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Bias in Qualitative Measures of Concordance for Rodent Carcinogenicity Tests

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According to current policy, chemicals are evaluated for possible cancer risk to humans at low dose by testing in bioassays, where high doses of the chemical are given to rodents. Thus, risk is extrapolated from high dose in rodents to low dose in humans. The accuracy of these extrapolations is generally unverifiable, since data on humans are limited. However, it is feasible to examine the accuracy of extrapolations from mice to rats. If mice and rats are similar with respect to carcinogenesis, this provides some evidence in favor of inter-species extrapolations; conversely, if mice and rats are different, this casts doubt on the validity of extrapolations from mice to humans.

One measure of inter-species agreement is concordance, the percentage of chemicals that are classied the same way as to carcinogenicity in mice and rats. Observed concordance in NCI/NTP bioassays is around 75% , which may seem on the low side because mice and rats are closely related species tested under the same experimental conditions. Theoretically, observed concordance could under-estimate true concordance, due to measurement error in the bioassays. Thus, bias in concordance is of policy interest. Expanding on previous work by Piegorsch et al. (1992), we show that the bias in observed concordance can be either positive or negative: an observed concordance of 75% can arise if the true concordance is anything between 20% and 100%. In particular, observed concordance can seriously overestimate true concordance.

We also consider quantitative correlations of carcinogenic potency. Following Bernstein et al. (1985), we show these correlations can be explained by statistical artifact. Our simulations expand on previous work by considering both carcinogens and non-carcinogens, while distinguishing between "observed" and "true" potencies. Thus, we develop a complete statistical model for chemicals and bioassays; within this model, biases in quantitative and qualitative concordance can be examined.

A variety of models more or less fit the data, with quite different implications for bias. Therefore, given our present state of knowledge, it seems unlikely that true concordance can be determined from bioassay data.

1. Introduction

According to current regulatory policy, chemicals are tested for safety. The most relevant data would come from human subjects. However, careful epidemiological studies have been done in relatively few cases, and screening is routinely done in animal experiments.

In a bioassay, rats and mice are exposed to near-toxic doses of the agent on test. High doses are needed in order to demonstrate a statistically signicant response with a limited number of animals. But there is an upper bound: if the dose level is set too high, animals will not live long enough to develop cancer. Thus, chemicals are administered at the \Maximum Tolerated Dose," or MTD. (Details on the MTD and bioassay design are in Section 2.)

Typically, the MTD is orders of magnitude higher than the environmental exposures of concern for the general population. To use bioassay results for risk assessment, then, two extrapolations are needed: (1) the species extrapolation from rats or mice to humans, and (2) the extrapolation from high dose to low dose. The first extrapolation is qualitative; the second is quantitative and depends on a dose-response model like the "one-hit model" (Section 2). In brief, if P (cancer) is the probability of developing cancer at dose D , the one-hit model says

$$
P(\text{cancer}) = p_0 + (1 - p_0)(1 - e^{-bD}).
$$

The model has two parameters, p_0 and b. The parameter p_0 is the background rate of cancer when the dose D is 0. The parameter b is called "potency." This parameter can be estimated from bioassay data and a chemical can be classied as carcinogenic $\scriptstyle\rm II$ its estimated potency is statistically significant—in other words, $\scriptstyle\rm 0$ exceeds zero by

an amount that is statistically signicant.

The focus of the present paper is the validity of the qualitative extrapolation (although the quantitative extrapolation and the one-hit model will be discussed too). Little direct evidence is available on the qualitative extrapolation because so few chemicals have been evaluated in human studies. It is often said that most known human carcinogens are also animal carcinogens. This familiar argument, however, faces certain empirical difficulties (Freedman and Zeisel, 1988). Moreover, the argument bypasses a question of considerable policy interest—are most animal carcinogens also human carcinogens?

Indirect evidence can be used to validate the species extrapolation; for example, the accuracy of extrapolations from mice to rats can be examined. If mice and rats are similar with respect to carcinogenesis, this provides some evidence in favor of inter-species extrapolation; conversely, if mice and rats are different, this casts doubt on extrapolations from rodents to humans. Data from National Cancer Institute/National Toxicology Program (NCI/NTP) are convenient for this purpose. NCI/NTP bioassays are run on a standard protocol and (with few exceptions) each chemical is tested both on rats and on mice.

Using the Carcinogenic Potency Data Base, we identied 297 chemicals tested by NCI/NTP in female mice and female rats (Gold et al., 1984, 1986, 1987, 1990; Gold and Manley et al., 1993). We classied each chemical as positive (+) or negative $(-)$ in the female mouse and in the female rat, based on significance at the .005 level, one sided. This rule produces a classification in good agreement with "authors' opinion" (Haseman, 1983b; Gold et al., 1989). Being mechanical, the rule is subject to simulation study; using females avoids complications created by sex-specific responses.

One measure of inter-species agreement is concordance, the percentage of chemicals that are classied the same way in both species. Results for NCI/NTP bioassays are shown in Table 1. There were $53 + 48 + 22 + 174 = 297$ chemicals; of them,

 $53 + 174 = 227$ were classified the same way in mice and in rats; the concordance is $227/297 = 76\%$. (Concordance has been computed by a number of authors, and 75%) is a typical figure; see Gold et al. 1989 or Krewski et al. 1993; other literature is reviewed below.)

			NCI/NTP
			Rats
		$^{+}$	
Mice	$^+$	53	48
		22	174

Table 1: Concordance table for 297 NCI/NTP bioassays

Mice and rats are, after all, very similar species being tested under virtually identical experimental conditions; it might be argued that a concordance of 75% is on the low side, bringing into question the validity of the extrapolation from rodents to humans. A possible counter-argument: the concordance observed in the NCI/NTP data is just an estimate based on limited data. Since each bioassay only involves a relatively small number of mice and rats, statistical power may be low. Theoretically, observed concordance could be lower than true concordance, due to measurement error in the bioassays; indeed, an observed concordance of 75% could imply a true concordance near 100%.

Here, we follow Piegorsch et al. (1992) in exploring this question via computer simulations of the bioassay process. We expand the framework used by those authors to include the case where true concordance is less than 100%, and we make the simulations more realistic in other ways too. The data generated in our simulations look rather like the real NCI/NTP data, with respect to summary statistics on potency and toxicity. We show that observed concordance can be 75% if true concordance is 20% , 100% , or anything in between—depending on the choice of parameters. In

other words, a variety of models more or less fit the data, but have radically different implications for bias in observed concordance. Thus, we doubt the data suffice to determine the bias, or give any very precise estimate of the true concordance of rats and mice—nor yet the validity of the species extrapolation from rodents to humans.

Work on the quantitative extrapolation may be summarized this way. Using NCI/NTP data, Crouch and Wilson (1979) found a strong correlation between estimated potencies in rats and mice. Following Bernstein et al. (1985), we show this correlation to be explicable in terms of statistical artifact. The correlation is due to (1) the choice of data set, namely, all chemicals with potency estimates that were statistically signicant in both species, (2) the high correlation between the MTDs in mice and rats, and (3) absence of 100% cancer rates in the NCI/NTP data.

We can set up our simulation model so the true classification of chemicals as carcinogens is independent from rats to mice; among the carcinogens, tumor yields in the two species are independent too. But estimated potencies—among those chemicals with statistically significant estimates—are highly correlated, as in the NCI/NTP data. In the simulation, the observed inter-species correlation is purely artifactual. This expands on previous work (Freedman et al., 1993) by explicitly considering both carcinogens and non-carcinogens, while distinguishing "observed" potencies from the \true" ones. Thus, we develop a statistical model for chemicals and bioassays; within this model, biases in quantitative and qualitative concordance can be examined.

Can risks be extrapolated from mice to rats? Previous arguments in the literature do not demonstrate the validity of the extrapolation. (Nor do we demonstrate invalidity.) The question remains open, as do more serious questions about extrapolations from rodents to humans. The statistical implications are worth stating explicitly: (1) simulation results may be driven by assumptions rather than data, and (2) correlations may be driven by selection of samples. When it comes to policy analysis, such possibilities should be carefully considered.

The balance of this paper is organized as follows. Section 2 gives some detail on bioassays and the one-hit dose-response model. Section 3 describes previous simulation studies, identies the crucial assumptions, and compares the results to real data. Section 4 describes our simulations. Section 5 extends the results to other measures of qualitative agreement such as the odds ratio. Section 6 discusses the quantitative extrapolation. Literature is reviewed in sections 5 and 6.

2. Background

In bioassays, animals are exposed to chemicals in order to determine carcinogenicity. Standard NCI/NTP protocols call for testing a chemical in two species (mice and rats) and in both sexes. For a given sex and species, there are three dose groups (high dose, low dose, control), each with 50 animals. The high dose group is given the Maximum Tolerated Dose (MTD), estimated using data from a preliminary experiment; the MTD is the dose that produces a 10% decrement in predicted weight gain but does not cause death or overt toxicity (Sontag et al., 1976). The low dose group receives half the MTD. The control group receives none of the chemical. For a detailed description of bioassay design, see (Freedman and Zeisel, 1988).

The probability that an animal develops cancer is often assumed to follow the one-hit model:

(1)
$$
P(\text{cancer}) = p_0 + (p_{\text{max}} - p_0)(1 - e^{-bD}).
$$

In equation (1), p_0 is the background rate of tumors, p_{max} is the maximum probability of developing cancer, and D is the dose; p_{max} is usually taken to be 1. Smaller values of p_{max} may be used to reflect residual genetic heterogeneity in the test animals, errors in tumor detection at necropsy, and other forms of miss-specification in the conventional

one-hit model. The parameter b in equation (1) is the potency; if a chemical is a not a carcinogen, its potency is zero, by definition. The one-hit model can be fit to bioassay data to estimate the potency, as in (Crouch et al., 1987) and (Shlyakhter et al., 1992). This model is often used, despite a number of difficulties (Freedman and Zeisel, 1988). The Cochran-Armitage Trend Test (Snedecor and Cochran, 1967; Gart et al., 1986) can be used to determine if bioassay results are "statistically significant," meaning they show a signicant (positive) trend with dose. On heterogeneity, see Gaylor et al. (1993), Peto et al. (1985, p.46); also see Peto et al. (1975), Peto et al. (1984).

The data in this paper cover 297 chemicals tested by NCI/NTP with results in female mice and female rats (Gold et al., 1984, 1986, 1987, 1990; Gold and Manley et al., 1993). Potencies were standardized to a two-year lifespan.

3. Previous Simulations

Piegorsch et al. (1992) use a simulation study to examine potential bias in observed concordance. The study is keyed to data from the Carcinogenic Potency Data Base of Gold et al. (1984,1986,1987). From this database, Piegorsch et al. select the 405 chemicals with results both in mice and in rats. Each chemical is characterized by six numbers: d_m , the MTD in mice; b_m , the estimated potency in mice; c_m , the "carcinogenicity" in mice $(\n+$ " for mouse carcinogens, " $-$ " for mouse noncarcinogens); and dr, but if compared for ratio α , for ratio α , and it is set to zero; likewise for cr and but α The study uses a new measure of carcinogenicity for mice:

(2)
$$
\theta_m = \ln\left(1 + \frac{b_m}{\ln 2}\right).
$$

A similar equation defines θ_r for rats. Finally, pairs (d, θ) are obtained by pooling data for mice and rats. (Piegorsch et al. use "the literature" as well as NCI/NTP, and

take the site with highest estimated potency in males or females; see their Appendix A.)

Piegorsch et al. report a regression of $\ln d$ on $\ln \theta$:

(3)
$$
\ln d = 4.103 - 0.097 \ln \theta.
$$

Substituting equation (2) into equation (3) yields

(4)
$$
\ln d = 4.103 - 0.097 \ln \left[\ln \left(1 + \frac{b}{\ln 2} \right) \right],
$$

where d is the MTD and b is the potency.

Each simulation is characterized by three parameters: p_0 , the background rate of cancer; ρ , a parameter that controls the inter-species correlation; and α , a one-sided significance level. Based on these parameters, 2000 sets of 100 "chemicals" are generated. A "chemical" is generated as follows. Choose a pair (z_m, z_r) from a bivariate normal distribution with mean 0, variance 1, and correlation ρ ; let $\theta_m = 10^{-4+2\Phi(z_m)}$ and $v_r =$ 10 \cdots , where Ψ is the standard normal distribution function, compute the simulated MTD in mice d_m from θ_m , using equation (3); compute the simulated potency in mice v_m from the identity $v_m = (e^{-m} - 1) \wedge$ in 2, for rats, compute the MTD r from r from r from r from r μ . The resulting quadruplet (dm; bm; d, f) and μ , and μ a simulated chemical.

Each "chemical" is then subjected to a simulated $\rm NCI/NTP$ bioassay involving two species (mice and rats), three dose groups (control, low dose, high dose), and 50 animals per dose group. The probability of cancer follows the standard one-hit model: equation (1) with $p_{\text{max}} = 1.0$. A chemical is classified as "+" if a Cochran-Armitage Test on the bioassay results shows a statistically significant positive trend at the α level, one-sided. This leads to a classification as "++", "+-", "-+", or "--", where the first and second symbols denote the observed carcinogenicity in mice and rats, respectively. The original carcinogenicity indicators c_m and c_r and

the initial measures θ_m and θ_r of carcinogenicity play no role in these simulations, except to derive equations (3) and (4). By construction, all simulated chemicals are carcinogenic in both species, with positive values for θ_m and θ_r chosen as described above. (The test for trend is applied to tumor rates in the three dose groups; time-totumor is not considered: in the jargon of the field, the analysis is based on summary data rather than *lifetable data*.)

For a given triple of parameters (p_0, ρ, α) , 2000 sets of 100 chemicals are generated and classified. For each set of 100 chemicals, the concordance is computed. Then, the 2000 concordances are averaged. This entire process is repeated for many different values of p_0 , ρ , and α . The principal finding is that the observed concordances were always less than the true concordance, with an upper bound of about 80%.

Piegorsch et al. report that $p_0 = .10$, $\rho = .9$, and $\alpha = .025$ give simulated concordances that are similar to NCI/NTP data (Table 1). However, other aspects of that simulation are quite unrealistic, as shown in Figure 1 for mice (the plot for rats would be similar). The horizontal axis shows log potency; the vertical axis shows $log(1/MTD)$. Each of the 143 dots corresponds to an NCI/NTP bioassay that had signicant results in mice at the .025 level. The dotted line is the graph of equation (4), which is the relationship between MTD and potency built into the simulations. The real NCI/NTP data do not follow the theoretical line.

The box in Figure 1 was computed by generating 100,000 statistically signicant $(\alpha = .025)$ chemicals according to the procedure described above, using $p_0 = .10$ and $\rho = 0.9$. The horizontal edges of the box show the mean log potency, plus or minus three standard deviations. The vertical edges of the box show the mean $log(1/MTD)$. plus or minus three standard deviations. Among the 100,000 simulated chemicals, 98.1% had values inside the box. By contrast, among the 143 NCI/NTP chemicals, only 8 had values inside the box. The box covers only a very small part of the real data. Adding points to represent experiments in "the literature" other than

Figure 1: Assumptions in Piegorsch et al. (1992) Compared to NCI/NTP Data; Chemicals that are Statistically Signicant Carcinogens in the Mouse

NCI/NTP only accentuates the discrepancy: Piegorsch et al.'s trend line does not follow the data. For further discussion, see (Lin, 1994).

There is another unrealistic assumption that drives the results. In the simulations, all chemicals are carcinogenic both for mice and for rats by construction, so the true concordance is 100% —by assumption. It is not surprising that concordance is underestimated: the observed concordance has nowhere to go but down.

4. New Simulations

This section presents results from new simulations, with more plausible assumptions. Each "chemical" is generated as a set of "true" values $(c_m, c_r, x_m, x_r, y_m, y_r)$. The values c_m and c_r indicate carcinogenicity: $c_m = 1$ for mouse carcinogens, and $c_m = 0$ otherwise; likewise for c_r . The values x_m and x_r are the log MTD's for mice and rats. The values y_m and y_r are the "true" log potencies for mice and rats. For mouse noncarcinogens, $y_m = -\infty$; for rat noncarcinogens, $y_r = -\infty$.

Each "chemical" is subjected to the simulated $\rm NCI/NTP$ bioassay described in the previous section. The probability of cancer follows the one-hit model, equation (1), with a background cancer rate of $p_0 = 10\%$ and an upper bound of $p_{\text{max}} = 90\%$. (Compare Shlyakhter et al., 1992, p. 78.) If $y_m = -\infty$ or $y_r = -\infty$, the corresponding probability of cancer is simply the background rate. In effect, this procedure fits the standard one-hit model ($p_{\text{max}} = 1$) to the data, although the true value for p_{max} is 0.9. This amount of specification error does not seem unrealistic (Section 2).

As before, chemicals are classied by the Cochran-Armitage Trend Test. After testing, a chemical is characterized by a set of "observed" values $(\hat{c}_m, \hat{c}_r, x_m, x_r, \hat{y}_m,$ \hat{y}_r). The values \hat{c}_m and \hat{c}_r indicate statistical significance: $\hat{c}_m = 1$ if the trend for mice is statistically significant at the .005 level, and $\hat{c}_m = 0$ otherwise, and similarly for \hat{c}_r ; recall that x_m and x_r are log MTD's. Finally, \hat{y}_m and \hat{y}_r are the maximum likelihood estimates for log potency. There is an artifactual constraint on estimated potencies (Bernstein et al., 1985): in essence, $x_m + \hat{y}_m$ must be around 0 for mice when $\hat{c}_m = 1$, and likewise for rats. However, there is no constraint on "true" potencies, that is, $x_m + y_m$ varies freely as does $x_r + y_r$. The artifact is discussed below, in Section 6.

Each "chemical" $(c_m, c_r, x_m, x_r, y_m, y_r)$ is generated as an independent and identically distributed observation from random variables C_m , C_r , X_m , X_r , Y_m , Y_r , which is the variable condition and r . The variables α and α and α and α and α and α and α C_m and C_r , the log MTD variables X_m and X_r have a bivariate normal distribution with $corr(X_m, X_r) = .93$. (In the NCI/NTP data, the correlation between X_m and X_r was .93 for the 53 "++" chemicals, and did not vary much from cell to cell in the \mathcal{L} - \mathcal{L} . The variable critical conditions of \mathcal{L} , the variable matrix \mathcal{L} and $\$ and of the pair (X_m, X_r) . If $C_m = 1$, then ϵ_m is normally distributed, and otherwise m and probability one; likewise for r and r variables \sim μ and \sim μ are defined by the equations \sim μ \sim \sim μ \sim μ \sim μ \sim μ \sim μ \sim Each model is completely specified by the joint distribution of $(C_m, C_r, X_m, X_r, Y_m,$ $Y_r, \epsilon_m, \epsilon_r$). The statistical power of a simulated bioassay is determined by the ϵ 's. Indeed, m and r govern turn to an and the one hit model (1): bD r and r e e de MTD, while both the MTD, when D is discussed a chemical contract of the chemical is not a carcinogen, it does not cause cancer at any dose; thus, $b = 0$, $bD = 0$, $Y = -\infty$, and $\epsilon = -\infty$. See (Freedman et al., 1993; Lin, 1994). In the simulations, we use the 0.005 level, one-sided; this closely matches classification by "authors' opinion" (Haseman, 1983b; Gold et al., 1989). In the NCI/NTP data, there were 53 chemicals signicant at the .005 level in both species; Freedman et al. (1993) used the .025 level and found 87 chemicals signicant in both species. (Changing levels from .005 to .025 in our simulations would not alter the concordances appreciably; however, the 2 - 2 table would no longer match the NCI/NTP data so well, unless other parameters were also changed.)

Model A

We chose the parameters for Model A (Table 2) so that summary characteristics of simulated data would match the real NCI/NTP data, while observed concordance would overestimate true concordance: the bias is about 25 percentage points. The first row in Table 2 gives parameters for simulated chemicals that are "true" carcinogens in the mouse and in the rat $(C_m = C_r = 1)$. As shown in the third column, this category has 20% of the probability. The remaining columns describe the conditional distribution for $\tau = m$, and $\tau = m$, and $\tau = m$, given that $\tau = m$. For example, given that the $C_m = C_r = 1$, the log MTD for mice X_m is normally distributed with a mean of 2.0 and a standard deviation of 1.0; the log MTD for rats X_r is normally distributed with a mean of 1.6 and a standard deviation of 1.0; and so forth. The other three rows are read similarly; the dots in Table 2 indicate that the corresponding ϵ is $-\infty$. recall that with the called row α and α and α and α is a correlation of .93, while α is α are independent of each other and of the pair (X_m, X_r) . (Appendix A explains how parameters were chosen.)

In Model A, the variables C_m and C_r are independent, due to the choice of probabilities in Table 2. Specifically, the probability that a chemical is a rat carcinogen is 50%, whether or not it is a mouse carcinogen; likewise, the probability that a chemical is a mouse carcinogen is 40%, whether or not it is a rat carcinogen. Furthermore, for chemicals carecinogenic in both species, the yields mandatory in the species of the yields mandatory in the yields mandatory i sense, mice and rats are qualitatively and quantitatively independent.

The primary statistic of interest is concordance. Classifying chemicals based on α - α and corresponding and $\overline{}$ and $\overline{}$ are concorded to concordance the chemical set of chemicals, the ch

		Dist. of (C_m, C_r) Dist. of X_m		Dist. of X_r	Dist. of ϵ_m	Dist. of ϵ_r	
	c_m c_r prob.	Mean SD		Mean SD	Mean SD		Mean SD
	$1 \quad 1 \quad .20$	$2.0 \ 1.0$		1.6 1.0	$0.35 \quad 0.50$		$0.25 \quad 0.50$
$1 \quad 0$.20	2.3	09	1.8 0.9	$-0.20 \quad 0.50$		and the company of the
Ω	.30	$2.1 \quad 1.5$		1.8 1.5	and the company of the company		$-1.01 \quad 0.50$
$0 \quad 0$.30	27 10		22 09	the contract of the contract of	the contract of the contract of the	

Table 2: Parameters in Model A

"true" and "observed" concordance tables are computed. In order to check on the realism of the simulation, we also compute the mean and standard deviation of the log MTD variables x_m and x_r , for each of the four cells in the observed concordance table. For each of the two cells with $\hat{c}_m = 1$, we compute the mean and standard deviation of the estimated log potency \hat{y}_m . Likewise, for each of the two cells with $\hat{c}_r = 1$, we compute the mean and standard deviation of \hat{y}_r . Finally, for chemicals with $\hat{c}_m = 1$ and $\hat{c}_r = 1$, the correlations among x_m, x_r, \hat{y}_m , and \hat{y}_r are computed.

Each simulated dataset contains 297 chemicals, the number of NCI/NTP bioassays. The whole procedure of generating, testing, and classifying a set of 297 chemicals is repeated 1000 times. At the end of each simulation, there are 1000 "true" and 1000 "observed" concordance tables; there are also 1000 sets of means and standard deviations; and 1000 correlation matrices. The results are averaged and compared to NCI/NTP data.

Results for Model A

Results are presented in Table 3. The left hand 2 - 2 table is the average of the 1000 "true" concordance tables in the simulation. For each set of 297 chemicals, the number of "true $++$ " chemicals is random; on average, 59.3 chemicals were truly " $++$ ", and

the average true concordance was $\mathcal{L}_{\mathcal{A}}$. The right hand $\mathcal{L}_{\mathcal{A}}$ is the average of the observed concordance tables: on average, 52.8 chemicals were classified as " $++$ ", and the average observed concordance was 76%. The average observed concordance table from Model A was virtually identical to the observed concordance table for the NCI/NTP data (Table 1). The bias in observed concordance is about 25 percentage points, because the true concordance is 50%.

The MTD's and potencies generated according to Model A are very similar to NCI/NTP data. For example, consider the chemicals with statistically signicant results in both species (observed " $++$ "). Over 1000 sets of 297 simulated chemicals, the mean log MTD in mice of the observed $++$'s averaged 2.00, and the standard deviation of the log MTD's averaged 1.00. In NCI/NTP data, the " $++$ " chemicals have a mean log MTD in mice of 1.99 and a standard deviation of 1.02. See Table 4. Finally, the correlations among the simulated $++$ " chemicals closely match the correlations from NCI/NTP (Table 5). For results on the "+-", "-+", and "--" chemicals, see Appendix B.

			Model A: "True" Model A: Observed					
	Rats				Rats			
Mice	$+$ 59.3 59.4	Mice			$+$ 52.8 48.4			
	89.4 89.0				-22.1 173.8			

Table 3: Concordance for 297 Chemicals tested both in Mice and Rats

	Model A		NCI/NTP	
	Average	Average		
	of Means	of SD's	Mean	SD.
log MTD in mice	2.00	1.00	1.99	1.02
log potency in mice	-1.82	1.04	-1.80	1.09
log MTD in rats	1.60	1.00	1.60	1.02
log potency in rats	-1.47	1.04	-1.46	1.16

Table 4: Means and SD's for "++" Chemicals ($\hat{c}_m = \hat{c}_r = 1$)

	Model A				NCI/NTP	
	X_m X_r Y_m				X_m X_r Y_m	
1.00				1.00		
X_r .93 1.00				X_r .93 1.00		
	\hat{Y}_m -.96 -.89 1.00			\hat{Y}_m -.92 -.85 1.00		
	$-.89$ $-.96$ $.85$ 1.00				$-.85$ $-.88$ $.86$ 1.00	

Table 5: Correlations for "++" Chemicals $(\hat{c}_m = \hat{c}_r = 1)$

The Source of Bias in Concordance

It is natural to think that errors in classifying chemicals will cause concordance to go down, but this is not necessarily so. Each chemical belongs to one of four categories, depending on "true" mouse- and rat-carcinogenicity (i.e., " $++$ ", " $+-$ ", and so forth); also, each chemical belongs to one of four categories, depending on "observed" carcinogenicity. This gives rise to a 4 - 2 matrix. Although the area are not more presented in Table 6. The row totals give the average "true" number of each type of chemical, as reported at the left in Table 3. The column totals give the average "observed" number of each type of chemical, as reported at the right in Table 3.

On the average, over the 1000 sets of 297 chemicals, 59.3 were "true $++$ ". Most of these (52.5) were observed as " $++$ " in the simulated bioassays, but an average of $3.9+2.7=6.6$ were misclassified as discordant $(\n+ - \n)$ or $\n- + \n)$. Also, 89.0 chemicals were "true $--$ "; of these, an average of $.4+.4=.8$ were misclassified as discordant. The average total number of "false discordances" can thus be computed from the first and fourth lines of the table as $3.9 + 2.7 + .4 + .4 = 7.4$. On the other hand, the average total number of "false concordances" is, from the second and third lines,

True		Observed								
					Total					
	52.5	3.9	27	-2	59.3					
	.2	43.7		15.4	59.4					
		-3	18.9	70.0	89.4					
	.0	.4	.4	88.1	89.0					
Total	52.8	48.4	22.1	173.8	297 O					

Table 6: Simulation Results for Model A: Matrix of Classications

 $.2 + 15.4 + .1 + 70.0 = 85.7$. The number of false concordances is much larger than the number of false discordances: in particular, the "observed $--$ " cell is inflated, due to lack of power in the bioassay. This is what makes the observed concordance much larger than the true concordance.

Model B

We chose the parameters for Model B (Table 7) so that summary characteristics of simulated data would match the real NCI/NTP data, while observed concordance would greatly overestimate true concordance. In Model B, all chemicals are carcinogenic in at least one species, but only 18% are carcinogenic in both species. Averaged over 1000 sets of 297 chemicals, the true concordance was 18%, and the observed concordance was 77%. As with Model A, the average observed concordance table was virtually identical to the concordance table for NCI/NTP. The MTD's, estimated potencies, and correlations generated according to Model B were similar to those for NCI/NTP data (Appendix B). In particular, Model B more or less fits the NCI/NTP data; yet mouse carcinogens are, in this model, much less likely than mouse noncarcinogens to be rat carcinogens— 25% versus 100%.

	Dist. of (C_m, C_r)	Dist. of X_m		Dist. of X_r		Dist. of ϵ_m		Dist. of ϵ_r	
	c_m c_r prob.	Mean SD		Mean SD		Mean SD		Mean SD	
	1 1 1 18	2.0 1.0		$1.6 - 1.0$		$0.90 \quad 0.50$		$0.90 \quad 0.50$	
$1 \quad 0$	- 53	2.3 0.9		1.8 0.9		-0.85 0.50		and the company of the	
	- 29	21 15			1.8 1.5	the contract of the contract of		$-0.95 \quad 0.50$	

Table 7: Parameters in Model B

Model C

Our next simulation (Model C, Table 8) is designed to show that current bioassay design allows observed concordance in excess of 90%, with a true concordance even higher-by a little. In this simulation, means and SD's of log MTD and log potency match the real data reasonably well, as do the correlations (Appendix B); of course, the simulated observed concordance is much larger than the concordance seen in NCI/NTP data. As it turns out, the simulated observed concordance of 92% overestimates the "true" concordance in Model C, by about two percentage points.

	Dist. of (C_m, C_r) Dist. of X_m			Dist. of X_r		Dist. of ϵ_m	Dist. of ϵ_r	
	c_m c_r prob.	Mean SD		Mean SD		Mean SD		Mean SD
	$1 \quad 1 \quad .20$	2.0 1.0		$1.6 \quad 1.0$		$0.35 \quad 0.50$		$0.25 \quad 0.50$
$1 \quad 0$.05	2.3	-0.9	18	0.9	$-0.20 \quad 0.50$		the contract of the contract of
	.05	$2.1 \quad 1.5$			1.8 1.5	and the company of the company	$-1.01 \quad 0.50$	
	.70	24	10	20 -	09	the contract of the contract of the	the control of the control of the con-	

Table 8: Parameters in Model C

Model D

Model D is characterized in Table 9. All chemicals are either carcinogenic in both species, or carcinogenic in neither species. The true concordance in Model D is 100%. Averaged over 1000 sets of 297 chemicals, the observed concordance was 77%; the average concordance table from Model D was virtually identical to the concordance table from NCI/NTP data. Furthermore, the MTD's, estimated potencies, and correlations generated according to Model D were similar to NCI/NTP data (Appendix B). Thus, the bias in observed concordance can be downward by a substantial amount, as suggested by Piegorsch et al. (1992).

			Dist. of (C_m, C_r) Dist. of X_m		Dist. of X_r		Dist. of ϵ_m		Dist. of ϵ_r	
	c_m c_r prob.	Mean SD			Mean SD		Mean SD		Mean SD	
	$1 \quad 1 \quad 47$	20 10			1.6 1.0				-0.24 0.50 -0.51 0.50	
	$0 \t 0 \t 53$	$-2.5 - 1.0$			21 10				the contract of	

Table 9: Parameters in Model D

Discussion

Piegorsch et al. (1992) suggest that true concordance is greater than observed concordance, especially for chemicals that are only weakly carcinogenic; indeed, an observed concordance of 75% may imply a true concordance of nearly 100%, and observed concordance may have an upper bound of about 80%:

\investigations, using computer simulations, illustrate that the concordance underestimation can be rather severe even when restricted to a narrow range of relatively low underlying potencies. At these levels, average observed concordance may be limited to only about 80%, suggesting that observed values at or near 75% may in fact be indicative of greater agreement than previously considered ...concordance information at relatively low levels of potency can be seriously underestimated, weakening the overall measure of agreement exhibited by the data, and leading to suspect or unsure inferences. [p.119]"

These results have been cited as showing that observed concordance is biased downward, so that 80% is an upper bound on observable concordance; see, for instance, (Huff et al., 1991) and (Haseman and Seilkop, 1992). However, the results are based on assumptions about the true (unobservable) parameters governing chemical carcinogenicity. These assumptions are somewhat unrealistic (figure 1). Furthermore, Piegorsch et al. have in effect assumed that all chemicals are carcinogenic in both species, so true concordance is 100%. On that basis, observed concordance has nowhere to go but down.

As Models A and B demonstrate, it is possible to have low true concordance but moderately high observed concordance. It is even possible to have a high true concordance and a higher observed concordance (Model C). In these models, observed concordance is biased high, on the average across all chemicals. Of course, it is also possible to have a true concordance of 100% but only moderately high observed concordance (Model D).

Piegorsch et al. pointed out that bias in concordance could depend on toxicity; if so, stratication by the MTD would help. We examined this idea in Model A, by computing concordance separately for chemicals with mouse MTDs above and below 100. (The units of dose are \milligrams per kilogram of body-weight per day.") As it turned out, observed concordance was higher than true concordance for both groups of chemicals, by about 25 percentage points. Stratication does not seem to resolve the problem.

So far, we have shown that a variety of models—with radically different true concordances—can be fitted to the NCI/NTP data. It therefore seems unlikely that the true concordance can be estimated with any reasonable degree of condence from bioassay data, without imposing further constraints. Like previous authors, we used a variant of the one-hit model; we made some allowance for specication error, because—if examined in detail—the one-hit model will be rejected. For reviews, see Food Safety Council (1980), Freedman and Zeisel (1988); also see Peto et al. (1984), *Cancer Research* (1991) Vol. 51 No. 23 Part 2 pp.6407–6491, Hoel and Portier (1994).

Too, there are familiar difficulties in using the data to discriminate among models; for a recent discussion, see Kopp-Schneider and Portier (1991). The one-hit model is a special case of the \multistage model"; even this more general model will not fit a number of data sets (Freedman and Navidi, 1989, 1990). Also see Moolgavkar (1990, 1991, 1993, 1994), who discusses alternative models. Because of uncertainties about dose-response models, simulation studies are rather idealized versions of reality. Such studies cannot give definitive evidence about concordance, but can indicate the complexities in estimating measures of inter-species agreement from bioassay data.

Other literature

There have been many studies of concordance, either to validate species extrapolation or to analyze possible modifications of bioassay design. Some papers have been cited above. Also see, for instance, Griesemer and Cueto (1980), Purchase (1980), Haseman and Huff (1987), Haseman et al. (1987), Byrd, Crouch and Wilson (1990), Krewski, Goddard, and Withey (1990), Gold and Slone (1993), or Haseman and Lockhart (1993). Reproducibility of bioassay results is considered by Gold et al. (1987). For studies with a policy analysis flavor, see Lave et al. (1988), who use concordance data to argue that the current regulatory framework is not cost-effective; Ennever et al. (1990) consider the costs of uncertainties about concordance.

Worst-case analysis

In a bioassay, some 25 target tissues are examined, and risk assessment is based on the most sensitive site. In other words, classication of carcinogenicity is based on the response at the most sensitive site, and extrapolations from rodent to human are based on the potency at this site. However, rodent carcinogens often increase the tumor rate at some sites but decrease the rate at other sites—even in the same sex-species group in the same experiment. (A further complication: animals in the treatment groups tend to weigh less, and body weight is associated with tumor incidence.) We think that both the positive and the negative trends should be considered when assessing carcinogenicity—a topic not addressed in our simulations. (In effect, like previous authors, we studied concordance of worst-case analyses in mice and rats.) For reviews, see Haseman (1983a), Salsburg (1983), Freedman and Zeisel (1988), Davies and Monro (1994), Haseman and Johnson (1995).

5. Other Measures

There are many possible alternative measures to concordance. "Correlation" is the Pearson product moment correlation of the carcinogenicity indicators c_m and c_r . The true correlation is denoted $corr(c_m, c_r)$ and is estimated by $corr(\hat{c}_m, \hat{c}_r)$. For NCI/NTP data, the correlation is 0.45; see Table 10. Over 1000 sets of chemicals, the observed correlations in our four models averaged about 0.45, 0.45, 0.78, and 0.45, respectively. The "true" correlations averaged $0.0, -0.68, 0.73,$ and 1.00. (Models C and D were constructed so the true association would be strong.)

The "odds ratio" is defined as follows. Let n_{11} be the number of chemicals with $c_m = 1$ and $c_r = 1$; let n_{10} be the number of chemicals with $c_m = 1$ and $c_r = 0$; and so forth. Then

true odds ratio =
$$
\frac{n_{11}/n_{10}}{n_{01}/n_{00}} = \frac{n_{11} n_{00}}{n_{10} n_{01}}
$$

The corresponding estimator is

observed odds ratio =
$$
\frac{\hat{n}_{11}/\hat{n}_{10}}{\hat{n}_{01}/\hat{n}_{00}} = \frac{\hat{n}_{11} \ \hat{n}_{00}}{\hat{n}_{10} \ \hat{n}_{01}},
$$

Table 10: Bias in Correlation and Odds Ratio

where \hat{n}_{11} is the number of chemicals with $\hat{c}_m = 1$ and $\hat{c}_r = 1$, and so on. The odds ratio for NCI/NTP data is 8.7. The models gave average observed odds ratios of 9.2, 9.5, 107, and 9.6; however, the "true" odds ratios averaged 1.0, 0.0, 56, and $+\infty$. Correlation coefficients and odds ratios, like concordance, can be seriously biased; and the bias can go in either direction.

6. Inter-species Correlations of Carcinogenic Potency

Inter-species agreement can also be measured quantitatively. Crouch and Wilson (1979) observed a high inter-species correlation of log potencies among chemicals with statistically signicant results in both mice and rats. Bernstein et al. (1985) demonstrated that this high correlation could be explained as a statistical artifact; also see (Freedman et al., 1993). This section extends previous work, using a statistical model which explicitly represents both carcinogens and non-carcinogens, and distinguishes between "observed" and "true" potencies. The context is the NCI/NTP data discussed above.

The correlation of log potencies is 0.86 for the 53 NCI/NTP chemicals with statistically significant ($p \leq 0.005$, one-sided) potencies in both species; see the bottom right panel of Figure 2. To demonstrate the artifact in this correlation, suppose 10% of the animals in the control group of a standard NCI/NTP bioassay develop cancer. If the bioassay results are statistically signicant and not all the dosed animals develop cancer, then the maximum likelihood estimate of log potency will be within 0.9 of $log(1/MTD)$; that is,

(5)
$$
\log(1/\text{MTD}) - 0.9 < \log(\text{estimated potency}) < \log(1/\text{MTD}) + 0.9
$$
.

Figure 2: MTD's and Potencies; Chemicals with Statistically Significant Potencies in NCI/NTP Bioassays; Logs to Base 10

Inequality (5) is essentially the one in Bernstein et al. (1985), except the bounds are appropriate for NCI/NTP data (Lin, 1994); also see Gaylor and Gold (1995). In (5) and in Figure 2, logs are to base 10. Variability in control tumor rates may widen the bounds a little; so do lifetable adjustments to the estimates.

Let a be the MTD for a chemical, and let v be the estimated potency. Use the \overline{a} subscripts m and r to denote species. As shown in the top left panel of Figure 2. $\log(a_m) \approx \log(a_r)$. Equation (2) says that $-0.9 \le \log(a_m) + \log(a_m) \le 0.9$ and $-0.9 < \log(v_r) + \log(u_r) < 0.9$. Thus, $\log(v_m) \approx -\log(u_m)$, as shown in the top right panel, also, $\log(\sigma_r) \approx -\log(a_r)$, as shown in the bottom left panel. It follows that $\log(\nu_m) \approx \log(\nu_r)$. This is the artifact, which explains the high correlation in the bottom right panel.

In our simulations, the correlations for chemicals classified as $++$ were similar to the correlations in NCI/NTP data. Take Model A, for instance, and restrict attention to chemicals with statistically signicant potency estimates: the inter-species correlation of estimated log potencies averaged 0.85, which is virtually identical to the correlation of 0.86 in NCI/NTP data (Table 5). Mice and rats were qualitatively independent in Model A, in the sense that the carcinogenicity indicators C_m and C_r are independent. Among the true carcinogens $(C_m = C_r = 1)$, the true tumor yields m and independent. These results suggests suggests that the inter-species correlation of log potencies could be almost entirely artifactual, which confirms the findings in Bernstein et al. (1985) and Freedman et al. (1993). The results would also seem to dispose of the suggestion by Goodman and Wilson $(1991, p.212)$ "that the relationship [between potencies in mice and rats] is indeed stronger than what is implied by the constraints alone."

If all the animals in the nonzero dose groups develop tumors at the same site, then the estimated potency is infinite. However, very few chemicals cause 100% tumor incidence. This might have some biological signicance, but it might also point to

other artifacts, such as errors in necropsy reports; for dicussion, see (Bernstein et al., 1985; Freedman et al., 1993; Krewski et al., 1993).

Crouch et al. (1987) responded to Bernstein et al. (1985) by claiming that the relationship between potency and MTD is based on biology, not statistics. Likewise, Goodman and Wilson (1992) observed that few chemicals have log(estimated potency - MTD)>1, and argued for biological signicance; however, on the whole, this seems to be another manifestation of the artifact—and the absence of 100% tumor rates.

The MTD is barely sub-toxic. Therefore, animals in the high dose group may experience chronic cell killing and cell replacement, which tends to increase the risk of cancer. Thus, toxicity is viewed as related to carcinogenicity. Inequality (5), on the other hand, derives from bioassay design; it is the design of the experiments that precludes estimated potencies in the range $(0, \text{MTD}/10)$ or $(10 \text{MTD}, \infty)$. Furthermore, the relationship between toxicity and carcinogenicity is a major complication in dose extrapolation, if tissue damage is much less—or much more easily repaired—at low environmental doses. For discussion of such issues, see Bernstein et al. (1985), Gold et al. (1989), Gold (1990), Ames and Gold (1990), Cunningham and Matthews (1991), Gold et al. (1992), Cohen and Ellwein (1992), Freedman et al. (1993), or Ames, Gold, and Willett (1995); the last is a compact introduction to cancer biology and epidemiology.

Recent papers on quantitative inter-species agreement and the artifact include Whipple (1985), Rieth and Starr (1989), (Krewski et al., 1990, 1993); Kodell et al. (1991) discuss the role of the model. The extrapolation from rodents to humans is discussed in (Freedman and Zeisel, 1988), (Gold et al., 1989), (Gold et al., 1992); also see (Gaylor et al., 1993); Allen et al. (1988) take a more optimistic view, as do Goodman and Wilson (1991, 1992). Kodell et al. (1995) suggest that the observed interspecies correlation in potency may be biased low; they use the one-hit model, assuming further that (1) all chemicals are carcinogenic in both species, and

(2) bioassays give unbiased estimates of potencies; in effect, measurement error attenuates the correlation. Our simulations indicate, however, that the situation may be more complicated than pure measurement error.

To avoid the artifact, various authors have suggested expanding the test set of chemicals, for instance, to include positive but insignicant potencies, or to replace estimates that are 0 by upper 95%-condence limits, or to truncate estimates from below at small, positive values. None of these strategies seem to be effective: see Bernstein et al. (1985), Freedman et al. (1993), or Lin (1994).

We turn now to the "true" values in our simulations. Recall that X is log MTD, Y is log potency, and $\epsilon = X + Y$ is the log tumor yield; X is observable, but Y and ϵ are unobservable. In all our models, the X 's for mice and rats are highly correlated and vary widely across experiments, just as in real data. Now, we restrict attention to chemicals carcinogenic in both species. The ϵ 's are independent and have a relatively small standard deviation (for instance, see line 1 of Table 2). It follows that the Y 's must be highly correlated, since $Y = -X + \epsilon$. The correlation in the Y's is purely artifactual, driven solely by the correlation between the X 's. This artifact holds at the level of "true" but unobservable quantities, and mimics the artifact discovered by Bernstein et al. (1985), which holds at the level of data.

On the other hand, if the X's are highly correlated but the Y's are made to be independent, then the ϵ 's would necessarily be correlated. In short, given the high correlation in the X's, either the Y's must be correlated or the ϵ 's; that is arithmetic, not biology. Of course, in Tables 2 and 7-8-9, the parameters for ϵ_m depend on C_r ; the same is true for μ and μ and is the constant α and non-carcinogens are considered as τ is a permitted value, and τ is a permitted value, η and τ are dependent.

7. Conclusions

In NCI/NTP data, the observed concordance between mice and rats is about 75%. However, true concordance may be much higher—or much lower. Simulation studies do not determine the direction of the bias, but suggest that bias can be substantial, and in either direction. Since a variety of models more or less fit the data, it does not seem likely that true concordance can be determined without making substantial additional modeling assumptions. Furthermore, previously reported quantitative correlations of interspecies potencies can easily be explained in terms of statistical artifact. In our present state of knowledge, it seems unlikely that the true correlation can be estimated from bioassay data.

Appendix A

This section explains how parameters were chosen. Use the letters C, X, Y, and ϵ for random variables. The variable C indicates "true" carcinogenicity: $C = 1$ for "true" carcinogens, and $C = 0$ otherwise. The variable X stands for log MTD. The variable Y stands for true log potency; if a chemical is not a carcinogen, $Y = -\infty$. Finally, the letter ϵ stands for true log yield. For the carcinogens, $\epsilon = X + Y$; for the noncarcinogens, $\epsilon = -\infty$.

Use "hats" to denote observed values from the bioassay. Among the random variables, \cup indicates whether the chemical was an $\,$ observed $\,$ carcinogen (i.e., had a \mathcal{S} ratistically significally trend at the .005 level), \mathcal{I} is the maximum intenflood estimate of log potency, and $\hat{\epsilon}$ is the maximum likelihood estimate of log yield. Among $\mathcal{N}(U)$ is the microsity of U is log $\mathcal{N}(U, V)$ is estimated log potency, D indicates whether ℓ is statistically significally, and $\ell = \nu + \ell$. (It is assumed that log MTD can be

		\bf{Model}			NCI/NTP
	Mice	Rats		Mice	Rats
"true" carcinogenicity	C_m	C_r			
"true" log MTD	X_m	X_r	U_m		U_r
"true" log potency	Y_m	Y_r			
"true" log yield	ϵ_m	ϵ_{r}			
statistical significance	\hat{C}_m	\hat{C}_r	\hat{D}_m		\hat{D}_r
estimated log potency	\hat{Y}_m	\hat{Y}_r	\hat{V}_m		\hat{V}_r
estimated log yield	$\hat{\epsilon}_m$	$\hat{\epsilon}_r$	$\hat{\delta}$		$\hat{\delta}_r$

Table 11: Notation

measured without error.) The notation is laid out in Table 11.

Use the subscripts m and r to denote species. Each of the pairs (ϵ_m, ϵ_r) and (X_m, X_r) is assumed to have a bivariate normal distribution. The pair (ϵ_m, ϵ_r) is assumed to be independent of the pair (X_m, X_r) , that is, tumor yields are independent of MTDs. These assumptions are at least approximately true for real data. For example, for the 33 NOI/NTT chemicals with $D_m = 1$ and $D_r = 1$, the pair (v_m, v_r) is approximately uncorrelated with the pair (U_m, U_r) ; see Table 12. (Of course, in real data, the "true" tumor yields are unobservable.)

Picking the parameters involves choosing the yields, the true concordance, and the MTD's. The first step was choosing parameters for the ϵ 's. Given $C_m = 1$ and $C_r = 1$, the conditional expected value for ϵ_m was chosen by judgment, and likewise for the conditional expected value for ϵ_m given $C_m = 1$ and $C_r = 0$. Also, given $C_m = 1$ and $\mathbf r$ for conditional expected value for $\mathbf r$ likewise for the condition expected value for α and α and α and α and α and α α

	U_m	U_r	
	U_m 1.00		
U_r		$.93 \quad 1.00$	
$\hat{\delta}_m$		$.04$ $.03$ 1.00	
$\hat{\delta}_r$	$-.07$ $-.01$ $.45$ 1.00		

Table 12: Correlations in NCI/NTP Data, the 53 " $++$ " Chemicals

the conditional expectations for the ϵ 's were set equal to the observed values from NCI/NTP data; for example, the conditional expectation for ϵ_m given $C_m = 1$ and $C_r = 1$ was set equal to the average value of v_m for chemicals with $D_m = 1$ and D_r = 1. The initial values for the conditional expectations were then modified by judgment.) Then, for chemicals with $C_m = 1$, the conditional standard deviation of ϵ_m was set at 0.5, which was the value for $SD(\ell_m|\mathcal{D}_m = 1)$, rounded to one decimal $\mathbf r$ and the chemical statement with Cr $\mathbf r$, $\mathbf r$, the conditional standard deviation of $\mathbf r$ was set at 0.9, which was the value for $SD(v_r | D_r = 1)$, again rounded to one decimal place. Finally, $corr(\epsilon_m, \epsilon_r)$ was set to zero; this makes the interspecies correlation of log potencies purely artifactual.

The next step was determining the probabilities for the "true" concordance table. There are four possible values for the pair (C_m, C_r) . Given a particular set of values for C_m and C_r , there are four possible classifications (C_m, C_r) . This gives rise to a 4 λ 4 transition matrix. Can this matrix M , the i _l entry of M gives the probability that a chemical of type i will be observed to be type j , where a type 1 chemical is " $++$ ", a type 2 chemical is " $+-$ ", and so forth. The matrix M controls the rate at which chemicals are misclassied. The various probabilities in ^M were found by numerical integration; of course, these depend on the mean and SD of the ϵ 's, which control the power of the trend test. (Table 6 is an empirical analog to M in Model

A, rescaled from probabilities to numbers.)

Let p be the row vector of proportions of NCI/NTP chemicals that are observed "++", "+-", "-+", and "--". For example, $p(++) = 53/297 = .178$; see Table 3. Let π be the row vector of probabilities for the model chemicals. The column vector μ for model A is shown in Column 3 or Table 2. The row vector μ was chosen for Model A as follows. Thist, π_0 was set equal to p_M \rightarrow , then π_0 was founded slightly to achieve independence. For Models B and D, some elements of π_0 were slightly negative; these were truncated at zero, then π_0 was scaled and rounded so that the sum of entries was equal to 1. For Model C, the vector π was chosen by judgment.

The final step was determining parameters for the log MTD's. The conditional distribution for the X's was chosen as follows. Given C_m and C_r , the conditional correlation $corr(X_m, X_r)$ was set at .93; see Table 12. Next, $SD{X_m|C_m = a}$ and $C_r =$ b} was set equal to the standard deviation of U_m for those NCI/NTP chemicals with $D^{}_m$ = a and $D^{}_r$ = v. The conditional standard deviation for $\Lambda^{}_r$ was chosen similarly. If $a > 0$ or $b > 0$, then $E{X_m|C_m = a}$ and $C_r = b$ was set equal to the mean of U_m for those NCI/NTI chemicals with $D_m = u$ and $D_r = v$, likewise for X_r . For chemicals with $C_m = 0$ and $C_r = 0$, the conditional mean of X_m was chosen so that the unconditional mean $E(X_m)$ would match the overall average of U_m for NCI/NTP chemicals; likewise for X_r . Finally, all the conditional means and conditional standard deviations for the X 's were rounded to one decimal place.

Other things being equal, the observed concordance depends on the parameters for the true log τ and τ and τ if the true σ true τ if the true τ chemicals, if the true τ are both either very high or very low, the observed concordance is maximized; if one true yield is high and the other is low (say, m is high and ^r is low), then observed concordance goes down. In the true " $+ -$ " and " $- +$ " cells, high true yields in one species lead to low observed concordance, and low true yields lead to high observed concordance (classification as " $---$ ").

Appendix B

This section presents results for the simulations. As before, X_m is log MTD in mice, Λ_r is log mTD in rats, T_m is estimated log potency in mice, and T_r is estimated log potency in rats. The " $++$ " part of Table 13 appears as Text Table 4.

		" $++$ " Chemicals			" $+-$ " Chemicals					
	Model A		NCI/NTP		Model A		NCI/NTP			
	Avg. of Avg.				Avg. of	Avg.				
	Means	of SD's	Means	SD.	Means	of SD's	Means	SD		
Mice:										
log dose	2.00	1.00	1.99	1.02	2.27	0.91	2.28	0.86		
log potency	-1.82	1.04	-1.80	1.09	-2.35	0.98	-2.30	1.05		
Rats:										
log dose	1.60	1.00	1.60	1.02	1.79	0.91	1.80	0.90		
log potency	-1.47	1.04	-1.46	-1.16	\bullet	\bullet	\bullet	\bullet		

		" $-+$ " Chemicals					" $-$ " Chemicals		
		Model A		NCI/NTP		Model A		NCI/NTP	
	Avg. of Avg.					Avg. of	Avg.		
	Means	of SD's	Means	SD.		Means	of SD's	Means	SD
Mice:									
log dose	-2.11	1.42	2.10	1.45		2.42	1.25	2.41	0.95
log potency	~ 100 km s $^{-1}$	~ 100	\bullet . 	\bullet		\bullet	\bullet	\bullet	\bullet
Rats:									
log dose	1.80	1.42	1.75 1.49			2.00	1.19	2.01	0.89
log potency -2.13		-1.47	-2.15	-1.58		\bullet	\bullet	\bullet	

Table 13: Means and SD's for Model A

Table 14: Concordance for 297 Chemicals tested both in Mice and Rats

		" $-+$ " Chemicals				" $-$ " Chemicals					
		Model B		NCI/\overline{NTP}		Model B		NCI/NTP			
	Avg. of Avg.					Avg. of	Avg.				
	Means	of SD's	Means	SD		Means	of SD's	Means	SD		
Mice:											
log dose	2.09	1.47	2.10	-1.45		2.23	1.16	2.41	0.95		
log potency	~ 100	~ 100 m $^{-1}$	\mathbf{A} and \mathbf{A} and \mathbf{A}	Contract Contract		\bullet	\bullet		\bullet		
Rats:											
log dose	1.79	1.47	1.75	- 1.49		1.80	1.16	2.01	0.89		
log potency	-2.15	1.49	-2.15	-1.58		\bullet	\bullet	\bullet	\bullet		

Table 15: Means and SD's for Model B

Model B						NCI/NTP						
	X_m	X_{r}	\boldsymbol{m}				X_m	X_{r}	m			
	$1.00\,$						1.00					
	.93	1.00						$.93 \quad 1.00$				
	\hat{Y}_m -.98 -.91 1.00							$-.92 - .85 1.00$				
$\hat{\mathbf{V}}$	$-.91$	$-.98$.90	$1.00\,$		V .		$-.85 - .88$.86	$1.00\,$		

Table 16: Average Correlations for "++" Chemicals $(\hat{c}_m = \hat{c}_r = 1)$ from Model B

	Model C: "True"				Model C: Observed	NCI/NTP		
		Rats			Rats			Rats
Mice		$+$ 58.9 14.7 Mice			$+$ 52.0 15.8 Mice		-53	-48
		$-$ 14.7 208.6		69	-222.3			-22 174

Table 17: Simulation Results for Model C: Concordance

		" $-+$ " Chemicals				" $-$ " Chemicals					
		Model C		NCI/NTP		Model C		NCI/NTP			
	Avg. of Avg.					Avg. of	Avg.				
	Means	of SD's	Means	SD.		Means	of SD's	Means	SD		
Mice:											
log dose	2.11	1.16	2.10	- 1.45		2.38	1.03	2.41	0.95		
log potency	~ 100	~ 100	$\sim 10^{-11}$	\bullet		\bullet	\bullet	\bullet	\bullet		
Rats:											
log dose	1.76	1.16	1.75	1.49		1.98	0.94	2.01	0.89		
log potency -1.85		1.04	-2.15 1.58			\bullet	\bullet	\bullet	\bullet		

Table 18: Means and SD's for Model C

Model C						NCI/NTP						
	X_m	X_r	\cdot m					X_r	Y_m			
X_m	1.00						1.00					
	X_r .93 1.00						X_r .93 1.00					
	\hat{Y}_m -.96 -.89 1.00							$-.92 - .85 1.00$				
		$-.89$ $-.96$ $.86$		1.00				$-.85 - .88$.86	1.00		

Table 19: Average Correlations for "++" Chemicals $(\hat{c}_m = \hat{c}_r = 1)$ from Model C

	Model D: "True"				Model D: Observed		TP		
	Rats				Rats				Rats
Mice	$+$ 139.6	0.0	Mice		$+$ 53.1 47.4	Mice		-53	- 48
	(1.0)	1574		-220	-174.5			99.	

Table 20: Simulation Results for Model D: Concordance

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		" $-+$ " Chemicals				" $-$ " Chemicals					
		Model D		NCI/NTP		Model D		NCI/NTP			
	Avg. of Avg.					Avg. of	Avg.				
	Means	of SD's	Means	SD		Means	of SD's	Means	SD		
Mice:											
log dose	2.02	0.99	2.10	-1.45		2.44	1.01	2.41	0.95		
log potency	~ 100	Contract Contract Ave	Contract Contract Ave			\bullet	\bullet				
Rats:											
log dose	1.61	0.99	1.75	-1.49		2.04	1.01	2.01	0.89		
log potency	-1.85	1.04	-2.15	- 1.58		\bullet	\bullet	\bullet	\bullet		

Table 21: Means and SD's for Model D

Model D						NCI/NTP						
	X_m	X_{r}	\boldsymbol{m}				X_m	X_{r}	m			
	1.00						1.00					
	.93	1.00						$.93 \quad 1.00$				
	\hat{Y}_m -.96 -.89 1.00							$-.92 - .85 1.00$				
	$-.89$	$-.96$.86	$1.00\,$		V .		$-.85 - .88$.86	$1.00\,$		

Table 22: Average Correlations for "++" Chemicals $(\hat{c}_m = \hat{c}_r = 1)$ from Model D

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