

ANTENATAL SCREENING FOR CHROMOSOMAL ABNORMALITIES

This invention relates to a method for antenatal screening for chromosomal abnormalities and to an apparatus for performing the method.

The risk of Down Syndrome and some other chromosomal abnormalities in a foetus is known to increase with the age of the mother and it is this knowledge which forms the basis for selection of pregnant women for further investigation. Further investigation in the case of Down Syndrome involves sampling of the amniotic fluid by amniocentesis, a procedure which itself carries a risk for the mother of the foetus, induction of a miscarriage being a recognised hazard of this procedure.

Maternal serum markers for Down Syndrome are widely used for antenatal screening for this chromosomal abnormality, the most common of these markers being alpha-fetoprotein (AFP), human chorionic gonadotropin (hCG) - either the intact molecule thereof or its beta subunit - and unconjugated estriol (UE). Disclosures relating to the use of these markers, which may be used in combination with maternal age, in antenatal screening for Down Syndrome include US Patent 4,874,693, WO 89/00696 and WO 90/08325. US Patent 5,100,806 discloses the use of the beta subunit of hCG as a marker in antenatal screening for Edwards Syndrome.

One method of prenatal screening for fetal Down Syndrome in the second trimester of pregnancy uses a combination of maternal age and maternal serum (AFP), (hCG) and (UE). In fetal Down Syndrome the maternal serum concentrations of (AFP) and (UE) are slightly lower than in normal pregnancies, when the concentrations are expressed relative to the median concentration found in unaffected pregnancies at the

same age of gestation (termed the multiple of the median in unaffected pregnancies or MoM). In contrast the concentration of maternal serum hCG MoM is higher in Down Syndrome affected pregnancies. The concentrations of all three markers (as log MoM) are approximately Gaussian distributed and the distributions for unaffected and affected pregnancies overlap. The overlap in values is such that it is impossible to choose a cut-off point which will clearly discriminate between the two populations.

Knowledge of the concentration of each analyte is of considerable value, as rather than revealing to which population the sample value belongs, it reveals the probability of the sample being taken from a particular population. The principles involved can be demonstrated by a graph of frequency against MoM (log scale) such as Figure 1 which relates to (AFP). This demonstrates the principles involved in calculating the likelihood that a sample has come from a Down Syndrome affected pregnancy, in this case for maternal serum (AFP), although the same principle applies to (hCG), (UE) or any marker, biochemical or otherwise in which the distributions in affected and unaffected pregnancies differ.

More information can be gained by combining markers than by using them individually. There is no theoretical limit to the number of markers which can be combined and the principle and practice of combining them is well known statistically. For Down Syndrome screening the likelihood ratio is derived from the two trivariate normal distributions for unaffected and affected pregnancies using maternal serum AFP, UE and hCG. Maternal age is another marker for Down Syndrome, the risk being much higher in older women. As none of the serum markers has been shown to

be related to any of the maternal serum analytes, then by Baye's theorem the final combined risk of having a child with Down Syndrome for an individual woman is obtained by multiplying the likelihood that the
5 maternal serum markers' values belong to an affected population by the a priori age risk.

The final combined risk may then be used to counsel women about their risk. If their judgement is that the risk is high then they may wish to proceed to
10 amniocentesis so that fetal cells may be obtained and a firm diagnosis made. The amniocentesis procedure carries with it a risk of miscarriage of the order of 0.5% to 1.0%. Thus for a woman with a combined risk of Down Syndrome of 1:400, her risk of losing the baby
15 through the amniocentesis is higher than her risk of having a child with Down Syndrome. Conversely a woman with a combined risk of 1:10, may feel that the risk is high enough to warrant amniocentesis.

It has been estimated that selecting the 5% of
20 women screened and found to have the highest risk would enable detection of approximately 60% of Down Syndrome affected pregnancies.

It is therefore desirable to develop improved methods of antenatal screening for chromosomal.
25 abnormalities.

According to the present invention we provide a method for antenatal screening for abnormalities in a foetus in which the gestational age of a pregnant woman is determined characterised in that the
30 gestational age is determined (a) by reference to the last menstrual period dates and (b) by a biometric measurement of the foetus, the difference between the ages as determined in (a) and (b) is calculated and the calculated difference is examined using reference
35 data to determine fetal chromosomal abnormalities.

Further according to the present invention we provide an apparatus comprising means adapted for receiving measurements relating to a foetus carried by a pregnant woman and computer means for comparing the
5 measurements to reference data to determine fetal abnormalities characterised in that the measurements relate to the difference between the gestational age of the woman as determined (a) by reference to the last menstrual period dates and (b) by a biometric
10 measurement of the foetus.

Some chromosomal and other abnormalities show growth retardation in a foetus, i.e. the foetus is not as large as would be expected from the gestational age. Gestational age is usually estimated from the
15 date of the last menstrual period. It can also be determined by a biometric measurement of the foetus. Usually biometric measurements are made using ultrasonography but other means are possible, for example nuclear magnetic resonance (NMR). The most
20 common estimate of gestational age by biometric measurement using e.g. ultrasonography is derived from measurement of the distance between the parietal lobes, the biparietal diameter (BPD). Other measurements that can be made include crown to rump,
25 humerus, orbit to orbit, abdominal circumference, ear size and femur length. Of these measurements the crown to rump measurement is usually made during the first trimester of pregnancy whilst the other measurements are best made later during the second trimester. The
30 preferred measurement to be made using ultrasonography in the method of the invention varies to some extent depending upon the chromosomal defect which is to be detected.

In the determination of the gestational age from
35 the last menstrual period, the calculation is made

using the elapsed days since the first day of the last menstrual period.

If the gestational age assessed by biometric measurement is significantly less than that calculated
5 from the last menstrual period there is the possibility that intra-uterine growth retardation has occurred. There are however other possible causes of such a discrepancy, the most notable being that the date of the last menstrual period has not been
10 recalled accurately.

The method of the invention can be used for antenatal screening for a wide range of chromosomal abnormalities. It is particularly useful for detection of Edwards Syndrome (Trisomy 18), Open Spina Bifida
15 and Patau Syndrome (Trisomy 13). Other abnormalities which may be detected include Down Syndrome (Trisomy 21), Turner Syndrome (Monosomy X) and Klinefelter's Syndrome. The method of the invention may be used to screen for individual abnormalities or to screen for
20 groups of abnormalities together, for example it could be used to screen for both Trisomy 18 and Open Spina Bifida.

The method of the invention can be used in combination with measurement of one or more other
25 markers such as maternal age and/or one or more components of a maternal fluid including urine, saliva, cerebrospinal fluid and in particular serum markers from maternal blood samples (from plasma or whole blood). In particular it can be used together
30 with measurement of the serum markers free beta hCG and pregnancy associated plasma protein A (PAPPA) as described in our copending UK Patent Application No. 9224965.5. Other markers which may be measured include alpha-fetoprotein (AFP), progesterone (Pr), 16-alpha-
35 hydroxy-dehydroepiandrosterone sulphate (16-alpha-

hydroxy-DHEAS) and dehydroepiandrosterone sulphate (DHEAS), intact inhibin (In) and its subunits, Schwangerschaft Protein 1 (SP1), free alpha subunit of hCG and precursors and metabolites of these markers.

5 Thus one or more of these other markers may be measured together with the principal markers used in the method of the invention. For example the method of the invention may be used with the gestational ages, hCG, PAPPa and AFP as the markers to be measured.

10 The method of the invention is suitably carried out in the period from 8 to 22 weeks of pregnancy with the period from 14 to 22 weeks being preferred.

The invention is illustrated by the accompanying drawings wherein :

15 Figure 1 is a graph of Frequency against AFP MoM (on a log scale) which shows the distribution of maternal serum AFP in a Down Syndrome pregnancy (Curve 1) and in a normal pregnancy (Curve 2).

20 Figure 2 is a graph of percentage frequency against the gestational discrepancy, i.e. the difference in days between the gestational ages determined by reference to the last menstrual period and by biometric measurement - in this case by ultrasonography.

25 Figure 3 is referred to in Example 1 and is a graph of relative frequency and gestational discrepancy (as in Figure 2) showing the difference between a Trisomy 18 affected pregnancy (Curve 3) and an unaffected pregnancy (Curve 4).

30 Figure 4 is referred to in Example 3 and is a graph of detection rate for Trisomy 18 against false-positive rate.

35 Figure 5 is referred to in Example 4 and is a graph of relative frequency against AFP multiple of median (log scale).

Figure 6 is referred to in Example 4 and is a graph of detection rate for Trisomy 18 against false-positive rate.

Figure 7 is referred to in Example 6 and is a
5 graph of detection rate for Trisomy 18 against screen-positive rate.

Figures 8 and 9 are referred to in Example 7 and are graphs of relative frequency against multiple of median (log scale) for hCG and UE respectively.

10 Figure 10 is referred to in Example 8 and is a graph of relative frequency against LMP-USS (days).

Figure 11 is referred to in Example 8 and is a graph of relative frequency against AFP multiple of median (log scale).

15 Figure 12 is referred to in Example 10 and is a graph of detection rate for Open Spina Bifida against screen-positive rate.

Figure 2 is the result of a clinical trial conducted at 6 centres throughout Europe from which
20 1761 pregnancies of known normal outcome were identified which had gestational age determined by ultrasound biometry and by reference to the last menstrual period. It shows that the difference in gestational ages (in days) between the ages as
25 determined by reference to the last menstrual period and by biometric measurement (ultrasonography) - termed the gestational discrepancy - has an approximately Gaussian distribution of values. The mean value of approximately +3 days reflects the fact
30 that more women will mistakenly overestimate their gestational ages than will mistakenly underestimate them, and that the dates determined using ultrasonography are constructed from formulae derived from women with well characterised dates for their
35 last menstrual periods.

If a chromosomal or other abnormality is associated with growth retardation then the Gaussian distribution of values will be shifted to the right. For example fetuses with Trisomy 18 are known on average to show a discrepancy in gestational ages of approximately 2 weeks. The two overlapping distributions of dating discrepancies are as shown in Figure 3. These two overlapping distributions are completely analogous to those with maternal serum markers, for example with AFP as shown in Figure 1.

It is possible therefore to derive a likelihood ratio that a given discrepancy in dates is due to Trisomy 18, or to another abnormality associated with intra-uterine growth retardation, in an exactly analogous manner to that illustrated for maternal serum AFP in Figure 1.

Furthermore it is possible to combine the discrepancies in gestational ages with other biochemical or other markers for the abnormality, in a multivariate calculation of risk, since it is known for example that maternal serum hCG, UE and AFP are all lower in uncomplicated Trisomy 18 pregnancies. The principle of combining several markers for foetal abnormality in multivariate models has been described by Reynolds and Penney (Ann. Clin. Biochem., 27, 452-458, 1990,)

The invention has been discussed generally in relation to Trisomy 18, but other chromosomal abnormalities are also associated with intra-uterine growth retardation, for example Open Spina Bifida, Triploidy and Turner Syndrome. All of these abnormalities have associated maternal serum biochemical markers.

Other markers used need not be restricted to maternal serum, but may also be measured in amniotic fluid.

5 The invention has the advantage that it enables the detection rate for foetal abnormalities to be increased using information which is routinely collected from many women.

EXAMPLE 1

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As part of large multicentre trials in the United Kingdom and elsewhere in Europe 7 cases of Trisomy 18 and 521 unaffected maternal serum control samples were identified. All samples were measured for maternal serum AFP, hCG and UE. In each case the gestational ages were known both by reference to the last menstrual period and by foetal biometry of the biparietal diameter. All three analytes measured change with gestational age. From the control data regressions were performed of the unaffected median value at each gestational week, versus the ultrasound measured gestation in weeks, weighted by the number of contributory samples at each week. For AFP and UE this took the form of a linear regression of the natural log of the MoM value $\{\ln(\text{MoM})\}$, versus gestational age in days. For hCG it took the form of an exponential decay.

20 Using these regression equations each analyte value from both Trisomy 18 and unaffected samples was divided by the unaffected median value for that gestational day, the latter being derived from the regression equations.

30 Table 1 gives the details of the Trisomy 18 cases. Table 2 gives a summary of the statistical analysis of the Trisomy 18 cases together with the 521

control samples. There was no statistically significant difference in standard deviations between the controls and Trisomy 18 cases; the standard deviations were therefore pooled. The gestational age discrepancy was calculated as last menstrual period derived gestation in days (LMP) - ultrasound derived gestation in days (USS).

TABLE 1

Women with Trisomy 18 affected pregnancies

Patient ID	USS	LMP	LMP-USS	AFP IU/ml	AFP MoM	AFP ln (MoM)
B0211	101	119	18	22.93	0.830	-0.186
B0250	136	155	19	61.87	1.192	0.176
B0289	115	140	25	34.85	0.980	-0.020
B0340	115	120	5	33.08	0.930	-0.072
B0379	113	141	28	18.42	0.537	-0.622
G0346	108	117	9	13.54	0.432	-0.839
G0347	136	145	9	28.56	0.550	-0.597

TABLE 2

Statistical parameters

	Trisomy 18	Unaffected Control
n	7	521
mean	16.14	
2.197		
pooled standard deviation	4.65	
4.65		

It can be seen that there is a marked difference in the distribution of the gestational age discrepancy between the Trisomy 18 cases and the controls. The Trisomy 18 cases show on average 16.1 days earlier gestation when assessed by ultrasound biometry than by LMP dating.

The discrepancies in dating were found to approximate to a Gaussian distribution for both Trisomy 18 cases and controls. These Gaussian distributions are shown in Figure 3.

This shows that there is a likelihood that a given gestational age discrepancy forms part of either the Gaussian distribution for Trisomy 18 or unaffected values can be calculated in an analogous fashion as is demonstrated for the use of maternal serum AFP in the assessment of Down Syndrome risk in Figure 1.

EXAMPLE 2

The calculation of an individual woman's risk of having a child with Trisomy 18 during the second trimester of pregnancy using the measured discrepancy in gestational ages is shown below.

For a 37 year old woman, her age related risk can be derived from epidemiological studies such as those reported by Crossley (Crossley et.al. Prenatal Diagnosis, 11,83-102, 1991).

Age risk = 1:245

This risk is modified according to the likelihood ratio derived from analysis of the gestational age

discrepancy between USS and LMP derived gestations as shown in Table 3. The final combined risk is calculated by dividing the right hand side of the risk odds ratio (245) by the likelihood ratio.

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TABLE 3

10 Individual risks using gestational age discrepancy and prior age-related risk for Trisomy 18 at second trimester for a 37 year old woman

Age risk = 1:245

15	gestational age discrepancy in days	likelihood ratio	combined risk
	-2	0.0007	1:344014
	0	0.0026	1:92737
20	2	0.0098	1:25000
	4	0.0364	1:6739
	6	0.1349	1:1817
	8	0.5003	1:490
	10	1.8558	1:132
25	12	6.8841	1:36
	14	25.5368	1:10
	16	94.7303	1:3

EXAMPLE 3

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The utility of any screening test is best described by the Receiver Operating Characteristics (ROC). This shows the relationship between the sensitivity (the proportion of Trisomy 18 cases that would be detected at a given risk cut-off level) and 1 - the specificity (the proportion of unaffected women who would be categorised incorrectly as being at high risk of Trisomy 18, i.e. the false-positive rate). The ROC curve for screening using the discrepancy in gestational age dating is shown in Figure 4.

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Table 4 shows the interpolated values from this ROC curve showing the sensitivity of the screening test at various false positive rates.

TABLE 4

Detection rates for given false positive rate: Trisomy 18: gestational age discrepancy alone

5		false-positive rate	detection rate
		1.0%	76.2%
		2.0%	83.9%
10		3.0%	87.8%
		4.0%	90.2%
		5.0%	92.0%

15 EXAMPLE 4

Several maternal serum biochemical markers may be used in screening for Trisomy 18. For example AFP, unconjugated oestriol (UE), human chorionic gonadotrophin (hCG), the free beta and alpha subunits of human chorionic gonadotrophin ((hCG), pregnancy associated placental protein A (PAPPA) are all known to be decreased in pregnancies where the foetus has Trisomy 18. AFP levels are raised in Trisomy 18 affected pregnancies where the foetus also has an associated neural tube defect.

None of the Trisomy 18 cases described in Table 1 were also affected by neural tube defects.

The AFP concentrations, multiple of the median levels (MoM) and the natural log of the AFP MoM levels $[\ln(\text{AFP MoM})]$, are shown in Table 1. The statistical summary of the AFP data for both the Trisomy 18 cases and the unaffected controls are shown in Table 5. There was no statistically significant difference in either the standard deviation or the correlations between the controls and Trisomy 18 cases ; the correlations and standard deviations were therefore pooled.

TABLE 5

Statistical parameters

	Trisomy 18	unaffected controls
5		
n	7	521
10		
mean ln(AFP MoM)	0.309	0.040
standard deviation		
ln(AFP MoM)	0.361	0.361
15		
correlation coefficient		
between ln(AFP MoM) and		
gestational age	0.135	0.135
discrepancy		
20	The Gaussian distributions of ln(AFP MoM) in	
	Trisomy 18 and control pregnancies is shown in Figure	
	5. It can be seen that likelihood ratios can be	
	calculated using these Gaussain distributions in the	
	same manner as was described when screening for Down	
25	Syndrome using maternal AFP, exemplified in Figure 1..	
	The calculation of an individual woman's risk	
	of having a child with Trisomy 18 at the time of	
	screening is shown below.	

30 Age related risk for 37 year old woman = 1:245

 The risk is modified according to the likelihood
ratio derived from analysis of the maternal serum AFP
level, expressed as the MoM value, as shown in Table
35 6. The final combined risk is calculated by dividing
the right hand side of the risk odds ratio (in this
case 245) by the likelihood ratio.

TABLE 6

5 Individual risks using maternal serum AFP and prior
age related risk of 1:245 for Trisomy 18, at second
trimester for a 37 year old woman

	AFP MoM	likelihood ratio	combined risk
10	0.5	4.4857	1:55
	1.0	0.6982	1:351
	2.0	0.1087	1:2255
	3.0	0.0366	1:6694

15 The ROC curve for screening for Trisomy 18 using
maternal serum AFP is shown in Figure 6. Table 7
shows the interpolated values from this ROC curve
showing the sensitivity of the screening test at
various false positive rates.

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TABLE 7

25 Detection rates for given false positive rate, Trisomy
18, maternal serum AFP alone

	1-specificity (false-positive rate)	sensitivity (detection rate)
30	1.0%	8.8%
	2.0%	13.9%
	3.0%	18.1%
	4.0%	21.7%
35	5.0%	25.0%

EXAMPLE 5

40 The optimal method of combining screening tests
is to use them simultaneously by calculating the
likelihood ratio from a multivariate, rather than
univariate, Gaussian distribution. The use of
multivariate Gaussian distributions in calculating
45 risk assessments for Down

Syndrome has been described by Reynolds (Reynolds, Annals of Clinical Biochemistry, 27, 452-458, 1990).

Knowledge is required of the correlation between the screening markers to allow for their dependence.

5 The statistical parameters in Tables 2 and 5 show the mean and standard deviations and correlations for $\ln(\text{AFP MoM})$ and for the gestational age discrepancies.

By way of illustration the risks assigned to a 37 year old woman with various levels of maternal serum
10 AFP and different gestational age dating discrepancies is shown in Table 8.

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TABLE 8

Individual risks for a 37 year old woman for Trisomy
18, using AFP and gestational age discrepancy combined
5 with maternal age risk of 1:245 at second trimester

Age related risk for 37 year old woman = 1:245

10	AFP MoM	gestational age discrepancy	combined likelihood ratio	combined risk
	0.5	0	0.0161	1:15199
	0.5	2	0.0649	1:3776
	0.5	6	1.0510	1:233
15	0.5	10	17.0267	1:14
	0.5	16	1110.1926	2:1
	1.0	0	0.0572	1:226025
	1.0	2	0.0829	1:56156
20	1.0	6	0.2237	1:3466
	1.0	10	0.8419	1:214
	1.0	16	11.4713	1:3
	3.0	0	0.0021	1:16303001
25	3.0	2	0.0032	1:4050525
	3.0	6	0.0093	1:250034
	3.0	10	0.0375	1:15434
	3.0	16	0.5691	1:237

30 EXAMPLE 6

Screening performance in the ordinary population

35 The estimates of risks in Example 5 do not allow
for the performance of such a test were it applied as
a routine screening test in the general population. In
such circumstances the incidence of the disorder must

be taken into account in the general population. Such estimates can be derived by integrating the bivariate Gaussian distribution of the discrepancy of gestational age dating and maternal serum AFP over the age distribution of pregnancies. The age related risk of Trisomy 18 varies with the age of the mother and age related risk factors have been published based on epidemiological surveys, see e,g, Crossley et al Prenatal Diagnosis,11,83-102, 1990).

10 The age distribution of pregnancies in England and Wales (Office of Population Census and Surveys, Birth Statistics 1987-1989, HMSO) for the years 1986-1988 were averaged and used as a reference population for this study. Repeated sets of 10000 sample
15 bivariate Gaussian distributions according to the statistical parameters described in Tables 2 and 5, for unaffected and Trisomy 18 affected populations were generated using the statistical package Minitab (Trade Mark). Likelihood ratios were calculated for
20 the use of gestational age discrepancy only, for maternal serum AFP only and using both tests combined according to the principle described by Reynolds and Penney (Annals of Clinical Biochemistry,27, 452-458, 1990) and the statistical parameters described in
25 Tables 2 and 5. The simulated screening performance was estimated for a range of risk cut-off levels, below which a woman would be considered to be at sufficiently high risk to be offered the diagnostic tests of amniocentesis and fetal karyotyping. For each
30 maternal age the likelihood ratio below which a woman at that age would be screen-positive was calculated. The proportion of likelihood ratios for unaffected or affected pregnancies above this limit were then calculated. These figures represent the percentage of
35 women at that specific age who would be at higher risk

than the cut-off (screen-positive), for unaffected or Trisomy 18 affected pregnancies respectively. Multiplication of these proportions by the actual numbers of unaffected or Trisomy 18 affected pregnancies at that maternal age gave the actual numbers of women. The procedure was repeated for all maternal ages and the numbers of affected and unaffected women who would be screen-positive obtained by summation of the numbers at each maternal age. The procedure was repeated for a range of risk-cut off values.

These data provided estimates of the detection rate (proportion of women with Trisomy 18 affected pregnancies who have risks higher than the cut-off value) and the corresponding false-positive rate (proportion of unaffected pregnancies who have risks higher than the cut-off value).

Such data enabled an ROC curve to be constructed showing the relationship between the screen-positive rate and detection rate should a test be applied routinely to all pregnant women in England and Wales. This ROC curve is shown in Figure 7. The ROC curve illustrates the additional increase in detection for the same false-positive rate when markers are combined in this fashion. Extrapolated detection rates for given false-positive rates are shown below in Table 9.

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TABLE 9

Detection rates for Trisomy 18 at specified false positive rates

5		Sensitivity	Sensitivity	Sensitivity
	1-Specificity	Maternal	Maternal age	Maternal age,
	(false-	age & AFP	& gestational	gestational
	positive rate)		age discrep-	age discrep-
10			ancy	ancy & AFP
	0.5%	16.2%	74.4%	83.3%
	1.0%	21.4%	81.8%	88.0%
	1.5%	25.3%	85.3%	90.3%
15	2.0%	28.4%	87.4%	92.2%

Thus for example if the test is applied routinely to the general population then 92.2% of Trisomy 18 cases can be identified, whilst performing
 20 amniocentesis and fetal karyotyping on only 2% of the population at highest risk.

EXAMPLE 7

25 Extension using other serum analytes

Maternal serum hCG and maternal serum UE are known to be lowered in Trisomy 18 affected pregnancies. Table 10, which presents information
 30 additional to Table 1, shows the individual maternal serum hCG and UE levels in the Trisomy 18 cases in this study. Table 11 shows the statistical distributions for the natural logarithm of maternal serum hCG {ln(hCG MoM)} and maternal serum UE {ln(UE

MoM) } in both unaffected pregnancies and Trisomy 18 affected pregnancies from this study.

TABLE 10

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Women with Trisomy 18 affected pregnancies

Patient ID	hCG IU/ml	UE nmole/l	MoM Values		ln (MoM)	
			hCG	UE	hCG	UE
10 B0211	8.89	3.31	0.199	1.020	-1.613	+0.019
B0250	3.62	3.97	0.190	0.514	-1.661	-0.665
B0289	8.80	1.98	0.320	0.431	-1.140	-0.841
B0340	5.11	1.81	0.186	0.394	-1.684	-0.931
15 B0379	3.65	4.61	0.125	1.055	-2.076	+0.054
G0346	13.58	1.15	0.398	0.298	-0.922	-1.211
G0347	8.43	3.88	0.443	0.503	-0.815	-0.688

TABLE 11

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Statistical parameters for hCG and UE, Trisomy 18 cases and controls using pooled standard deviations

	ln (hCG MoM)	ln (UE MoM)
25 Mean normal controls	-0.0099	-0.0212
Mean Trisomy 18	-1.4159	-0.6089
Pooled standard	0.4969	0.3349
30 deviation		

Figures 8 and 9 show the Gaussian distributions for ln(hCG MoM) and ln(UE MoM) respectively. Both demonstrate the further potential for the inclusion of such maternal serum markers together with the

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discrepancy in gestational age dating in multivariate Gaussian models to calculate likelihood ratios. The mathematical combination of multiple screening markers has been described in detail (Reynolds and Penney, 5 Annals of Clinical Biochemistry, 27, 452-458, 1990).

Other maternal serum or foetal biometric measurements could also be included with the gestational age discrepancy in a multivariate model to improve the screening performance further.

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EXAMPLE 8

Screening for open spina bifida

15 25 cases of open spina bifida were examined as part of the above clinical trials. Maternal serum AFP was measured and MoM values were calculated for both cases and controls as described in Example 1. Table 12 shows the individual data relating to the open spina bifida 20 cases. Table 13 shows the statistical summary of the distributions of gestational age dating discrepancies and the natural logarithm of maternal serum AFP MoM $\{\ln(\text{AFP MoM})\}$. There was no statistically significant difference in either the standard deviations or, 25 correlations between open spina bifida cases and controls and the correlations and standard deviations were therefore pooled.

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TABLE 12

Women with Open Spina Bifida affected pregnancies

5	Patient ID	USS	GA(days)		AFP IU/ml	MoM AFP	ln MoM AFP
			LMP	LMP-USS			
	G0405	122	129	9	190.6	4.727	1.553
	NTD021	122	136	15	109.4	2.713	0.998
10	NTD022	129	136	4	216.4	4.729	1.554
	NTD023	129	129	1	178.2	3.896	1.360
	NTD024	122	129	9	342.4	8.489	2.139
	NTD025	115	115	-1	103.7	2.916	1.070
	NTD027	122	136	19	265.1	6.573	1.883
15	NTD028	115	115	-2	124.9	3.514	1.257
	NTD030	122	122	5	144.3	3.577	1.275
	NTD032	122	129	8	260.0	6.446	1.863
	NTD033	122	157	37	169.6	4.205	1.436
	NTD034	122	136	19	286.7	7.108	1.961
20	NTD035	115	136	20	228.6	6.431	1.861
	NTD036	101	122	23	105.9	3.834	1.344
	NTD037	115	122	11	91.0	2.561	0.940
	NTD038	115	122	9	214.4	6.030	1.797
	NTD039	115	115	6	173.1	4.868	1.583
25	NTD040	136	101	-30	123.2	2.375	0.865
	NTD041	115	122	6	122.9	3.457	1.241
	NTD043	122	122	-5	84.0	2.083	0.734
	NTD045	122	136	15	197.4	4.894	1.588
	NTD057	122	136	18	92.8	2.301	0.834
30	NTD059	122	136	12	141.5	3.507	1.255
	RA044	122	136	17	175.2	4.343	1.469
	RA045	122	136	19	217.1	5.384	1.683

TABLE 13

Statistical parameters

5		Gestational Age		Natural log	
		Discrepancy		AFP MoM	
		OSB	Control	OSB	Control
	n	25	521	25	521
10	mean	10.30	1.97	1.422	
	0.041				
	pooled SD	4.44	4.44	0.362	
	0.362				
	pooled correlation	0.1490	0.1490		
15	(gestational age				
	discrepancy & natural				
	log AFP MoM)				
	OSB = Open Spina Bifida				
20	SD = Standard Deviation				

Figure 10 shows the distribution of gestational age dating discrepancies for open spina bifida and for unaffected control pregnancies. It is apparent that open spina bifida fetuses have a significantly smaller biparietal diameter and hence lower ultrasound estimated gestational age than in control pregnancies.

The discrepancy in gestational age can be used as a marker for open spina bifida in an analogous fashion to its use for Trisomy 18 in Example 1.

Maternal serum AFP has been used for many years as a maternal serum marker for open spina bifida. The distribution of $\ln(\text{AFP MoM})$ found in this study is shown in Figure 11. Data is in accord with previously published data.

EXAMPLE 9

Estimating individual spina bifida risk

5 The background risk of open spina bifida varies
temporally, geographically and racially. In addition
there are known to be various genetic, social and
nutritional determinants of risk. In practice local
10 epidemiological surveillance is used to determine the
background (pre-test) risk. In this example the
background risk is assumed to be 1:500.

 The background risk is modified according to the
likelihood ratio derived from analysis of the
gestational age discrepancy between USS and LMP, from
15 analysis of the maternal serum AFP or by using both
markers in a bivariate combination. The final risk is
calculated by dividing the right hand side of the risk
odds ratio (in this case 500) by the likelihood ratio.
The modified risks for various combinations of
20 gestational age dating discrepancies and maternal
serum AFP MoM alone or in combination are shown in
Table 14.

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TABLE 14

Individual risks for Open Spina Bifida using AEP and gestational age discrepancy and a priori pre-test risk (incidence) of 1:500

	AFP MoM	Gestational Age Discrepancy	Likelihood Ratio	Final Risk
10	not used	0	0.0751	1:6662
	not used	2	0.1745	1:2865
	not used	4	0.4058	1:1232
	not used	8	2.1943	1:228
15	not used	16	64.1535	1:8
	1.0	not used	0.00044	1:1126254
	2.0	not used	0.66867	1:748
	2.5	not used	7.05111	1:71
20	3.0	not used	48.32238	1:10
	1.0	0	0.00010	1:4765230
	1.0	2	0.00019	1:2612053
	1.0	4	0.00035	1:1431792
25	1.0	8	0.00116	1:430206
	1.0	16	0.01287	1:38839
	2.0	0	0.1080	1:4633
	2.0	2	0.1969	1:2540
30	2.0	4	0.3592	1:1392
	2.0	8	0.1953	1:418
	2.0	16	13.2401	1:38
	2.5	0	1.0064	1:497
	2.5	2	1.8361	1:272
35	2.5	4	3.3496	1:149

TABLE 14 (continued)

	2.5	8	11.1478	1:45
	2.5	16	123.4804	1:4
5	3.0	0	6.2387	1:80
	3.0	2	11.3813	1:44
	3.0	4	20.7633	1:24
	3.0	8	69.1034	1:7
10	3.0	16	765.4331	1:1

EXAMPLE 10

Routine population screening performance estimate

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The predicted performance of a spina bifida test when applied to the entire population can be estimated in a manner analogous to that demonstrated for screening for Trisomy 18 in Example 6, except that the incidence is not related to maternal age, and hence integration over the maternal age distribution is not required. Repeated sets of 10000 sample bivariate Gaussian distributions were generated according to the statistical parameters described in Table 13, for unaffected and Open Spina Bifida affected populations. Likelihood ratios were calculated for the use of gestational age discrepancy only, for maternal serum AFP only and using both tests combined. The simulated screening performance was estimated for a range of risk cut-off levels, below that at which a woman is considered to be at sufficiently high risk to be offered the diagnostic test of amniocentesis and/or detailed ultrasonographic examination of the foetal spine. The likelihood ratio above which a woman is screen-positive was calculated. The proportion of

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likelihood ratios for unaffected or affected pregnancies above this critical likelihood ratio was then calculated from the data for unaffected and affected pregnancies. These proportions represent the percentage of women who are at higher risk than the risk cut-off (screen-positive), for unaffected or Open Spina Bifida pregnancies respectively. Multiplication of these proportions by the total number of unaffected or Open Spina Bifida pregnancies at that maternal age gave the actual numbers of women. The procedure was repeated for a range of risk cut-off values.

These data provided estimates of the detection rate (proportion of women with Open Spina Bifida affected pregnancies who have risks higher than the cut off value) and the corresponding false-positive rate (proportion of unaffected pregnancies who have risks higher than the cut-off value). Such values enable an ROC curve to be constructed showing the relationship between the screen-positive rate and the detection rate when such a test is applied routinely to all pregnant women in England and Wales. This ROC curve is shown in Figure 12. The ROC curve illustrates the detection rates predicted using gestational age dating discrepancies (GA diff) alone, maternal serum AFP alone or both in combination (both combined). Extrapolated detection rates for given false-positive rates are shown in Table 15.

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TABLE 15

Detection rate for Open Spina Bifida at specified false positive rates

False positive rate	Sensitivity		
	GA Discrepancy Alone	AFP Alone	Both Combined
0.5%	21.5%	84.86%	89.3%
1.0%	32.1%	91.2%	94.4%
1.5%	38.7%	94.06%	96.1%
2.0%	43.1%	95.2%	97.4%

Table 15 shows that the combination of both gestational age discrepancy and maternal serum AFP as a marker for Open Spina Bifida is better than either test used alone. For example 91% of cases of Open Spina Bifida can be identified in the 1% of the population at highest risk with maternal serum AFP alone, whilst the addition of gestational age dating discrepancy has the potential to raise this to 94% whilst maintaining the same 1% screen-positive rate.

A further common diagnostic test performed on those women at highest risk is amniocentesis and the measurement of amniotic fluid AFP. Although amniotic fluid AFP measurement is a highly sensitive test, a very small but significant number of women will have a false-positive result. This is particularly distressing as this may lead to the effective termination of a healthy unaffected child by mistake. The use of gestational age dating discrepancies in a bivariate risk calculation with amniotic fluid AFP would also be of benefit in reducing the incidence of such errors.



CLAIMS

1. A method for antenatal screening for chromosomal abnormalities in a fetus in which the gestational age of a pregnant woman is determined characterised in that the gestational age is determined (a) by reference to the last menstrual period dates and (b) by a biometric measurement of the fetus, the difference between the ages as determined in (a) and (b) is calculated and the calculated difference is examined using reference data to determine fetal abnormalities.
2. A method according to claim 1 characterised in that chromosomal abnormalities screened for include Edwards Syndrome (Trisomy 18) and/or Open Spina Bifida.
3. A method according to claim 1 or claim 2 characterised in that chromosomal abnormalities screened for include at least one of Down's Syndrome, Patau's Syndrome (Trisomy 13), Turner Syndrome, Monosomy X and Klinefelter's Syndrome.
4. A method according to any one of the preceding claims characterised in that the biometric measurement is made by ultrasonography.
5. A method according to any one of the preceding claims characterised in that maternal age and/or measurement of a component from a maternal fluid are combined with the gestational age measurements in a multivariate analysis.





6. A method according to claim 6 characterised in that measurement of hCG, either the intact molecule thereof, its alpha subunit and/or its beta subunit is included.

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7. A method according to claim 6 or claim 7 characterised in that measurement of at least one marker selected from the group AFP, PAPP_A, UE, In, Pr, 16-alpha-hydroxy-DHEAS and DHEAS is included.

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8. A method according to any one of the preceding claims characterised in that measurements are made in the period from week 8 to week 22 of pregnancy.

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9. An apparatus comprising means adapted for receiving measurements relating to a foetus carried by a pregnant woman and computer means for comparing the measurements to reference data to determine fetal abnormalities characterised in that the measurements relate to the difference between the gestational age of the woman as determined (a) by reference to the last menstrual period dates and (b) by a biometric measurement of the foetus.

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10. An apparatus according to claim 9 characterised in that maternal age and/or measurement of a component from a maternal fluid are combined with the gestational age measurements in a multivariate analysis.

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