Contents

OH Stats: Complete Statistical Analysis Guide

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1. Introduction

What is oh_stats?

`oh_stats` is a statistical analysis package built on top of `oh_parser`. While `oh_parser` handles the extraction and loading of Occupational Health (OH) profile data from JSON files, `oh_stats` provides the statistical inference layer for analyzing this data.

Why was it built?

The OH profile data has specific characteristics that require specialized handling:

1. **Repeated measures**: Each subject contributes multiple observations across days
2. **Hierarchical structure**: Observations nested within subjects
3. **Multiple outcomes**: Many EMG metrics measured simultaneously
4. **Laterality**: Separate measurements for left and right sides
5. **Non-normal distributions**: Many outcomes are skewed or bounded

Standard statistical approaches (t-tests, ANOVA) are inappropriate because they: - Ignore the correlation structure within subjects - Inflate Type I error rates - Lose power by ignoring the design

Key Design Principles

1. **Registry-driven**: Each outcome is registered with its measurement type (continuous, ordinal, proportion, count), guiding model selection

2. **Multilevel inference**: Linear Mixed Models (LMM) account for subject-level clustering
3. **Two-layer multiplicity control**: FDR across outcomes, Holm within outcomes
4. **Diagnostic-first**: Check assumptions before trusting results
5. **Function-based architecture**: All data containers use TypedDicts with factory functions for code homogeneity

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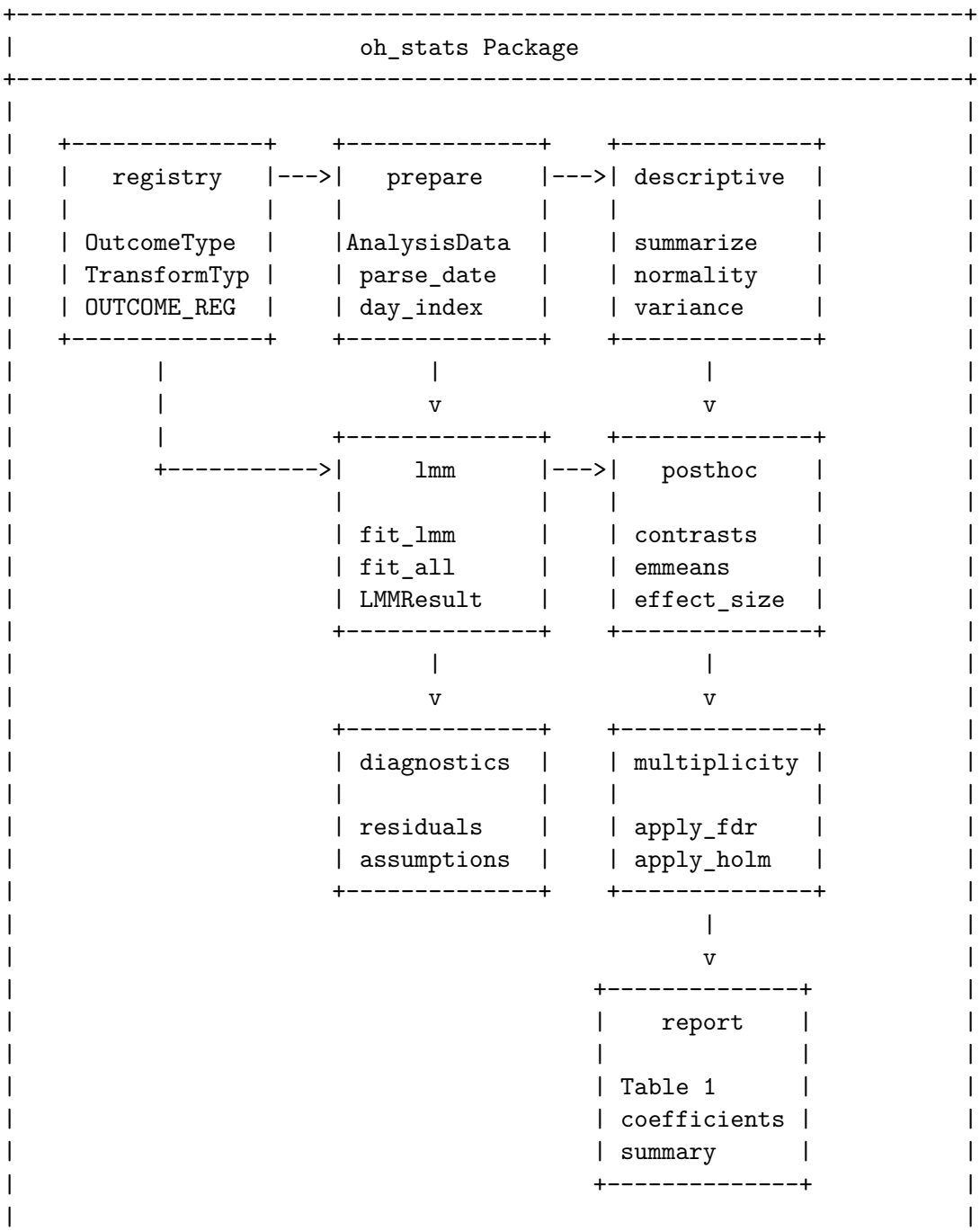
2. Architecture Overview



```
+---------------------------------------------------------------------+
```

Module Dependencies

```
registry.py      <-- No dependencies (foundational)
    |
    v
prepare.py       <-- Uses registry for outcome metadata
    |
    v
descriptive.py   <-- Uses prepare output (AnalysisDataset)
    |
    v
lmm.py           <-- Uses prepare output + registry for transforms
    |
    v
posthoc.py       <-- Uses LMM results
    |
    v
multiplicity.py  <-- Uses p-values from any source
    |
    v
diagnostics.py   <-- Uses LMM results
    |
    v
report.py        <-- Uses all of the above
```

Function-Based Architecture

The `oh_stats` package uses a **function-based architecture** with TypedDicts for all data containers. This design:

- Maintains code homogeneity with the rest of the `oh_parser` project
- Provides type hints without OOP overhead
- Uses factory functions (`create_*()`) for data container construction
- Uses helper functions instead of instance methods

Example Pattern:

```python
# TypedDict defines the structure
class LMMResult(TypedDict):
    outcome: str
    converged: bool
    # ... other fields

# Factory function creates instances
def create_lmm_result(outcome: str, converged: bool, ...) -> LMMResult:
    return {
        'outcome': outcome,
        'converged': converged,
```

```
        # ... other fields
    }

# Helper functions operate on the data
def summarize_lmm_result(result: LMMResult) -> str:
    return f"Model for {result['outcome']}: converged={result['converged']}"
```

---

3. Data Flow Pipeline

Standard Analysis Workflow

```
# Step 1: Load OH profiles (oh_parser)
from oh_parser import load_profiles
profiles = load_profiles("/path/to/profiles")

# Step 2: Prepare data for analysis (oh_stats)
from oh_stats import prepare_daily_emg
ds = prepare_daily_emg(profiles, side="both")

# Step 3: Coverage & missingness report (ALWAYS DO THIS FIRST)
from oh_stats import summarize_outcomes, check_variance, missingness_report
coverage = summarize_outcomes(ds)  # Days per subject, sensors present
variance = check_variance(ds)       # Flag degenerate metrics
missing = missingness_report(ds)    # % missing per outcome

# Step 4: Descriptive statistics
from oh_stats import check_normality
summary = summarize_outcomes(ds, ["EMG_intensity.mean_percent_mvc"])
normality = check_normality(ds, ["EMG_intensity.mean_percent_mvc"])

# Step 5: Fit models
from oh_stats import fit_lmm, fit_all_outcomes
result = fit_lmm(ds, "EMG_intensity.mean_percent_mvc")
all_results = fit_all_outcomes(ds)

# Step 6: Multiple testing correction
from oh_stats import apply_fdr
fdr_results = apply_fdr(all_results)

# Step 7: Post-hoc contrasts (if needed)
from oh_stats import pairwise_contrasts
contrasts = pairwise_contrasts(result, "day_index", ds)

# Step 8: Diagnostics
from oh_stats import residual_diagnostics
diag = residual_diagnostics(result)
```

```python
# Step 9: Generate reports
from oh_stats import descriptive_table, results_summary
table1 = descriptive_table(ds)
summary_df = results_summary(all_results, fdr_results)
```

Critical Pre-Modeling Step: Coverage Report

Before any modeling, always generate a coverage/missingness report. This is the difference between "statistics" and "statistics you can defend in peer review."

```python
# What to check BEFORE modeling:
from oh_stats import summarize_outcomes, check_variance, missingness_report

# 1. Coverage: Days per subject, total observations
print(f"Subjects: {ds['data']['subject_id'].nunique()}")
print(f"Total observations: {len(ds['data'])}")
print(f"Days per subject: {ds['data'].groupby('subject_id')['day_index'].max().describe()}")

# 2. Missingness: % missing per outcome
miss = missingness_report(ds)
high_missing = miss[miss['pct_missing'] > 10]
if len(high_missing) > 0:
    print(f"[WARNING] High missingness (>10%): {high_missing['outcome'].tolist()}")

# 3. Degenerate metrics: Near-zero variance
var = check_variance(ds)
degenerate = var[var['is_degenerate']]['outcome'].tolist()
if degenerate:
    print(f"[EXCLUDE] Exclude from modeling: {degenerate}")
```

The AnalysisDataset Container

The `AnalysisDataset` TypedDict is the central data container:

```python
class AnalysisDataset(TypedDict):
    """Container for analysis-ready data."""
    data: pd.DataFrame          # The actual data
    outcome_vars: List[str]     # Column names of outcomes
    id_var: str                 # Subject identifier column
    time_var: str               # Time variable column
    grouping_vars: List[str]    # Additional grouping (e.g., ["side"])
    sensor: str                 # "emg" or "questionnaire"
    level: str                  # "daily", "session", etc.
    metadata: Dict[str, Any]    # Additional info

# Create using factory function:
ds = create_analysis_dataset(
    data=df,
```

```
    outcome_vars=["EMG_intensity.mean_percent_mvc"],
    id_var="subject_id",
    time_var="day_index",
    grouping_vars=["side"],
    sensor="emg",
    level="daily"
)

# Access using dictionary syntax:
print(f"Subjects: {ds['data']['subject_id'].nunique()}")
print(f"Outcomes: {ds['outcome_vars']}")

# Helper functions for common operations:
description = describe_dataset(ds)  # Get summary
subset = subset_dataset(ds, outcomes=["EMG_intensity.mean_percent_mvc"])
```

Why this design? - Encapsulates all information needed for downstream analysis - Self-documenting: you know what variables are outcomes vs. metadata - Enables consistent handling across all analysis functions - Dictionary access is explicit and homogeneous with rest of project

---

4. Module Reference

4.1 Registry (registry.py)

Purpose Maps each outcome variable to its statistical properties, enabling automatic model selection and transform recommendations.

```
class OutcomeType(Enum):
    """Classification of outcome variable measurement type."""
    CONTINUOUS = "continuous"   # Unbounded numeric (e.g., %MVC)
    ORDINAL = "ordinal"         # Ordered categories (e.g., pain 0-10)
    PROPORTION = "proportion"   # Bounded [0, 1] (e.g., rest_percent)
    COUNT = "count"             # Non-negative integers (e.g., gap_count)
    BINARY = "binary"           # 0/1 outcomes
    UNKNOWN = "unknown"         # Not yet classified

class TransformType(Enum):
    """Variance-stabilizing transformations."""
    NONE = "none"               # No transformation
    LOG = "log"                 # log(x), requires x > 0
    LOG1P = "log1p"             # log(1 + x), for x >= 0 with zeros
    SQRT = "sqrt"               # sqrt(x), for x >= 0
    LOGIT = "logit"             # log(x/(1-x)), for proportions (PREFERRED)
    ARCSINE = "arcsine"         # [!] DEPRECATED - see note below

class AnalysisLevel(Enum):
```

```
    """Level of data aggregation."""
    DAILY = "daily"
    SESSION = "session"
    SUBJECT = "subject"
```

Core Types (Enums)

> **[!] ARCSINE Transform Deprecation Notice**
>
> The arcsine-square-root transform (`arcsin(sqrt(x))`) for proportions is **widely discouraged** in modern statistical practice. It is less interpretable than logit and often unnecessary when you can model the outcome distribution directly (e.g., beta regression).
>
> See: Warton & Hui (2011) "The arcsine is asinine" - *Ecology* 92(1):3-10
>
> **Recommendation**: Use `LOGIT` for proportions. `ARCSINE` is retained only for legacy compatibility.

```
class OutcomeInfo(TypedDict, total=False):
    """Metadata for a registered outcome variable."""
    name: str                                  # Variable name (required)
    outcome_type: OutcomeType                  # Measurement type (required)
    transform: TransformType                   # Recommended transform
    level: str                                 # Aggregation level
    is_primary: bool                           # Primary endpoint?
    description: str                           # Human-readable description
    min_value: Optional[float]                 # Theoretical minimum
    max_value: Optional[float]                 # Theoretical maximum
    unit: str                                  # Measurement unit

# Create using factory function:
info = create_outcome_info(
    name="EMG_intensity.mean_percent_mvc",
    outcome_type=OutcomeType.CONTINUOUS,
    transform=TransformType.NONE,
    level="daily",
    is_primary=True,
    description="Mean muscle activation as percentage of MVC",
    unit="%MVC"
)
```

The OutcomeInfo TypedDict

Pre-registered Outcomes The following EMG outcomes are pre-registered:

Outcome	Type	Transform	Description	Notes
`EMG_intensity.mean_percent_mvc`	CONTINUOUS	NONE	Mean muscle activation	Primary

Outcome	Type	Transform	Description	Notes
`EMG_intensity.max_percent_mvc`	CONTINUOUS	NONE	Peak activation	
`EMG_intensity.iemg_percent_seconds`	CONTINUOUS	LOG	Integrated EMG	Right-skewed
`EMG_apdf.active.p50`	CONTINUOUS	NONE	Median active amplitude	Primary
`EMG_rest_recovery.rest_percent`	PROPORTION	LOGIT	Time at rest	Bounded [0,1]
`EMG_rest_recovery.gap_count`	COUNT	LOG1P	Number of rest periods	[!] Fallback approach*
...	...	...	...	

COUNT outcomes: The `LOG1P` transform + Gaussian LMM is a **pragmatic fallback, not the principled solution. True count data should use Poisson/Negative Binomial GLMMs. This is acceptable for exploratory analysis but consider proper count models for publication.

Primary vs. Secondary Outcomes: Multiplicity Strategy The `is_primary` field in the registry enables **differentiated multiplicity control**:

Outcome Class	Correction Method	Rationale
Primary (confirmatory)	FWER (Holm-Bonferroni)	Strong control for main hypotheses
Secondary (exploratory)	FDR (Benjamini-Hochberg)	Discovery-oriented, accepts some false positives

Enforcement Pattern:

```
from oh_stats import list_outcomes, apply_fdr, apply_holm

# Get outcomes by class
primary = list_outcomes(is_primary=True)
secondary = list_outcomes(is_primary=False)

# Fit models
primary_results = fit_all_outcomes(ds, outcomes=primary)
secondary_results = fit_all_outcomes(ds, outcomes=secondary)

# Apply appropriate correction
primary_corrected = apply_holm(primary_results)      # FWER for primaries
secondary_corrected = apply_fdr(secondary_results)   # FDR for secondaries
```

Default Report Behavior:

- `results_summary()` displays primary outcomes first
- Primary outcomes are flagged in output tables
- This matches how occupational health papers are typically structured and defended

Recommendation: Pre-specify 2-4 primary outcomes based on research questions. Everything else is exploratory. This distinction should be documented in your analysis plan BEFORE seeing results.

```
from oh_stats import get_outcome_info, register_outcome, OutcomeType, TransformType

# Get info for existing outcome
info = get_outcome_info("EMG_intensity.mean_percent_mvc")
print(f"Type: {info['outcome_type']}")  # CONTINUOUS
print(f"Transform: {info['transform']}")  # NONE

# Register a new outcome
register_outcome(
    name="my_custom_metric",
    outcome_type=OutcomeType.CONTINUOUS,
    transform=TransformType.LOG,
    level="daily",
    description="Custom metric from EMG processing"
)

# List all outcomes
from oh_stats import list_outcomes
outcomes = list_outcomes(outcome_type=OutcomeType.CONTINUOUS)
```

Usage

Why a Registry?

1. **Automatic model family dispatch**: Maps outcome types to appropriate models (see table below)
2. **Transform recommendations**: Skewed data -> LOG transform
3. **Validation**: Catch misspecified analyses early
4. **Documentation**: Centralized knowledge about each variable

Model Family Dispatch Table

Outcome Type	Preferred Model	Fallback (Current)	Notes
CONTINUOUS	Gaussian LMM	[OK] Implemented	`statsmodels.MixedLM`
ORDINAL	Ordered logistic/probit	[STUB] (future: Bayesian)	Requires specialized tooling
PROPORTION	Beta mixed model *or* Logit+LMM	[OK] Logit transform + Gaussian LMM	NOT logistic regression (that's for binary)

Outcome Type	Preferred Model	Fallback (Current)	Notes
COUNT	Poisson/Negative Binomial GLMM	[STUB] LOG1P + Gaussian LMM	NB if overdispersed
BINARY	Logistic GLMM	[STUB] Stub	True logistic regression

> [!] **Important Distinction**: "Logistic regression" is for **binary** (0/1) outcomes only. For **proportions** (values in 0-1), we use the **logit transform** on the continuous outcome, then fit a **Gaussian** LMM on the transformed scale. This is statistically defensible and often works well in practice.

4.2 Data Preparation (prepare.py)

Purpose Transform raw `oh_parser` output into analysis-ready `AnalysisDataset` dictionaries.

Main Functions

```
def prepare_daily_emg(
    profiles: Dict[str, dict],
    side: str = "both",           # "left", "right", "both", "average"
    add_day_index: bool = True,   # Add ordinal day within subject
    add_weekday: bool = True,     # Add day name
) -> AnalysisDataset:
    """
    Prepare EMG data at the daily aggregation level.

    Parameters
    ----------
    profiles : dict
        Output from oh_parser.load_profiles()
    side : str
        How to handle laterality:
        - "left": Only left side data
        - "right": Only right side data
        - "both": Keep as separate rows (doubles observations)
        - "average": Average left and right into single value
    add_day_index : bool
        Add within-subject ordinal day (1, 2, 3, ...)
    add_weekday : bool
        Add day-of-week name column

    Returns
```

```
    -------
    AnalysisDataset
        Ready for analysis with all EMG outcomes (TypedDict)
    """
```

`prepare_daily_emg()` Side Handling Strategies:

Strategy	Effect	When to Use
`"both"`	Left and right as separate rows	When laterality is of interest
`"average"`	Mean of left/right	When laterality is nuisance
`"left"` / `"right"`	Keep only one side	When sides have different meaning

> **[!] Statistical Implication of `side="both"`**
>
> When keeping both sides as separate rows, left and right observations from the **same subject-day are NOT independent**. The current model with only a subject-level random intercept doesn't fully account for this within-day correlation.
>
> **Options to handle this properly:** 1. **Add subject-day clustering** (more complex model): `(1|subject_id/day_index)` 2. **Use `side="average"`** if laterality is not the research question 3. **Analyze each side separately** as a sensitivity check
>
> For the current EMG analysis where `side` is a fixed effect of interest, the subject random intercept is a reasonable approximation.

Multi-Channel Correlation: The Subject-Day Clustering Pattern The side handling issue is a specific case of a **general pattern**: any sensor with multiple channels per day (left/right EMG, multi-axis accelerometer, multiple device placements) creates correlated observations that share a subject-day context.

Documented Variance Structure Options:

Model Complexity	Formula	Use When
Simple (current)	`(1|subject_id)`	Single channel per day, or channels averaged
Intermediate	`(1|subject_id) + (1|subject_day_id)`	Multiple channels, day-level correlation matters
Full nested	`(1|subject_id/day_index/channel)`	Complex multi-level structure

Implementation Pattern:

```
# Create subject-day identifier for intermediate clustering
ds['data']['subject_day_id'] = (
    ds['data']['subject_id'].astype(str) + '_' +
    ds['data']['day_index'].astype(str)
```

```
)

# Fit with subject-day random effect (future enhancement)
result = fit_lmm(
    ds, outcome,
    random_intercept="subject_id",
    nested_random="subject_day_id",  # Planned feature
)
```

> **Current Status**: v0.2.0 supports subject-level random intercept only. Subject-day clustering is documented here for (1) methodological transparency and (2) preventing misuse when multi-channel data is involved. Full nested random effects are planned for v0.3.0.

Example:

```
# Keep both sides (320 obs = 160 days × 2 sides)
ds_both = prepare_daily_emg(profiles, side="both")
print(ds_both['data'].shape)  # (320, 27)

# Average sides (160 obs = 160 days)
ds_avg = prepare_daily_emg(profiles, side="average")
print(ds_avg['data'].shape)  # (160, 25)
```

`create_analysis_dataset()` Factory function for creating AnalysisDataset containers:

```
def create_analysis_dataset(
    data: pd.DataFrame,
    outcome_vars: List[str],
    id_var: str = "subject_id",
    time_var: str = "day_index",
    grouping_vars: Optional[List[str]] = None,
    sensor: str = "emg",
    level: str = "daily",
    metadata: Optional[Dict[str, Any]] = None
) -> AnalysisDataset:
    """Create an AnalysisDataset TypedDict."""
```

```
# Describe a dataset
def describe_dataset(ds: AnalysisDataset) -> Dict[str, Any]:
    """Get summary statistics for an AnalysisDataset."""

# Subset a dataset
def subset_dataset(
    ds: AnalysisDataset,
    outcomes: Optional[List[str]] = None,
    subjects: Optional[List[str]] = None,
```

```
    time_range: Optional[Tuple[int, int]] = None
) -> AnalysisDataset:
    """Subset an AnalysisDataset by outcomes, subjects, or time range."""

# Validate a dataset
def validate_dataset(ds: AnalysisDataset) -> List[str]:
    """Validate an AnalysisDataset structure. Returns list of warnings."""
```

Helper Functions

Day Index Computation Within each subject, days are assigned ordinal indices:

```
Subject 103:
  2025-10-13 -> day_index = 1
  2025-10-14 -> day_index = 2
  2025-10-15 -> day_index = 3
  ...

Subject 104:
  2025-09-22 -> day_index = 1  (different calendar date!)
  2025-09-23 -> day_index = 2
  ...
```

Why ordinal, not calendar day? - Subjects start on different dates - Interest is in "day 1 vs day 5 of monitoring," not "October 13 vs October 17" - Makes between-subject comparison meaningful

---

4.3 Descriptive Statistics (descriptive.py)

Purpose Summarize data and check assumptions before modeling.

```
class NormalityResult(TypedDict):
    """Result of normality testing for an outcome."""
    outcome: str
    n: int
    n_missing: int
    skewness: float
    kurtosis: float
    shapiro_stat: Optional[float]
    shapiro_p: Optional[float]
    is_normal: bool
    recommended_transform: str

class VarianceCheckResult(TypedDict):
    """Result of variance/degeneracy check for an outcome."""
    outcome: str
    n: int
```

```
    n_unique: int
    pct_mode: float
    variance: float
    is_degenerate: bool
    reason: str
```

Data Containers (TypedDicts)

Main Functions

```python
def summarize_outcomes(
    ds: AnalysisDataset,
    outcomes: Optional[List[str]] = None,  # None = all outcomes
    by_group: bool = False,                 # Group by side?
) -> pd.DataFrame:
    """
    Generate comprehensive summary statistics.

    Returns
    -------
    DataFrame with columns:
        outcome, n, n_missing, pct_missing, mean, std, min,
        p25, median, p75, max, skewness, kurtosis, cv
    """
```

`summarize_outcomes()` **Output Example:**

outcome	n	n_missing	mean	std	min	p25	median
EMG_intensity.mean_percent_mvc	320	0	9.126	6.992	1.080	4.424	7.443
EMG_apdf.active.p50	320	0	6.811	5.901	0.696	3.015	5.378

```python
def check_normality(
    ds: AnalysisDataset,
    outcomes: Optional[List[str]] = None,
    alpha: float = 0.05,
) -> pd.DataFrame:
    """
    Test normality of each outcome using Shapiro-Wilk test.

    Returns
    -------
    DataFrame with:
        outcome, n, skewness, shapiro_stat, shapiro_p,
        is_normal, recommended_transform
    """
```

`check_normality()`

[!] Don't Over-Interpret Normality Tests

The Shapiro-Wilk p-value should be treated as a **signal, not a verdict**:

- **With moderate-to-large N**: Tests become "significant" for trivial deviations
- **With small N**: Tests lack power to detect real departures

Better approach: 1. Use **visual diagnostics** first (QQ plots, histograms) 2. Treat Shapiro p-value as one input, not a gatekeeper 3. Check whether fixed-effect estimates are **stable** under transformation 4. LMMs are fairly robust to mild normality violations

```
def check_variance(
    ds: AnalysisDataset,
    outcomes: Optional[List[str]] = None,
    threshold_unique: int = 5,        # Minimum distinct values
    threshold_mode_pct: float = 95.0, # Maximum mode percentage
) -> pd.DataFrame:
    """
    Detect degenerate or near-constant outcomes.

    A variable is DEGENERATE if:
    - Fewer than 5 unique values, OR
    - Mode accounts for >95% of observations

    Degenerate outcomes should NOT be modeled.
    """
```

```
check_variance()
```

4.4 Linear Mixed Models (lmm.py)

Purpose Fit Linear Mixed Effects Models accounting for repeated measures within subjects.

Why Linear Mixed Models? The Problem: Each subject provides multiple observations (days). These observations are **not independent**—values from the same subject are more similar than values from different subjects.

Standard approaches fail: - **T-tests/ANOVA**: Assume independence -> inflated Type I error - **Paired t-tests**: Only handle 2 time points - **Repeated measures ANOVA**: Requires complete data, sphericity assumption

LMM Solution:

```
Y_ij = B0 + B1*Day_ij + B2*Side_ij + u_i + e_ij

Where:
- Y_ij: Outcome for subject i on observation j
- B0: Grand mean (intercept)
- B1: Effect of day
```

```
- B2: Effect of side
- u_i ~ N(0, sigma^2_u): Subject-specific random intercept
- e_ij ~ N(0, sigma^2): Residual error
```

```python
class LMMResult(TypedDict):
    """Container for all model output."""
    outcome: str                    # Which outcome was modeled
    model: Any                      # The statsmodels model object
    formula: str                    # Formula used (e.g., "Y ~ C(day)")
    coefficients: pd.DataFrame      # Fixed effects estimates (Wald tests)
    fit_stats: Dict[str, float]     # AIC, BIC, log-likelihood, LRT results
    random_effects: Dict[str, float]  # Variance components + ICC
    n_obs: int                      # Number of observations
    n_groups: int                   # Number of subjects
    converged: bool                 # Did optimization succeed?
    transform_applied: str          # What transform was used
    warnings: List[str]             # Any issues encountered

# Create using factory function:
result = create_lmm_result(
    outcome="EMG_intensity.mean_percent_mvc",
    model=fitted_model,
    formula="Y ~ C(day_index) + C(side)",
    coefficients=coef_df,
    fit_stats={
        'aic': 478.4,
        'bic': 502.1,
        'loglik': -234.2,
        'lrt_stat': 12.5,        # LRT chi-square for day effect
        'lrt_df': 4,             # Degrees of freedom
        'lrt_pvalue': 0.014,     # P-value for FDR correction
    },
    random_effects={
        'group_var': 24.0,       # sigma^2_u
        'residual_var': 23.9,    # sigma^2
        'icc': 0.50,             # Intraclass correlation
    },
    n_obs=320,
    n_groups=37,
    converged=True,
    transform_applied="none",
    warnings=[]
)

# Access using dictionary syntax:
print(f"AIC: {result['fit_stats']['aic']}")
```

```
print(f"ICC: {result['random_effects']['icc']}")

# Summarize result:
print(summarize_lmm_result(result))
```

The LMMResult TypedDict

Main Functions

```
def fit_lmm(
    ds: AnalysisDataset,
    outcome: str,
    fixed_effects: Optional[List[str]] = None,
    random_intercept: str = "subject_id",
    transform: Optional[TransformType] = None,
    day_as_categorical: bool = True,
    include_side: bool = True,
    formula: Optional[str] = None,
    reml: bool = False,
) -> LMMResult:
    """
    Fit a Linear Mixed Model for a single outcome.

    Parameters
    ----------
    ds : AnalysisDataset
        Prepared data
    outcome : str
        Name of outcome variable to model
    fixed_effects : list, optional
        Custom fixed effects. Default: [C(day_index), C(side)]
    random_intercept : str
        Grouping variable for random intercept (default: subject_id)
    transform : TransformType, optional
        Override registry transform recommendation
    day_as_categorical : bool
        Treat day as categories (True) or linear trend (False)
    include_side : bool
        Include side effect if present
    formula : str, optional
        Complete formula override (advanced)
    reml : bool
        Use REML estimation. Default False (ML for valid AIC/BIC)

    Returns
    -------
```

```
    LMMResult
        TypedDict containing model output
    """
```

`fit_lmm()` Day as Categorical vs. Linear:

```
# Categorical (default): Estimate separate effect for each day
# Formula: Y ~ C(day_index) + C(side)
# Coefficients: Day2 vs Day1, Day3 vs Day1, Day4 vs Day1, ...
# Use when: Pattern over days is non-linear

# Linear trend: Assume linear change per day
# Formula: Y ~ day_index + C(side)
# Coefficients: slope (change per day)
# Use when: Expecting monotonic trend

result_cat = fit_lmm(ds, outcome, day_as_categorical=True)
result_lin = fit_lmm(ds, outcome, day_as_categorical=False)
```

```
def fit_all_outcomes(
    ds: AnalysisDataset,
    outcomes: Optional[List[str]] = None,
    outcome_type: Optional[OutcomeType] = None,
    skip_degenerate: bool = True,
    max_outcomes: Optional[int] = None,
    **kwargs,
) -> Dict[str, LMMResult]:
    """
    Fit LMM for multiple outcomes in batch.

    Returns
    -------
    dict
        {outcome_name: LMMResult} for each fitted model
    """
```

`fit_all_outcomes()`

Understanding the Output Coefficients DataFrame:

term	estimate	std_error	z_value	p_value	ci_lower	ci_upper
C(day_index)[T.2]	-0.411170	0.825203	-0.498265	0.618297	-2.028538	1.206198
C(day_index)[T.3]	-0.028058	0.838860	-0.033448	0.973318	-1.672194	1.616078
C(day_index)[T.4]	-1.930854	0.840079	-2.298419	0.021538	-3.577380	-0.284329
C(side)[T.right]	0.902430	0.549862	1.641193	0.100757	-0.175280	1.980140
Intercept	9.405613	1.035062	9.087006	0.000000	7.376929	11.434297

Interpretation: - `Intercept (9.41)`: Mean %MVC on Day 1, Left side - `C(day_index)[T.4]`

(-1.93, p=0.02): Day 4 is 1.93 %MVC lower than Day 1 (significant) - C(side)[T.right] (0.90, p=0.10): Right side is 0.90 %MVC higher (not significant)

Random Effects (accessed via dictionary):

```
print(result['random_effects'])
# {
#     'group_var': 24.048,      # Between-subject variance (sigma^2_u)
#     'residual_var': 23.884,   # Within-subject variance (sigma^2)
#     'icc': 0.502              # Intraclass correlation
# }
```

ICC (Intraclass Correlation):

```
ICC = sigma^2_u / (sigma^2_u + sigma^2)
    = 24.048 / (24.048 + 23.884)
    = 0.502
```

Interpretation: - ICC = 0.50 means **50% of total variance is between subjects** - This justifies using mixed models—observations within subjects are indeed correlated

---

4.5 Post-Hoc Comparisons (posthoc.py)

Purpose When an overall effect is significant, identify which specific comparisons drive the effect.

```
class ContrastResult(TypedDict):
    """Result of a single contrast comparison."""
    contrast: str               # e.g., "Day1-Day4"
    estimate: float             # Difference estimate
    std_error: float            # Standard error
    z_value: float              # Test statistic
    p_value: float              # Raw p-value
    p_adjusted: float           # Adjusted p-value
    ci_lower: float             # Lower CI bound
    ci_upper: float             # Upper CI bound
    cohens_d: Optional[float]   # Effect size

# Factory function:
contrast = create_contrast_result(
    contrast="Day1-Day4",
    estimate=1.931,
    std_error=0.840,
    z_value=2.298,
    p_value=0.022,
    p_adjusted=0.043,
    ci_lower=0.284,
    ci_upper=3.577,
    cohens_d=0.276
```

```
)

# Summarize:
print(summarize_contrast_result(contrast))
```

The ContrastResult TypedDict

Main Functions

```
def pairwise_contrasts(
    result: LMMResult,
    factor: str,                    # "day_index" or "side"
    ds: AnalysisDataset,
    adjustment: str = "holm",       # "holm", "bonferroni", "none"
) -> pd.DataFrame:
    """
    Compute all pairwise comparisons for a factor.

    Returns DataFrame with columns:
        contrast, estimate, std_error, z_value, p_value,
        p_adjusted, ci_lower, ci_upper, cohens_d
    """
```

pairwise_contrasts()

```
def compute_emmeans(
    result: LMMResult,
    factor: str,
    ds: AnalysisDataset,
) -> pd.DataFrame:
    """
    Compute Estimated Marginal Means (EMMs).

    EMMs are model-predicted means for each level of a factor,
    averaging over other factors.
    """
```

compute_emmeans()

```
def compute_effect_size(
    contrast_estimate: float,
    pooled_sd: float,
    effect_type: str = "cohens_d",
) -> float:
    """
```

```
    Compute standardized effect size.

    Cohen's d interpretation:
        |d| < 0.2: Negligible
        0.2 <= |d| < 0.5: Small
        0.5 <= |d| < 0.8: Medium
        |d| >= 0.8: Large
    """
```

`compute_effect_size()`

Effect Size Definition for Mixed Models In LMMs, variance is decomposed into components (subject random intercept + residual), so there is no single "pooled SD." We adopt the following **explicit definition**:

Default: Residual-Standardized Effect Size

`d = Delta / sigma_residual`

Where: - `Delta` = contrast estimate (e.g., Day1 - Day4 difference) - `sigma_residual` = square root of residual variance from LMM

This standardizes by **within-subject variability**, which is appropriate for repeated-measures designs where subject-level variance is nuisance.

Alternative Definitions (for sensitivity analysis):

Definition	Formula	When to Use
Residual-standardized (default)	d = Delta / sigma_res	Within-subject comparisons
Total-standardized	d = Delta / sqrt(sigma^2_u + sigma^2)	Between-subject interpretability
Raw units	Report Delta + 95% CI directly	Clinical/practical interpretation

> **Recommendation**: Always report raw-unit effects with confidence intervals as the primary result. Cohen's d is supplementary for readers who want standardized comparisons across studies.

4.6 Multiplicity Correction (multiplicity.py)

Purpose Control false positive rate when testing many hypotheses simultaneously.

Critical: Which P-Value Feeds FDR? LMM output contains **multiple p-values** (one per coefficient). For outcome-wise FDR correction, we need **one p-value per outcome** representing the overall "day effect."

Default Strategy (Omnibus Test):

We use a **Likelihood Ratio Test (LRT)** comparing: - **Full model**: `Y ~ C(day_index) + C(side) + (1|subject_id)` - **Reduced model**: `Y ~ C(side) + (1|subject_id)` (day removed)

The LRT p-value tests: "Does including day improve model fit?" This is the p-value used for across-outcome FDR correction.

```
# LRT is computed automatically in fit_lmm() and stored in:
result['fit_stats']['lrt_pvalue']  # P-value for day effect (omnibus)
result['fit_stats']['lrt_stat']    # Chi-square statistic
result['fit_stats']['lrt_df']      # Degrees of freedom
```

> [!] **Important Distinction**
>
> - **LRT p-value (omnibus)**: Used for FDR across outcomes ("Is there ANY day effect?")
> - **Coefficient p-values (Wald)**: Used for interpretation tables ("Which specific days differ?")
>
> Never apply FDR correction to arbitrary coefficient-level p-values - this conflates the multiplicity layers and inflates false discovery.

Two-Layer Correction Strategy

```
Layer 1: ACROSS outcomes (FDR correction)
+-- Outcome 1: p_raw = 0.001 -> p_adj = 0.005 [PASS]
+-- Outcome 2: p_raw = 0.02  -> p_adj = 0.04  [PASS]
+-- Outcome 3: p_raw = 0.08  -> p_adj = 0.10  [FAIL]
+-- ...

Layer 2: WITHIN significant outcomes (Holm correction for post-hoc)
+-- Outcome 1 post-hocs:
|   +-- Day1-Day2: p = 0.50 -> p_adj = 0.50
|   +-- Day1-Day4: p = 0.02 -> p_adj = 0.04 [PASS]
|   +-- ...
+-- Outcome 2 post-hocs:
    +-- ...
```

Main Functions

```python
def apply_fdr(
    results: Dict[str, LMMResult],
    alpha: float = 0.05,
    method: str = "fdr_bh",       # Benjamini-Hochberg
) -> pd.DataFrame:
    """
    Apply False Discovery Rate correction across outcomes.

    Returns DataFrame with:
```

```
        outcome, p_raw, p_adjusted, significant
    """
```

apply_fdr()

```
def apply_holm(
    p_values: List[float],
    alpha: float = 0.05,
) -> pd.DataFrame:
    """
    Apply Holm-Bonferroni correction (step-down procedure).
    More powerful than Bonferroni while controlling FWER.
    """
```

apply_holm()

```
def adjust_pvalues(
    p_values: np.ndarray,
    method: str = "fdr_bh",
) -> np.ndarray:
    """
    Wrapper for multiple testing correction methods.

    Supported methods:
    - "fdr_bh": Benjamini-Hochberg FDR
    - "fdr_by": Benjamini-Yekutieli FDR (more conservative)
    - "holm": Holm-Bonferroni FWER
    - "bonferroni": Classical Bonferroni FWER
    - "none": No adjustment
    """
```

adjust_pvalues()

4.7 Model Diagnostics (diagnostics.py)

Purpose Verify that model assumptions are met before trusting results.

```
class DiagnosticsResult(TypedDict):
    """Comprehensive diagnostics output for an LMM."""
    outcome: str
    residuals: np.ndarray           # Raw residuals
    fitted: np.ndarray              # Fitted values
    standardized: np.ndarray        # Standardized residuals
    normality_stat: float           # Shapiro-Wilk statistic
```

```
    normality_p: float              # Normality p-value
    heteroscedasticity_stat: Optional[float]  # Breusch-Pagan statistic
    heteroscedasticity_p: Optional[float]     # Heteroscedasticity p-value
    outlier_indices: List[int]      # Indices of outliers (|z| > 3)
    n_outliers: int
    assumptions_met: bool           # Overall assessment

# Factory function:
diag = create_diagnostics_result(
    outcome="EMG_intensity.mean_percent_mvc",
    residuals=residuals,
    fitted=fitted_values,
    standardized=std_residuals,
    normality_stat=0.98,
    normality_p=0.12,
    heteroscedasticity_stat=1.45,
    heteroscedasticity_p=0.23,
    outlier_indices=[45, 156],
    n_outliers=2,
    assumptions_met=True
)

# Summarize:
print(summarize_diagnostics(diag))
```

The DiagnosticsResult TypedDict

Main Functions

```
def residual_diagnostics(result: LMMResult) -> DiagnosticsResult:
    """
    Comprehensive residual analysis.

    Returns DiagnosticsResult TypedDict with:
        - residuals: Raw residuals
        - fitted: Fitted values
        - standardized: Standardized residuals
        - normality_stat/p: Shapiro-Wilk test (use as signal, not verdict)
        - heteroscedasticity_stat/p: Breusch-Pagan test (screening only)
        - outlier_indices: Observations with |z| > 3
    """
```

residual_diagnostics()

[!] Heteroscedasticity Testing Caveat

The Breusch-Pagan test assumes **independent residuals**, but LMM residuals have correlation structure (observations within subjects are dependent). Therefore:

- Use BP as a **screening heuristic**, not a definitive test
- The **residual vs. fitted plot** is more informative for detecting patterns
- If heteroscedasticity is suspected:
  1. Try variance-stabilizing transforms (LOG, SQRT)
  2. Consider robust standard errors as sensitivity analysis
  3. Check if patterns differ by subject or time

The same "signal, not verdict" philosophy from normality testing applies here.

```
def check_assumptions(
    result: LMMResult,
    alpha: float = 0.05,
) -> Dict[str, Dict[str, Any]]:
    """
    Automated assumption checking with pass/fail status.

    Note: "FAIL" means the test flagged an issue, not that
    the model is invalid. Use judgment and visual inspection.
    """
```

`check_assumptions()` Example (recommended approach):

```
diag = residual_diagnostics(result)

# 1. Check summary
print(summarize_diagnostics(diag))

# 2. Visual check (most important)
import matplotlib.pyplot as plt
from scipy import stats

fig, axes = plt.subplots(1, 2, figsize=(10, 4))

# QQ plot
stats.probplot(diag['standardized'], dist="norm", plot=axes[0])
axes[0].set_title("QQ Plot of Residuals")

# Residual vs Fitted
axes[1].scatter(diag['fitted'], diag['residuals'], alpha=0.5)
axes[1].axhline(y=0, color='r', linestyle='--')
axes[1].set_xlabel("Fitted Values")
axes[1].set_ylabel("Residuals")
axes[1].set_title("Residuals vs Fitted")

plt.tight_layout()
plt.show()

# 3. Check for outliers
```

```python
if diag['n_outliers'] > 0:
    print(f"[WARNING] {diag['n_outliers']} potential outliers - investigate these")
```

4.8 Report Generation (report.py)

Purpose Generate publication-quality tables and summaries.

Main Functions

```python
def descriptive_table(
    ds: AnalysisDataset,
    outcomes: Optional[List[str]] = None,
    by_group: Optional[str] = None,
    format_spec: str = ".2f",
) -> pd.DataFrame:
    """
    Generate "Table 1" style descriptive statistics.

    Output format:
        | Outcome | N | Mean (SD) | Median [IQR] | Range |
    """
```

descriptive_table()

```python
def coefficient_table(
    result: LMMResult,
    format_spec: str = ".3f",
    include_ci: bool = True,
) -> pd.DataFrame:
    """
    Format model coefficients for publication.

    Output format:
        | Term | Estimate (95% CI) | SE | p-value |
    """
```

coefficient_table()

```python
def results_summary(
    results: Dict[str, LMMResult],
    fdr_results: Optional[pd.DataFrame] = None,
) -> pd.DataFrame:
    """
```

```
    Comprehensive summary across all models.
    Combines model fit statistics with FDR-adjusted p-values.
    """
```

```
results_summary()
```

Variance Explained: ICC and R-Squared Measures For longitudinal models, reviewers often want measures of variance explained. The LMMResult includes several complementary metrics:

Intraclass Correlation (ICC)

Already computed in `result['random_effects']['icc']`:

`ICC = sigma^2_u / (sigma^2_u + sigma^2_residual)`

Interpretation: Proportion of total variance attributable to between-subject differences.

R-Squared Measures for Mixed Models

Measure	Formula	Interpretation
Marginal R^2	Var(fixed) / Var(total)	Variance explained by fixed effects only
Conditional R^2	Var(fixed + random) / Var(total)	Variance explained by full model

```
# Access R² measures (when available):
print(result['fit_stats']['r2_marginal'])      # Fixed effects only
print(result['fit_stats']['r2_conditional'])  # Fixed + random effects

# Typical interpretation:
# - Marginal R² = 0.15: Fixed effects explain 15% of variance
# - Conditional R² = 0.65: Full model explains 65% (random effects add 50%)
```

> **Current Status**: ICC is implemented in v0.2.0. Marginal and conditional R^2 (Nakagawa & Schielzeth, 2013) are planned for v0.3.0. When implemented, they will appear in `results_summary()` output automatically.

Recommended Reporting:

For OH/biomedical papers, report: 1. **ICC**: Shows clustering strength (justifies mixed model) 2. **Marginal R^2**: Shows practical effect of predictors 3. Raw variance components (sigma^2_u, sigma^2_residual) for reproducibility

---

5. Statistical Methods Deep Dive

5.1 Linear Mixed Models: Mathematical Foundation

The Model Full LMM specification:

$$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}\mathbf{u} + \varepsilon$$

Where: - $\mathbf{Y}$: $n \times 1$ vector of observations - $\mathbf{X}$: $n \times p$ fixed effects design matrix - β: $p \times 1$ vector of fixed effect coefficients - $\mathbf{Z}$: $n \times q$ random effects design matrix - $\mathbf{u}$: $q \times 1$ vector of random effects, $\mathbf{u} \sim N(\mathbf{0}, \mathbf{G})$ - ε: $n \times 1$ residual vector, $\varepsilon \sim N(\mathbf{0}, \mathbf{R})$

For Random Intercept Model

$$Y_{ij} = \beta_0 + \beta_1 \text{Day}_{ij} + \beta_2 \text{Side}_{ij} + u_i + \varepsilon_{ij}$$

Variance structure: - Var(u_i) = sigma^2_u (between-subject variance) - Var(e_ij) = sigma^2 (within-subject variance) - Cov(Y_ij, Y_ik) = sigma^2_u for same subject (compound symmetry)

5.2 Variance Transforms

Transform Reference

Transform	Formula	Use When	Status
LOG	$\log(Y)$	Y > 0, right-skewed	[OK] Recommended
LOG1P	$\log(1 + Y)$	Y >= 0 with zeros	[~] Fallback
SQRT	$\sqrt{Y}$	Y >= 0, moderate skew	[OK] Recommended
LOGIT	$\log \frac{Y}{1-Y}$	Y in (0,1), proportions	[OK] **Preferred**
ARCSINE	$\arcsin(\sqrt{Y})$	Legacy only	[X] **Deprecated**

5.3 Multiple Testing Correction

FDR (False Discovery Rate)

$$\text{FDR} = E\left[\frac{V}{R}\right]$$

Benjamini-Hochberg Procedure: 1. Order p-values: p_(1) <= p_(2) <= ... <= p_(m) 2. Find largest k such that p_(k) <= (k/m) * alpha 3. Reject all H_(1), H_(2), ..., H_(k)

FWER (Family-Wise Error Rate) **Holm Procedure:** 1. Order p-values 2. Compare p_(i) to alpha / (m - i + 1) 3. Reject until first non-rejection, then stop

---

6. Complete Workflow Examples

6.1 Basic Analysis: Day Effect on EMG Intensity

```
"""
Research Question: Does EMG intensity change over the monitoring period?
"""

from oh_parser import load_profiles
from oh_stats import (
```

```
    prepare_daily_emg,
    summarize_outcomes,
    check_normality,
    check_variance,
    fit_lmm,
    pairwise_contrasts,
    residual_diagnostics,
    coefficient_table,
    summarize_lmm_result,
)

# Step 1: Load and Prepare Data
profiles = load_profiles("/path/to/profiles")
ds = prepare_daily_emg(profiles, side="both")

outcome = "EMG_intensity.mean_percent_mvc"

# Step 2: Descriptive Statistics
print("=== Descriptive Statistics ===")
summary = summarize_outcomes(ds, [outcome])
print(summary)

# Step 3: Fit Model
print("\n=== Linear Mixed Model ===")
result = fit_lmm(ds, outcome)

if not result['converged']:
    print(f"WARNING: Model did not converge! {result['warnings']}")
else:
    print(summarize_lmm_result(result))
    print("\nCoefficients:")
    print(coefficient_table(result))

# Step 4: Diagnostics
print("\n=== Diagnostics ===")
diag = residual_diagnostics(result)
print(f"Normality p = {diag['normality_p']:.4f}")
print(f"Outliers detected: {diag['n_outliers']}")

# Step 5: Post-Hoc Comparisons
print("\n=== Post-Hoc Contrasts ===")
contrasts = pairwise_contrasts(result, "day_index", ds)
print(contrasts[["contrast", "estimate", "p_adjusted", "cohens_d"]])
```

6.2 Multi-Outcome Analysis with FDR Correction

```
"""
Research Question: Which EMG metrics change significantly over time?
"""

from oh_stats import (
    prepare_daily_emg,
    fit_all_outcomes,
    apply_fdr,
    results_summary,
    list_outcomes,
    OutcomeType,
    check_variance,
)

# Load Data
profiles = load_profiles("/path/to/profiles")
ds = prepare_daily_emg(profiles, side="both")

# Pre-modeling Checks
continuous_outcomes = list_outcomes(outcome_type=OutcomeType.CONTINUOUS)
variance_check = check_variance(ds, continuous_outcomes)
degenerate = variance_check[variance_check["is_degenerate"]]["outcome"].tolist()
print(f"Degenerate outcomes (excluded): {degenerate}")

# Fit All Models
results = fit_all_outcomes(
    ds,
    outcome_type=OutcomeType.CONTINUOUS,
    skip_degenerate=True,
)
print(f"\nFitted {len(results)} models")

# Apply FDR Correction
fdr_df = apply_fdr(results, alpha=0.05)
print("\n=== FDR-Corrected Results ===")
print(fdr_df)

# Summary Table
summary = results_summary(results, fdr_df)
print("\n=== Complete Summary ===")
print(summary)
```

---

7. Edge Cases and Error Handling

7.1 Missing Data

```
# Check missingness before modeling
miss = missingness_report(ds)
print(f"Total missing: {miss['total_missing'].iloc[0]} cells")

# If >10% missing, investigate patterns
if miss['pct_missing'].iloc[0] > 10:
    print("Warning: High missingness - check if MAR is plausible")
```

7.2 Non-Convergence

```
result = fit_lmm(ds, outcome)

if not result['converged']:
    print("Model did not converge!")
    print(f"Warnings: {result['warnings']}")

    # Try simpler model
    result_simple = fit_lmm(ds, outcome, include_side=False)

    # Or try transformation
    result_log = fit_lmm(ds, outcome, transform=TransformType.LOG)
```

7.3 Degenerate Outcomes

```
variance_check = check_variance(ds, [outcome])
if variance_check['is_degenerate'].iloc[0]:
    print(f"Outcome {outcome} is degenerate")
    print("This outcome cannot be meaningfully modeled.")
```

7.4 Small Sample Sizes

```
result = fit_lmm(ds, outcome)

if result['n_groups'] < 30:
    print(f"Warning: Only {result['n_groups']} subjects - results may be unstable")
```

[!] Model-Aware Sample Size Considerations

The "<30 clusters" heuristic is a rough guideline. Actual stability depends on:

1. **Number of clusters (subjects)**: More important than total observations
2. **Fixed-effect complexity**: More coefficients require more clusters
3. **Observations per cluster**: Sparse designs amplify instability
4. **Missingness patterns**: Systematic dropout is worse than random

When clusters are limited (<30 subjects): - Prefer simpler models (fewer fixed effects) - Consider wider confidence intervals or bootstrap CIs - Interpret random effect variance estimates with caution (often imprecise) - Report sensitivity analyses with different model specifications

There is no magic threshold - use judgment based on design complexity.

---

8. Best Practices

8.1 Pre-Analysis Checklist

1. **Check data quality**
   - Run `missingness_report()`
   - Verify sample sizes are adequate
2. **Examine distributions**
   - Run `summarize_outcomes()` for all outcomes
   - Run `check_normality()` to identify skewness
   - Run `check_variance()` to identify degenerate variables
3. **Document analysis plan**
   - Specify primary vs. secondary outcomes
   - Pre-specify alpha level and correction method
   - Justify model specification

8.2 Working with TypedDicts

```
# Access data using dictionary syntax
print(ds['data'].shape)
print(result['fit_stats']['aic'])
print(diag['n_outliers'])

# Use helper functions for common operations
description = describe_dataset(ds)
summary = summarize_lmm_result(result)
diag_summary = summarize_diagnostics(diag)

# Factory functions ensure proper structure
ds = create_analysis_dataset(data=df, outcome_vars=outcomes, ...)
result = create_lmm_result(outcome=name, model=model, ...)
```

8.3 Reporting Results

Example results paragraph: > "EMG mean %MVC was analyzed using linear mixed models with subjects as random intercepts, day (categorical) and side as fixed effects. The ICC was 0.50, indicating substantial between-subject variation. After FDR correction (alpha = 0.05), day showed a significant overall association with mean %MVC (p_adj = 0.03). Post-hoc contrasts (Holm-adjusted) revealed significantly lower activation on Day 4 compared to Day 1 (Delta = -1.93 %MVC, 95% CI [-3.58, -0.28], Cohen's d = 0.28, p_adj = 0.04)."

9. Glossary

Term	Definition
AIC	Akaike Information Criterion. Lower = better fit.
AnalysisDataset	TypedDict container for analysis-ready data.
Cohen's d	Standardized effect size: (M1 - M2) / SD_pooled.
ContrastResult	TypedDict for post-hoc comparison output.
DiagnosticsResult	TypedDict for model diagnostics output.
FDR	False Discovery Rate. Expected proportion of false positives.
ICC	Intraclass Correlation. Between-subject variance proportion.
LMMResult	TypedDict for linear mixed model output.
OutcomeInfo	TypedDict for outcome variable metadata.
TypedDict	Python dict with type hints (function-based alternative to dataclass).

Quick Reference Card

```
# ===== MINIMAL WORKFLOW =====

from oh_parser import load_profiles
from oh_stats import (
    prepare_daily_emg,
    summarize_outcomes,
    fit_all_outcomes,
    apply_fdr,
    results_summary,
)

# 1. Load & Prepare
profiles = load_profiles("/path/to/data")
ds = prepare_daily_emg(profiles, side="both")

# 2. Describe
summary = summarize_outcomes(ds)
print(summary)

# 3. Model
results = fit_all_outcomes(ds, skip_degenerate=True)

# 4. Correct
fdr = apply_fdr(results)
print(fdr[fdr['significant']])
```

```
# 5. Report
report = results_summary(results, fdr)
print(report)
```

---

10. Future Extensions: Multi-Modal Ready

The `oh_stats` architecture is designed to generalize beyond EMG.

Planned Extensions

Feature	Current Status	Future Direction
Count models	LOG1P + Gaussian LMM	Poisson/NB GLMMs
Ordinal models	Stub only	Ordered logistic (Bayesian)
Beta regression	Logit transform	`statsmodels` beta regression
Multi-channel	Subject random intercept	Subject -> Day -> Channel hierarchy

References

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