

BINGHAM McCUTCHEN LLP
DONN P. PICKETT (SBN 72257)
GEOFFREY M. HOWARD (SBN 157468)
HOLLY A. HOUSE (SBN 136045)
ZACHARY J. ALINDER (SBN 209009)
BREE HANN (SBN 215695)
Three Embarcadero Center
San Francisco, CA 94111-4067
Telephone: (415) 393-2000
Facsimile: (415) 393-2286
donn.pickett@bingham.com
geoff.howard@bingham.com
holly.house@bingham.com
zachary.alinder@bingham.com
bree.hann@bingham.com

BOIES, SCHILLER & FLEXNER LLP
DAVID BOIES (Admitted *Pro Hac Vice*)
333 Main Street
Armonk, NY 10504
Telephone: (914) 749-8200
Facsimile: (914) 749-8300
dboies@bsfllp.com
STEVEN C. HOLTZMAN (SBN 144177)
FRED NORTON (SBN 224725)
1999 Harrison St., Suite 900
Oakland, CA 94612
Telephone: (510) 874-1000
Facsimile: (510) 874-1460
sholtzman@bsfllp.com
fnorton@bsfllp.com

DORIAN DALEY (SBN 129049)
JENNIFER GLOSS (SBN 154227)
500 Oracle Parkway, M/S 5op7
Redwood City, CA 94070
Telephone: (650) 506-4846
Facsimile: (650) 506-7114
dorian.daley@oracle.com
jennifer.gloss@oracle.com

Attorneys for Plaintiffs Oracle USA, Inc., *et al.*

UNITED STATES DISTRICT COURT
NORTHERN DISTRICT OF CALIFORNIA
OAKLAND DIVISION

ORACLE USA, INC., *et al.*,

Plaintiffs,

v.

SAP AG, *et al.*,

Defendants.

CASE NO. 07-CV-01658 PJH (EDL)

**EXHIBIT 7 TO THE DECLARATION OF
DANIEL S. LEVY, PH.D. IN SUPPORT OF
MOTION NO. 1: TO EXCLUDE TESTIMONY
OF DEFENDANTS' EXPERT STEPHEN
CLARKE**

FILED PURSUANT TO DKT. NO. 915

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EXHIBIT 7

Mathematical Statistics and Data Analysis

Second Edition

John A. Rice

University of California, Berkeley



Duxbury Press
An Imprint of Wadsworth Publishing Company
Belmont, California

Duxbury Press

*An Imprint of Wadsworth Publishing Company
A Division of Wadsworth, Inc.*

Assistant Editor: *Jennifer Burger*
Editorial Assistant: *Michelle O'Donnell*
Production: *The Wheatley Company, Inc.*
Cover and Text Designer: *Cloyce Wall*
Print Buyer: *Barbara Britton*
Copy Editor: *Linda Thompson*
Compositor: *Interactive Composition Corporation*
Printer: *R. R. Donnelley & Sons*
(Credits continue in the back of the book.)



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International Thomson Publishing

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Beginning February 22, 1999, you can request permission to use material from this text through the following phone and fax numbers: Phone: 1-800-730-2214; Fax: 1-800-730-2215.

Printed in the United States of America

14 - 04

Library of Congress Cataloging-in-Publication Data

Rice, John A.,

Mathematical statistics and data analysis / John A. Rice. — 2nd
ed.

p. cm.

Includes bibliographical references and indexes.

ISBN 0-534-20934-3 (acid-free)

1. Statistics. I. Title.

QA276.12.R53 1995

519.5—dc20

93-28340

The normality assumption, or its approximation, makes possible the construction of confidence intervals and hypothesis tests. It can then be shown that

$$\frac{\hat{\beta}_i - \beta_i}{s_{\hat{\beta}_i}} \sim t_{n-2}$$

which implies that the t distribution can be used for confidence intervals and hypothesis tests.

EXAMPLE A We apply these procedures to the 21 data points on chromatographic peak area. The following table presents some of the statistics from the fit (tables like this are produced by regression programs of software packages):

Coefficient	Estimate	Standard Error	t Value
β_0	.0729	.0297	2.45
β_1	10.77	.27	40.20

The estimated standard deviation of the errors is $s = .068$. The standard error of the intercept is $s_{\hat{\beta}_0} = .0297$. A 95% confidence interval for the intercept, β_0 , based on the t distribution with 19 df is

$$\hat{\beta}_0 \pm t_{19}(.025)s_{\hat{\beta}_0}$$

or (.011, .135). Similarly, a 95% confidence interval for the slope, β_1 , is

$$\hat{\beta}_1 \pm t_{19}(.025)s_{\hat{\beta}_1}$$

or (10.21, 11.33). To test the null hypothesis $H_0: \beta_0 = 0$, we would use the t statistic $\hat{\beta}_0/s_{\hat{\beta}_0} = 2.45$. The hypothesis would be rejected at significance level $\alpha = .05$, so there is strong evidence that the intercept is nonzero. ■

14.2.2 Assessing the Fit

As an aid in assessing the quality of the fit, we will make extensive use of the residuals, which are the differences between the observed and fitted values:

$$\hat{e}_i = y_i - \hat{\beta}_0 - \hat{\beta}_1 x_i$$

It is most useful to examine the residuals graphically. Plots of the residuals versus the x values may reveal systematic misfit or ways in which the data do not conform to the standard statistical model. Ideally, the residuals should show no relation to the x values, and the plot should look like a horizontal blur.