# Hypercap CC NLP Analysis

## Table of contents


**1 Workbook for MIMIC Hypercapnia Presenting Chief Concern Analysis 1**

1.1 Environment Gate . . . 1
1.2 Load Data . . . 2
1.3 Descriptive Checks . . . 8
1.4 ED Vitals Data Quality (cleaned-column preference) . . . 10
1.5 Cohort Blood-Gas QC Snapshot . . . 12
1.6 ICD And Inclusion Categories . . . 14
1.7 Symptom Composition By Hypercapnia Definition . . . 17
1.8 Symptom Distribution By Ascertainment Overlap . . . 22
1.9 ICD Diagnostic Performance (ICD as predictor) . . . 26
1.10 Ascertainment overlap UpSet . . . 28
1.11 PDF-ready long tables . . . 30
1.12 Association Model . . . 35
1.13 Export Verification . . . 37


# 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.

```
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`.

```
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))
```

```
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 307 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)
```

| gender | Count | Percent |
|---|---|---|
| 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.

```
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",
 ↪  {})
    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": "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 | 0.362484 |
| 2 | POC OTHER quarantined hadm count | 0 |
| 3 | POC OTHER leakage into threshold | 0 |
| 4 | first_gas_without_pco2_anchor_n | 0 |
| 5 | 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)
```

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

| symptom_group | No | Yes | Percent_yes |
|---|---|---|---|
| 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")
```

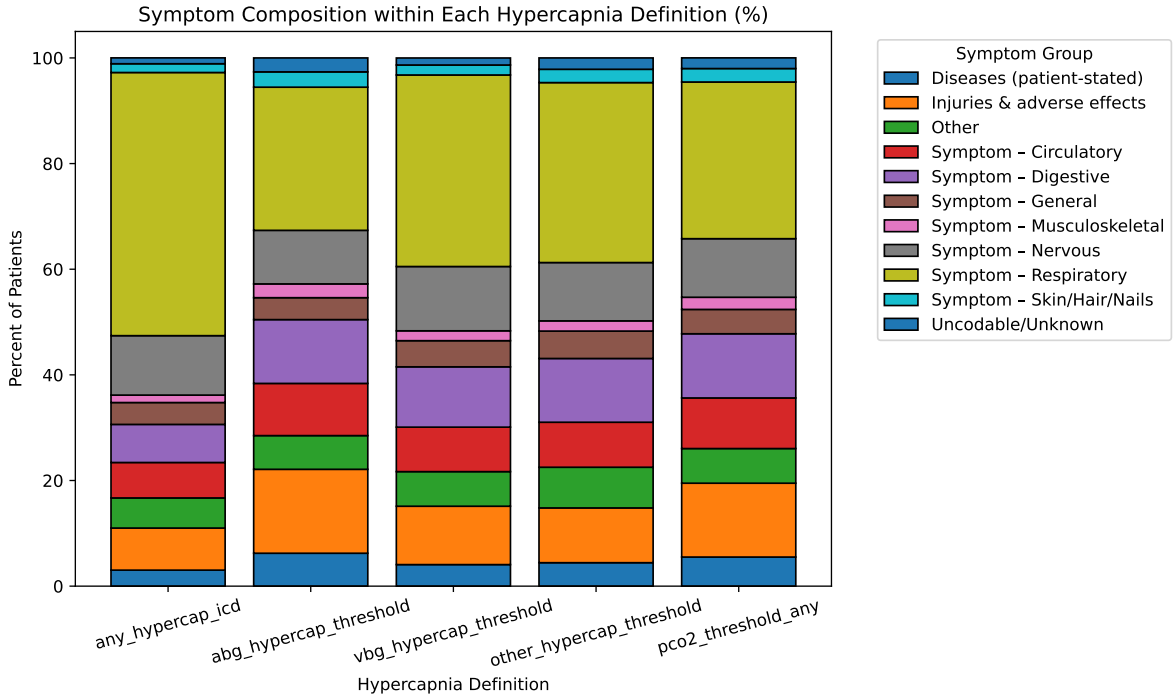
```
definition_counts_df["Percent"] = definition_counts_df["Count"] /
 ↪  definition_counts_df["Total"] * 100

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 |

| | Hypercapnia_Definition | symptom_group | Count | Total | Percent | CI_lower | CI_uppe |
|---|---|---|---|---|---|---|---|
| 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 |

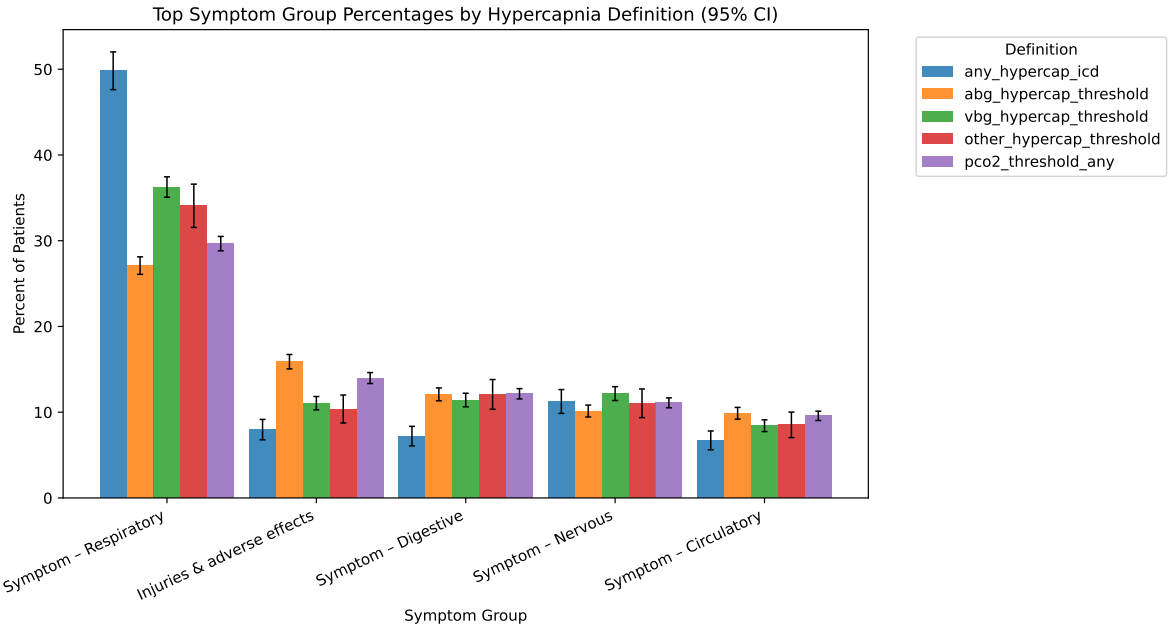
```
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Symptom_Composition_by_Hypercapnia_Definition.xlsx
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/Symptom_Composition_Pivot_ChartReady.xlsx
```

```
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<br>symptom_group | ABG+VBG | ABG-only | VBG-only |
|---|---|---|---|
| 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)

```
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 |

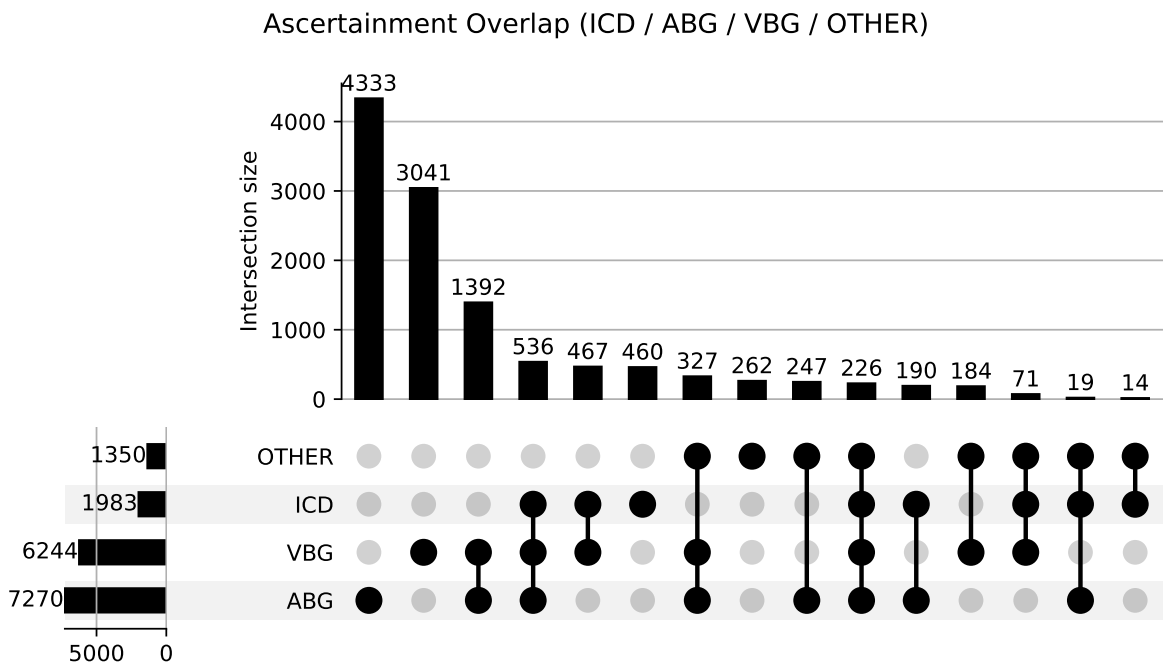
```
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/ICD_Positive_Subset_Breakdown.xlsx
Exported: /Users/blocke/Box Sync/Residency Personal Files/Scholarly Work/Locke Research Proje
CC-NLP/ICD_vs_Gas_Performance.xlsx
```

### 1.10 Ascertainment overlap UpSet

```
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:pr
\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}{llrrrrrrrrrr}
\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

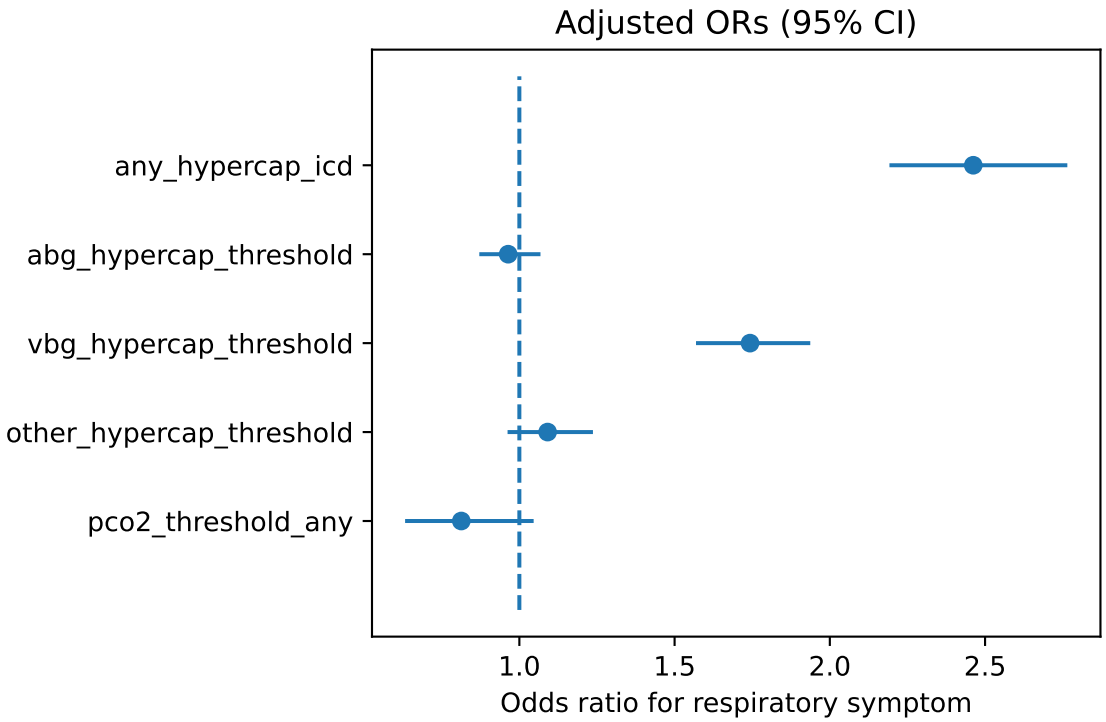
Logistic regression of respiratory symptom flag on hypercapnia definitions.

```
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 |

```
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 | 5283 |

```
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 Projects
CC-NLP/MIMIC tabular data/prior runs/2026-02-18 analysis_run_manifest.json
```