



9.2 Neyman-Pearson Paradigm Let $\underline{X} = (X_1, ..., X_n)$ denote a sample from population $f(x|\theta)$. Decide on H_0 vs. H_A based on the sample. A decision on whether or not to reject H_0 in favor of H_A is made on the basis of a statistic $T=T(\underline{X})=T(X_1, ..., X_n)$.

The set of values of T for which H_0 is accepted is called the <u>acceptance region</u> and the set of values of T for which H_0 is rejected is the <u>rejection region of the test</u>.

Two kinds of error may occur: 1. H_0 is rejected when it is true: <u>Type I error</u>. P(type I error) = α = P(T \in rejection region | H_0 true). If H_0 is simple, α is called the <u>significance level</u> of the test.

5

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2. H₀ is accepted when it is false: <u>Type II error</u>.
P(type II error) = β
= P(T in acceptance region | H₀ false)
If H_A is composite, β depends on which member of H_A is the true pdf. Power of the test =P(H₀ is rejected when false) = 1 - P(H₀ is accepted | H₀ false) = 1 - β . <u>Ideally</u>, we would want α = β =0, but this not possible since the decision is based on <u>data</u>.

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<u>P-value</u> The p-value is the probability of observing a test statistic at least as extreme as the one observed if the null hypothesis is true.

The null hypothesis is rejected when p-value is $\leq \alpha$. It is the smallest α for which H₀ would be rejected.

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For a composite test the significance level α is the maximum (supremum) of the probabilities of a Type I error over all the possible alternatives.

11

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