |
| Symptom – Circulatory | 7.4 | 11.2 | 9.1 |
| Symptom – Digestive | 10.4 | 12.9 | 12.1 |
| Symptom – General | 4.3 | 4.1 | 5.4 |
| Symptom – Musculoskeletal | 2.1 | 2.9 | 1.8 |
| Symptom – Nervous | 11.3 | 9.5 | 12.8 |
| Symptom – Respiratory | 38.6 | 21.2 | 34.7 |
| Symptom – Skin/Hair/Nails | 2.0 | 3.4 | 1.8 |
| Uncodable/Unknown | 2.0 | 3.0 | 0.9 |

```
Symptom distribution by ABG/VBG/OTHER overlap (expanded output):
```

| gas_source_overlap<br>symptom_group | ABG+OTHER | ABG+VBG | ABG+VBG+OTHER | ABG-only | OTHER-o |
|---|---|---|---|---|---|
| Diseases (patient-stated) | 5.3 | 4.3 | 3.4 | 7.5 | 6.2 |
| Injuries & adverse effects | 17.7 | 12.6 | 9.0 | 18.0 | 10.5 |
| Other | 8.3 | 5.5 | 8.0 | 6.4 | 7.2 |
| Symptom – Circulatory | 9.4 | 7.2 | 8.1 | 11.3 | 8.0 |
| Symptom – Digestive | 15.4 | 10.6 | 9.8 | 12.8 | 14.9 |
| Symptom – General | 4.1 | 4.3 | 4.5 | 4.1 | 6.2 |
| Symptom – Musculoskeletal | 2.6 | 2.0 | 2.2 | 2.9 | 1.4 |
| Symptom – Nervous | 5.6 | 11.3 | 11.2 | 9.8 | 13.4 |
| Symptom – Respiratory | 22.6 | 38.2 | 40.0 | 21.1 | 27.9 |
| Symptom – Skin/Hair/Nails | 3.8 | 2.0 | 2.2 | 3.3 | 3.3 |
| Uncodable/Unknown | 5.3 | 2.1 | 1.6 | 2.9 | 1.1 |

```
Symptom distribution by ICD/Gas overlap:
```

| icd_gas_overlap<br>symptom_group | Gas-only | ICD+Gas | ICD-only |
|---|---|---|---|
| Diseases (patient-stated) | 5.9 | 2.9 | 3.5 |
| Injuries & adverse effects | 14.9 | 8.3 | 6.7 |
| Other | 6.8 | 5.2 | 7.4 |
| Symptom – Circulatory | 10.1 | 6.4 | 7.8 |
| Symptom – Digestive | 12.9 | 7.5 | 6.3 |
| Symptom – General | 4.8 | 3.6 | 5.9 |
| Symptom – Musculoskeletal | 2.5 | 1.1 | 2.4 |
| Symptom – Nervous | 11.0 | 11.5 | 10.4 |
| Symptom – Respiratory | 26.3 | 51.3 | 44.8 |
| Symptom – Skin/Hair/Nails | 2.7 | 1.3 | 2.8 |
| Uncodable/Unknown | 2.2 | 0.9 | 2.0 |

```
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Symptom_Composition_by_ABG_VBG_Overlap.xlsx
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Symptom_Composition_by_Gas_Source_Overlap.xlsx
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Symptom_Composition_by_ICD_Gas_Overlap.xlsx
```

## 1.9 ICD Diagnostic Performance (ICD as predictor)

```python
performance_targets = [
    ("pco2_threshold_any", "Gas any"),
    ("abg_hypercap_threshold", "ABG threshold"),
    ("vbg_hypercap_threshold", "VBG threshold"),
    ("other_hypercap_threshold", "PCO2 OTHER threshold"),
]

icd_positive = to_binary_flag(df["any_hypercap_icd"])
performance_rows = []
for target_col, target_label in performance_targets:
    target_positive = to_binary_flag(df[target_col])
    tp = int(((icd_positive == 1) & (target_positive == 1)).sum())
    fp = int(((icd_positive == 1) & (target_positive == 0)).sum())
    fn = int(((icd_positive == 0) & (target_positive == 1)).sum())
    tn = int(((icd_positive == 0) & (target_positive == 0)).sum())

    sens_denom = tp + fn
    ppv_denom = tp + fp
    sensitivity = float(tp / sens_denom) if sens_denom else np.nan
    ppv = float(tp / ppv_denom) if ppv_denom else np.nan
    sens_ci = (
        proportion_confint(tp, sens_denom, alpha=0.05, method="wilson")
        if sens_denom
        else (np.nan, np.nan)
    )
    ppv_ci = (
        proportion_confint(tp, ppv_denom, alpha=0.05, method="wilson")
        if ppv_denom
        else (np.nan, np.nan)
    )
    performance_rows.append(
        {
            "Target": target_label,
            "Target_Column": target_col,
            "TP": tp,
            "FP": fp,
            "FN": fn,
            "TN": tn,
            "Sensitivity": sensitivity,
            "Sensitivity_CI_Lower": sens_ci[0],
            "Sensitivity_CI_Upper": sens_ci[1],
                "PPV": ppv,
                "PPV_CI_Lower": ppv_ci[0],
                "PPV_CI_Upper": ppv_ci[1],
            }
        )

icd_performance_df = pd.DataFrame(performance_rows)
icd_performance_df[[
    "Sensitivity",
    "Sensitivity_CI_Lower",
    "Sensitivity_CI_Upper",
    "PPV",
    "PPV_CI_Lower",
    "PPV_CI_Upper",
]] = icd_performance_df[[
    "Sensitivity",
    "Sensitivity_CI_Lower",
    "Sensitivity_CI_Upper",
    "PPV",
    "PPV_CI_Lower",
    "PPV_CI_Upper",
]].clip(lower=0.0, upper=1.0)

icd_subset_output_path = OUTPUT_DIR / "ICD_Positive_Subset_Breakdown.xlsx"
icd_performance_output_path = OUTPUT_DIR / "ICD_vs_Gas_Performance.xlsx"
with pd.ExcelWriter(icd_subset_output_path, engine="openpyxl") as writer:
    icd_positive_breakdown.to_excel(writer, index=False,
 ↪  sheet_name="Gas_criteria")
    icd_positive_category_summary.reset_index().to_excel(
        writer, index=False, sheet_name="ICD_categories"
    )
icd_performance_df.to_excel(icd_performance_output_path, index=False)

display(icd_positive_breakdown)
display(icd_performance_df)
print(f"Exported: {icd_subset_output_path}")
print(f"Exported: {icd_performance_output_path}")
```

| | Definition | Count | Percent | Denominator_N |
|---|---|---|---|---|
| 0 | ABG threshold positive | 971 | 49.0 | 1983 |
| 1 | VBG threshold positive | 1300 | 65.6 | 1983 |
| 2 | PCO2 OTHER threshold positive | 330 | 16.6 | 1983 |

|   | Definition | Count | Percent | Denominator_N |
|---|---|---|---|---|
| 3 | Any gas threshold positive | 1523 | 76.8 | 1983 |

|   | Target | Target_Column | TP | FP | FN | TN | Sensitivity | Sensitivi |
|---|---|---|---|---|---|---|---|---|
| 0 | Gas any | pco2_threshold_any | 1523 | 460 | 9786 | 0 | 0.134672 | 0.128504 |
| 1 | ABG threshold | abg_hypercap_threshold | 971 | 1012 | 6299 | 3487 | 0.133563 | 0.125936 |
| 2 | VBG threshold | vbg_hypercap_threshold | 1300 | 683 | 4944 | 4842 | 0.208200 | 0.198310 |
| 3 | PCO2 OTHER threshold | other_hypercap_threshold | 330 | 1653 | 1020 | 8766 | 0.244444 | 0.222266 |

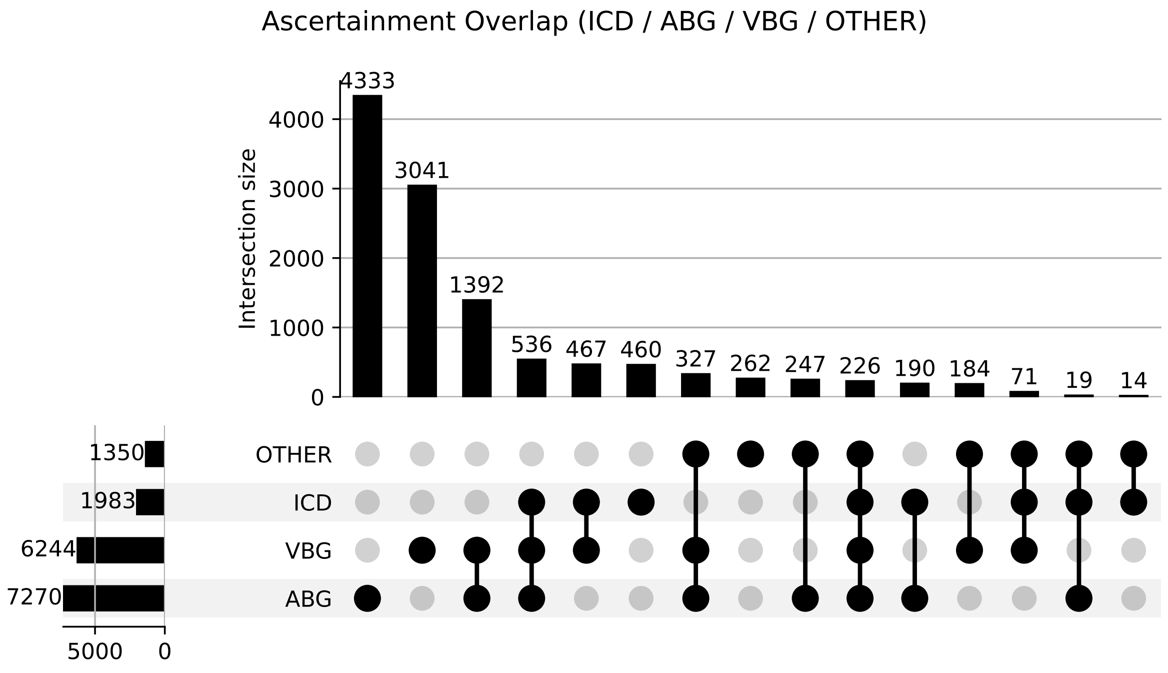
```
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/ICD_Positive_Subset_Breakdown.xlsx
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/ICD_vs_Gas_Performance.xlsx
```

### 1.10 Ascertainment overlap UpSet

```python
ascertainment_flags = pd.DataFrame(
    {
        "ICD": to_binary_flag(df["any_hypercap_icd"]).astype(bool),
        "ABG": to_binary_flag(df["abg_hypercap_threshold"]).astype(bool),
        "VBG": to_binary_flag(df["vbg_hypercap_threshold"]).astype(bool),
        "OTHER": to_binary_flag(df["other_hypercap_threshold"]).astype(bool),
    }
)

upset_series = from_indicators(ascertainment_flags.columns.tolist(),
 ↪  ascertainment_flags)
plt.figure(figsize=(12, 7))
upset_plot = UpSet(
    upset_series,
    subset_size="count",
    show_counts=True,
    sort_by="cardinality",
)
upset_plot.plot()
plt.suptitle("Ascertainment Overlap (ICD / ABG / VBG / OTHER)")
plt.tight_layout()

upset_output_path = OUTPUT_DIR / "Ascertainment_Overlap_UpSet.png"
```

```
plt.savefig(upset_output_path, dpi=300, bbox_inches="tight")
plt.show()

intersection_counts = (
    ascertainment_flags.groupby(["ICD", "ABG", "VBG", "OTHER"], dropna=False)
    .size()
    .reset_index(name="Count")
    .sort_values("Count", ascending=False)
    .reset_index(drop=True)
)
intersection_output_path = OUTPUT_DIR /
↪   "Ascertainment_Overlap_Intersections.xlsx"
intersection_counts.to_excel(intersection_output_path, index=False)

display(intersection_counts.head(20))
print(f"Exported: {upset_output_path}")
print(f"Exported: {intersection_output_path}")
```

```
<Figure size 3600x2100 with 0 Axes>
```



|  | ICD | ABG | VBG | OTHER | Count |
|---|---|---|---|---|---|
| 0 | False | True | False | False | 4333 |
| 1 | False | False | True | False | 3041 |
| 2 | False | True | True | False | 1392 |
| 3 | True | True | True | False | 536 |
| 4 | True | False | True | False | 467 |
| 5 | True | False | False | False | 460 |
| 6 | False | True | True | True | 327 |
| 7 | False | False | False | True | 262 |
| 8 | False | True | False | True | 247 |
| 9 | True | True | True | True | 226 |
| 10 | True | True | False | False | 190 |
| 11 | False | False | True | True | 184 |
| 12 | True | False | True | True | 71 |
| 13 | True | True | False | True | 19 |
| 14 | True | False | False | True | 14 |

```
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Ascertainment_Overlap_UpSet.png
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Ascertainment_Overlap_Intersections.xlsx
```

## 1.11 PDF-ready long tables

```
print(
    render_latex_longtable(
        hypercap_prevalence.reset_index(),
        caption=f"Hypercapnia prevalence summary (denominator = full cohort
↪   N={cohort_n:,}).",
        label="tab:prevalence_summary",
        index=False,
    )
)
print(
    render_latex_longtable(
        icd_category_summary.reset_index(),
        caption=f"ICD category composition (denominator = full cohort
↪   N={len(df):,}).",
        label="tab:icd_category",
        index=False,
    )
)
print(
    render_latex_longtable(
        inclusion_summary.reset_index(),
        caption=f"Inclusion source composition (denominator = full cohort
 ↪  N={len(df):,}).",
        label="tab:inclusion_type",
        index=False,
    )
)
print(
    render_latex_longtable(
        icd_positive_breakdown,
        caption=f"Among ICD-positive encounters, which gas criteria are also
 ↪  met (denominator = ICD-positive N={icd_positive_n:,}).",
        label="tab:icd_positive_breakdown",
        index=False,
    )
)
print(
    render_latex_longtable(
        icd_positive_category_summary.reset_index(),
        caption=f"Among ICD-positive encounters, ICD category distribution
 ↪  (denominator = ICD-positive N={icd_positive_n:,}).",
        label="tab:icd_positive_categories",
        index=False,
    )
)
print(
    render_latex_longtable(
        icd_performance_df,
        caption="ICD diagnostic performance vs gas-confirmed hypercapnia
 ↪  definitions (Wilson 95% CI).",
        label="tab:icd_performance",
        landscape=True,
        index=False,
    )
)
```

```
\begin{longtable}{llrrr}
\caption{Hypercapnia prevalence summary (denominator = full cohort N=11,769).} \label{tab:pre
\toprule
Definition & Column & Count & Denominator_N & Percent \\
\midrule
\endfirsthead
\caption[]{Hypercapnia prevalence summary (denominator = full cohort N=11,769).} \\
\toprule
Definition & Column & Count & Denominator_N & Percent \\
\midrule
\endhead
\midrule
\multicolumn{5}{r}{Continued on next page} \\
\midrule
\endfoot
\bottomrule
\endlastfoot
PCO2 threshold any source & pco2_threshold_any & 11309 & 11769 & 96.100000 \\
ABG hypercapnia threshold & abg_hypercap_threshold & 7270 & 11769 & 61.800000 \\
VBG hypercapnia threshold & vbg_hypercap_threshold & 6244 & 11769 & 53.100000 \\
Hypercapnic RF ICD (any) & any_hypercap_icd & 1983 & 11769 & 16.800000 \\
PCO2 OTHER threshold & other_hypercap_threshold & 1350 & 11769 & 11.500000 \\
\end{longtable}

\begin{longtable}{lrrr}
\caption{ICD category composition (denominator = full cohort N=11,769).} \label{tab:icd_categ
\toprule
ICD Category & Count & Percent & Denominator_N \\
\midrule
\endfirsthead
\caption[]{ICD category composition (denominator = full cohort N=11,769).} \\
\toprule
ICD Category & Count & Percent & Denominator_N \\
\midrule
\endhead
\midrule
\multicolumn{4}{r}{Continued on next page} \\
\midrule
\endfoot
\bottomrule
\endlastfoot
Other / None & 9786 & 83.200000 & 11769 \\
Acute RF with hypoxia & 793 & 6.700000 & 11769 \\
Obesity hypoventilation syndrome & 524 & 4.500000 & 11769 \\
Acute RF with hypoxia & hypercapnia & 386 & 3.300000 & 11769 \\
Respiratory failure, unspecified & 187 & 1.600000 & 11769 \\
Acute RF with hypercapnia & 93 & 0.800000 & 11769 \\
\end{longtable}

\begin{longtable}{lrrr}
\caption{Inclusion source composition (denominator = full cohort N=11,769).} \label{tab:inclu
\toprule
Inclusion Type & Count & Percent & Denominator_N \\
\midrule
\endfirsthead
\caption[]{Inclusion source composition (denominator = full cohort N=11,769).} \\
\toprule
Inclusion Type & Count & Percent & Denominator_N \\
\midrule
\endhead
\midrule
\multicolumn{4}{r}{Continued on next page} \\
\midrule
\endfoot
\bottomrule
\endlastfoot
Gas_only & 9786 & 83.200000 & 11769 \\
Both & 1523 & 12.900000 & 11769 \\
ICD_only & 460 & 3.900000 & 11769 \\
\end{longtable}

\begin{longtable}{lrrr}
\caption{Among ICD-positive encounters, which gas criteria are also met (denominator = ICD-
positive N=1,983).} \label{tab:icd_positive_breakdown} \\
\toprule
Definition & Count & Percent & Denominator_N \\
\midrule
\endfirsthead
\caption[]{Among ICD-positive encounters, which gas criteria are also met (denominator = ICD-
positive N=1,983).} \\
\toprule
Definition & Count & Percent & Denominator_N \\
\midrule
\endhead
\midrule
\multicolumn{4}{r}{Continued on next page} \\
\midrule
\endfoot
\bottomrule
\endlastfoot
```

```
ABG threshold positive & 971 & 49.000000 & 1983 \\
VBG threshold positive & 1300 & 65.600000 & 1983 \\
PCO2 OTHER threshold positive & 330 & 16.600000 & 1983 \\
Any gas threshold positive & 1523 & 76.800000 & 1983 \\
\end{longtable}

\begin{longtable}{lrrr}
\caption{Among ICD-positive encounters, ICD category distribution (denominator = ICD-
positive N=1,983).} \label{tab:icd_positive_categories} \\
\toprule
ICD Category (ICD-positive subset) & Count & Percent & Denominator_N \\
\midrule
\endfirsthead
\caption[]{Among ICD-positive encounters, ICD category distribution (denominator = ICD-
positive N=1,983).} \\
\toprule
ICD Category (ICD-positive subset) & Count & Percent & Denominator_N \\
\midrule
\endhead
\midrule
\multicolumn{4}{r}{Continued on next page} \\
\midrule
\endfoot
\bottomrule
\endlastfoot
Acute RF with hypoxia & 793 & 40.000000 & 1983 \\
Obesity hypoventilation syndrome & 524 & 26.400000 & 1983 \\
Acute RF with hypoxia & hypercapnia & 386 & 19.500000 & 1983 \\
Respiratory failure, unspecified & 187 & 9.400000 & 1983 \\
Acute RF with hypercapnia & 93 & 4.700000 & 1983 \\
\end{longtable}

\begin{landscape}\n\begin{longtable}{llrrrrrrrrr}
\caption{ICD diagnostic performance vs gas-confirmed hypercapnia definitions (Wilson 95% CI)
\toprule
Target & Target_Column & TP & FP & FN & TN & Sensitivity & Sensitivity_CI_Lower & Sensitivity
\midrule
\endfirsthead
\caption[]{ICD diagnostic performance vs gas-confirmed hypercapnia definitions (Wilson 95% CI
\toprule
Target & Target_Column & TP & FP & FN & TN & Sensitivity & Sensitivity_CI_Lower & Sensitivity
\midrule
\endhead
```

```
\midrule
\multicolumn{12}{r}{Continued on next page} \\
\midrule
\endfoot
\bottomrule
\endlastfoot
Gas any & pco2_threshold_any & 1523 & 460 & 9786 & 0 & 0.134672 & 0.128504 & 0.141087 & 0.768
ABG threshold & abg_hypercap_threshold & 971 & 1012 & 6299 & 3487 & 0.133563 & 0.125936 & 0.1
VBG threshold & vbg_hypercap_threshold & 1300 & 683 & 4944 & 4842 & 0.208200 & 0.198310 & 0.2
PCO2 OTHER threshold & other_hypercap_threshold & 330 & 1653 & 1020 & 8766 & 0.244444 & 0.222
\end{longtable}
\n\end{landscape}\n
```

## 1.12 Association Model

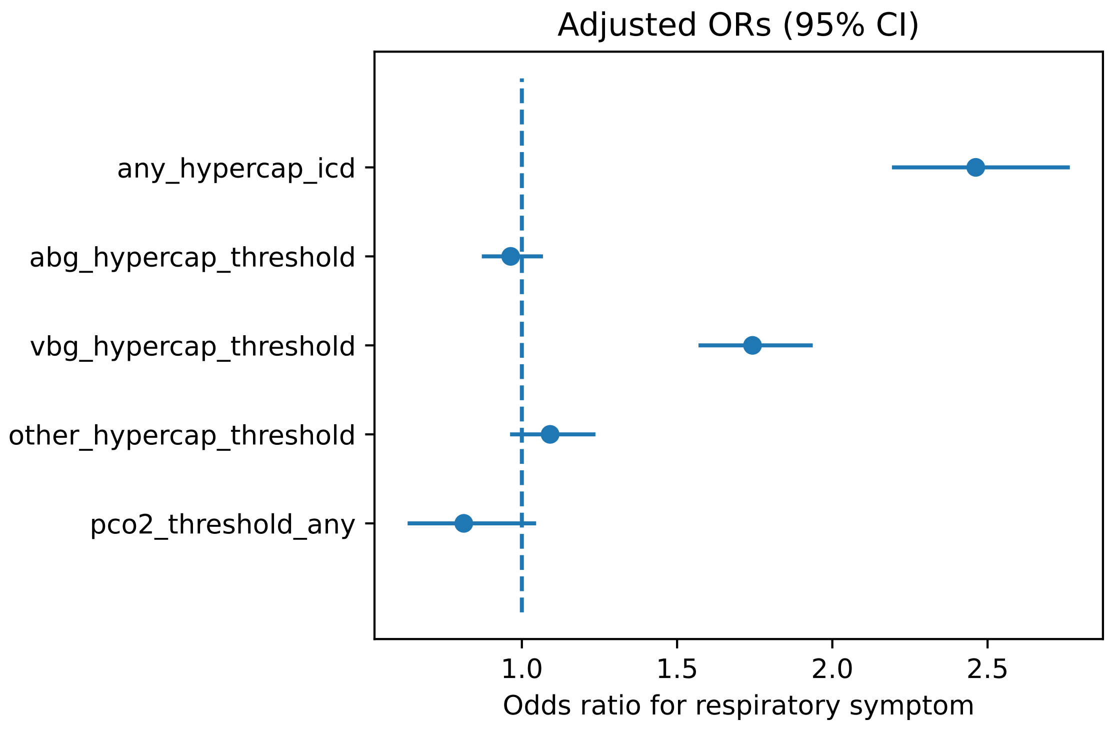
Logistic regression of respiratory symptom flag on hypercapnia definitions.

```python
model_df = df.dropna(subset=[SYMPTOM_COL]).copy()
model_df["is_respiratory"] = model_df[SYMPTOM_COL].astype(str).str.contains(
    r"\brespir", case=False, na=False
).astype(int)

design_matrix = sm.add_constant(model_df[HYPERCAP_CRITERIA],
 ↪ has_constant="add")
outcome = model_df["is_respiratory"]
logit_result = sm.Logit(outcome, design_matrix,
 ↪ missing="drop").fit(disp=False)

or_table = pd.DataFrame(
    {
        "OR": np.exp(logit_result.params),
        "CI_lo": np.exp(logit_result.conf_int()[0]),
        "CI_hi": np.exp(logit_result.conf_int()[1]),
        "p": logit_result.pvalues,
    }
).round(3)

display(or_table.loc[HYPERCAP_CRITERIA])
```

| | OR | CI_lo | CI_hi | p |
|---|---|---|---|---|
| any_hypercap_icd | 2.462 | 2.192 | 2.765 | 0.000 |
| abg_hypercap_threshold | 0.964 | 0.871 | 1.068 | 0.484 |

|  | OR | CI_lo | CI_hi | p |
|---|---|---|---|---|
| vbg_hypercap_threshold | 1.743 | 1.569 | 1.937 | 0.000 |
| other_hypercap_threshold | 1.091 | 0.962 | 1.237 | 0.175 |
| pco2_threshold_any | 0.813 | 0.632 | 1.046 | 0.107 |

```python
or_plot_df = or_table.loc[HYPERCAP_CRITERIA]
y_positions = np.arange(len(or_plot_df))[::-1]

plt.figure(figsize=(6, 4))
plt.hlines(y=y_positions, xmin=or_plot_df["CI_lo"], xmax=or_plot_df["CI_hi"],
 ↪  linewidth=1.5)
plt.plot(or_plot_df["OR"], y_positions, "o")
plt.vlines(1, ymin=-1, ymax=len(or_plot_df), linestyles="dashed")
plt.yticks(y_positions, or_plot_df.index)
plt.xlabel("Odds ratio for respiratory symptom")
plt.title("Adjusted ORs (95% CI)")
plt.tight_layout()
plt.show()
```



## 1.13 Export Verification

```
expected_outputs = [
    definition_output_path,
    pivot_output_path,
    gas_source_output_path,
    gas_source_expanded_output_path,
    icd_gas_output_path,
    icd_subset_output_path,
    icd_performance_output_path,
    upset_output_path,
    intersection_output_path,
]

verification_rows = []
for output_path in expected_outputs:
    verification_rows.append(
        {
            "path": str(output_path),
            "exists": output_path.exists(),
            "size_bytes": output_path.stat().st_size if output_path.exists()
             ↪  else 0,
        }
    )

output_verification = pd.DataFrame(verification_rows)
display(output_verification)
```

| | path | exists | size_bytes |
|---|---|---|---|
| 0 | /Users/blocke/Box Sync/Residency Personal File... | True | 7363 |
| 1 | /Users/blocke/Box Sync/Residency Personal File... | True | 5557 |
| 2 | /Users/blocke/Box Sync/Residency Personal File... | True | 5367 |
| 3 | /Users/blocke/Box Sync/Residency Personal File... | True | 5612 |
| 4 | /Users/blocke/Box Sync/Residency Personal File... | True | 5381 |
| 5 | /Users/blocke/Box Sync/Residency Personal File... | True | 5856 |
| 6 | /Users/blocke/Box Sync/Residency Personal File... | True | 5571 |
| 7 | /Users/blocke/Box Sync/Residency Personal File... | True | 146181 |
| 8 | /Users/blocke/Box Sync/Residency Personal File... | True | 5284 |

```
from datetime import datetime
```

```
prior_runs_dir = WORK_DIR / "MIMIC tabular data" / "prior runs"
prior_runs_dir.mkdir(parents=True, exist_ok=True)
run_date = datetime.now().strftime("%Y-%m-%d")

analysis_manifest = collect_run_manifest(
    WORK_DIR,
    run_id=f"analysis_{datetime.now().strftime('%Y%m%d_%H%M%S')}",
)
analysis_manifest["stage"] = "analysis"
analysis_manifest["analysis_input_path"] = str(ANALYSIS_INPUT_PATH)
analysis_manifest["outputs"] = {
    "definition_output_path": str(definition_output_path),
    "pivot_output_path": str(pivot_output_path),
    "abg_vbg_overlap_output_path": str(gas_source_output_path),
    "gas_source_overlap_output_path": str(gas_source_expanded_output_path),
    "icd_gas_overlap_output_path": str(icd_gas_output_path),
    "icd_subset_output_path": str(icd_subset_output_path),
    "icd_performance_output_path": str(icd_performance_output_path),
    "upset_output_path": str(upset_output_path),
    "intersection_output_path": str(intersection_output_path),
}
analysis_manifest["output_verification"] = verification_rows
analysis_manifest_path = prior_runs_dir / f"{run_date}
 ↪  analysis_run_manifest.json"
analysis_manifest_path.write_text(json.dumps(analysis_manifest, indent=2))
print(f"Wrote: {analysis_manifest_path}")
```

```
Wrote: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Project
CC-NLP/MIMIC tabular data/prior runs/2026-02-20 analysis_run_manifest.json
```