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Table S1. Baseline characteristics of men and women by diabetes status at follow-up

	Men			Women		
	Diabetes n=316	Without diabetes n=2753	*P value	Diabetes n=427	Without diabetes n=3667	*P value
Age (years)	45.4 (12.1)	39.7 (13.2)	<0.001	43.8 (11.8)	37.7 (12.3)	<0.001
BMI (kg/m^2)	27.4 (3.7)	25.3 (3.9)	<0.001	29.8 (5.0)	26.6 (4.6)	<0.001
FPG (mmol/L)	5.2 (0.5)	4.9 (0.4)	<0.001	5.2 (0.5)	4.8 (0.4)	<0.001
SBP (mmHg)	123.3 (17.6)	116.5 (15.0)	<0.001	121.1 (17.6)	113.3 (16.3)	<0.001
DBP (mmHg)	81.3 (10.4)	76.0 (10.1)	<0.001	79.6 (10.1)	75.1 (10.2)	<0.001
HDL-C (mmol/L)	0.96 (0.21)	0.98 (0.24)	0.067	1.10 (0.28)	1.18 (0.29)	<0.001
TC (mmol/L)	5.61 (1.02)	5.08 (1.08)	<0.001	5.74 (1.23)	5.19 (1.17)	<0.001
Ln-TG (mmol/L)	0.74 (0.49)	0.48 (0.54)	<0.001	0.64 (0.51)	0.29 (0.52)	<0.001
2-hPG (mmol/L)	6.5 (1.7)	5.4 (1.4)	<0.001	6.9 (1.5)	5.7 (1.3)	<0.001
Smokers	83 (26.3)	835 (30.5)	0.136	12 (2.8)	140 (3.8)	0.345
Family history of diabetes (yes)	116 (36.7)	620 (22.5)	<0.001	147 (34.4)	903 (24.6)	<0.001
Physical activity (low)	245 (79.3)	1861 (70.6)	0.001	303 (73.2)	2415 (69.6)	0.140

Values are mean (SD) for continuous variables and frequency (percentage) for categorical variables.

P values show statistical differences based on t-test and chi-square test for continuous and categorical variables, respectively.

BMI: body mass index; **FPG:** fasting plasma glucose; **TC:** total cholesterol; **SBP:** systolic blood pressure, **DBP:** diastolic blood pressure;

HDL-C: high-density lipoprotein cholesterol; **2-hPG:** 2-h post-load plasma; **Ln-TG:** natural logarithm of triglyceride; **SD:** standard deviation

Table S2. Baseline characteristics of participants and non-participants

	Non-Participants n=3905	Participants n=7163	*P value
Male (%)	1731 (44.3)	3069 (42.8)	0.069
Age (years)	39.6 (14.0)	39.2 (12.8)	0.180
BMI (kg/m^2)	26.8 (5.1)	26.3 (4.5)	<0.001
FPG (mmol/L)	5.1 (0.6)	4.9 (0.5)	<0.001
SBP (mmHg)	117.9 (18.5)	115.4 (16.2)	<0.001
DBP (mmHg)	77.4 (11.1)	76.0 (10.3)	<0.001
HDL (mmol/L)	1.07 (0.3)	1.09 (0.3)	0.017
TC (mmol/L)	5.2 (1.2)	5.2 (1.1)	0.364
Ln-TG (mmol/L)	0.45 (0.57)	0.40 (0.57)	<0.001
2-hPG (mmol/L)	6.1 (1.7)	5.7 (1.4)	<0.001
Smokers	769 (20.9)	1070 (15.0)	<0.001
Family history of diabetes (yes)	1010 (25.9)	1786 (24.9)	0.146
Physical activity (low)	2481 (70.6)	4824 (70.6)	0.481

Values are mean (SD) for continuous variables and frequency (percentage) for categorical variables.
P values show statistical differences based on t-test and chi-square test for continuous and categorical variables, respectively.
BMI: body mass index; **FPG:** fasting plasma glucose; **TC:** total cholesterol; **SBP:** systolic blood pressure, **DBP:** diastolic blood pressure; **HDL-C:** high-density lipoprotein cholesterol; **2-hPG:** 2-h post-load plasma; **Ln-TG:** natural logarithm of triglyceride; **SD:** standard deviation

Table S3. Characteristics of different submodels and final growth model for body mass index (BMI) in men

	Notation							
		Value (Standard error), P value						
	Notation	**Model 1**	**Model 2**	**Model 3**	**Model 4**	**Model 5**	**Model 6**	**Final model**
Intercept	β_0	26.73(0.07), <0.001	26.70 (0.07), <0.001	27.37(0.07), <0.001	27.41 (0.07), <0.001	27.44 (0.08), <0.001	27.41 (0.07), <0.001	27.42 (0.08), <0.001
Age	β_1		0.11(0.002), <0.001	0.11(0.002), <0.001	0.08 (0.002), <0.001	0.08 (0.003), <0.001	0.075 (0.003), <0.001	0.077 (0.003), <0.001
Age^2	β_2			-0.03(0.001), <0.001	-0.03(0.001), <0.001	-0.03 (0.001), <0.001	-0.04 (0.001), <0.001	-0.04 (0.001), <0.001
Age^3	β_3				0.001(0.0001), <0.001	0.001(0.0001), <0.001	0.001 (0.0001), <0.001	0.001 (0.0001)
Variance of random intercept	$\sigma^2\, u_0$	14.44 (0.38)	17.44 (0.47)	16.71 (0.44)	16.44 (0.43)	16.57 (0.11)	17.01 (0.48)	17.01 (0.48)
Variance of random Age term	$\sigma^2\, u_1$					0.01 (0.06)	0.012 (0.0008)	0.012 (0.0009)
Variance of random Age^2 term	$\sigma^2\, u_2$						0.0006 (0.0001)	0.0006 (0.0001)
AIC			65360.16	63219.39	61684.86	61522.01	60651.5	60400.9	60272.06
Log Likelihood (P value for LR test)		-32677.08	-31605.7 (<0.001)	-30837.43 (<0.001)	-30755 (<0.001)	-30317.8 (<0.001)	-30189.4 (<0.001)	-30123.0 (<0.001)

Model 1: Unconditional mean
Level 1: $BMI_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $BMI_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $BMI_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Cubic unconditional growth model
Level 1: $BMI_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Model 5: Cubic growth model with the intercept and slope variability
Level 1: $BMI_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Model 6: Cubic growth model with the intercept and slopes variability
Level 1: $BMI_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2 + u_{2i}$
Level 2: $b_{3i} = \beta_3$

Final Model: Was obtained with adding following error structure into Model 6:
RCS: First-Order Autoregressive
RH: $\sigma^2 \times |Age|^{2\delta}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 6 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (LR) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times |Age|^{2\delta}$: Variance proportional to the absolute value of Age raised to a constant power

Table S4. Characteristics of different submodels and final growth model for body mass index (BMI) in women

	Notation	Value (Standard Error), P value						
		Model 1	**Model 2**	**Model 3**	**Model 4**	**Model 5**	**Model 6**	**Final model**
Intercept	β_0	28.55(0.07), <0.001	28.83 (0.07), <0.001	29.29 (0.07), <0.001	29.29 (0.07), <0.001	29.30 (0.07), <0.001	29.30 (0.07), <0.001	29.30 (0.07), <0.001
Age	β_1		0.17 (0.002), <0.001	0.17 (0.002), <0.001	0.16 (0.003), <0.001	0.15 (0.003), <0.001	0.15 (0.003), <0.001	0.16(0.003), <0.001
Age ^{2}	β_2			-0.03 (0.0009), <0.001	-0.03 (0.0009), <0.001	-0.02 (0.001), <0.001	-0.03 (0.001), <0.001	-0.03 (0.001), <0.001
Age ^{3}	β_3				0.0002(0.0001), <0.001	0.0007 (0.0001), <0.001	0.0004 (0.0001), <0.01	0.0003 (0.0001), <0.01
Variance of random intercept	$\sigma^2 u_0$	20.94 (0.48)	20.25 (0.46)	19.41 (0.44)	19.40 (0.44)	21.29 (0.11)	21.68 (0.52)	21.27 (0.52)
Variance of random Age term	$\sigma^2 u_1$					0.02 (0.08)	0.02 (0.0009)	0.01(0.001)
Variance of random Age^2 term	$\sigma^2 u_2$						0.0009 (0.0001)	0.0008 (0.0001)
AIC		95547.99	89746.35	88894.02	88888.71	87158.5	86827.63	86691.11
Log Likelihood (P value for LR test)		-47771.00	-44869.17 (<0.001)	-44442.01 (<0.001)	-44438.36 (0.006)	-43571.30 (<0.001)	-43402.82 (<0.001)	-43332.56 (<0.001)

Model 1: Unconditional mean
Level 1: BMI$_{ij}$= b$_{oi}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$

Model 2: Unconditional growth model
Level 1: BMI$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1

Model 3: Quadratic unconditional growth model
Level 1: BMI$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ +e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1
Level 2: b$_{2i}$ = β_2

Model 4: Cubic unconditional growth model
Level 1: BMI$_{ij}$= b$_{oi}$ +b$_1$Age$_{ij}$ +b$_2$Age$^2_{ij}$ + b$_3$Age$^3_{ij}$+e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1
Level 2: b$_{2i}$ = β_2
Level 2: b$_{3i}$ = β_3

Model 5: Cubic growth model with the intercept and slope variability
Level 1: BMI$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ + b$_3$Age$^3_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1 + u$_{1i}$
Level 2: b$_{2i}$ = β_2
Level 2: b$_{3i}$ = β_3

Model 6: Cubic growth model with the intercept and slopes variability
Level 1: BMI$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ + b$_3$Age$^3_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1 + u$_{1i}$
Level 2: b$_{2i}$ = β_2 + u$_{2i}$
Level 2: b$_{3i}$ = β_3

Final Model: Was obtained with adding following error structure into Model 6:
RCS: First-Order Autoregressive
RH: $\sigma^2 \times e^{2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; **b$_{ki}$** represent individual component or random effects; **u$_{ki}$** represents the deviation of **b$_{ki}$** from the value of **β_k** in the population for individual **i**.

Models 1 to 6 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (LR) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; **$\sigma^2 \times e^{2\delta \times Age}$:** variance proportional to the exponential of Age multiplied by a constant

Table S5. Characteristics of different submodels and final growth model for fasting plasma glucose (FPG) in men

	Notation	Value (Standard Error), P value				
		Model 1	Model 2	Model 3	Model 4	Final model
Intercept	β_0	5.14 (0.01), <0.001	5.13 (0.01), <0.001	5.18 (0.01), <0.001	5.18 (0.01), <0.001	5.18 (0.01), <0.001
Age	β_1		0.01 (0.0004), <0.001	0.01 (0.0004), <0.001	0.01 (0.0004), <0.001	0.01 (0.0004), <0.001
Age ^{2}	β_2			-0.002 (0.0002), <0.001	-0.002 (0.0002), <0.001	-0.002 (0.0002), <0.001
Variance of random intercept	$\sigma^2 u_0$	0.10 (0.004)	0.11 (0.004)	0.11 (0.004)	0.11 (0.004)	0.11 (0.004)
Variance of random Age term	$\sigma^2 u_1$				0.00003 (0.00001)	0.00003 (0.00001)
AIC		18565.28	17405.42	17263.34	17170.78	17157.73
Log Likelihood (P value for LR test)		-9279.641	-8698.711 (<0.001)	-8626.670 (<0.001)	-8578.39 (<0.001)	-8570.864 (<0.001)

Model 1: Unconditional mean
Level 1: $FPG_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $FPG_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $FPG_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Quadratic growth model with the intercept and slope variability
Level 1: $FPG_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$

Final Model: Was obtained with adding following error structure into Model 4:
RCS: Was not adjusted for residual correlation structure
RH: $\sigma^2 \times e^{2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 4 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{2\delta \times Age}$: variance proportional to the exponential of Age multiplied by a constant

Table S6. Characteristics of different submodels and final growth model for fasting plasma glucose (FPG) in women

	Notation	Value (Standard Error), P value				
		Model 1	Model 2	Model 3	Model 4	Final model
Intercept	β_0	5.02 (0.01), <0.001	5.05 (0.006), <0.001	5.08 (0.01), <0.001	5.08 (0.01), <0.001	5.08 (0.01), <0.001
Age	β_1		0.02 (0.0003), <0.001	0.02 (0.0003), <0.001	0.02 (0.0004), <0.001	0.02 (0.0004), <0.001
Age ^{2}	β_2			-0.002 (0.0002), <0.001	-0.001 (0.0002), <0.001	-0.001 (0.0002), <0.001
Variance of random intercept	$\sigma^2 u_0$	0.12 (0.003)	0.11 (0.003)	0.11 (0.003)	0.11 (0.003)	0.11 (0.003)
Variance of random Age term	$\sigma^2 u_1$				0.00006 (0.00001)	0.00006 (0.00001)
AIC		25245.79	22857.62	22737.6	22480.27	22408.66
Log Likelihood (P value for LR test)		-12619.9	-11424.81 (<0.001)	-11363.8 (<0.001)	-11233.13 (<0.001)	-11196.33 (<0.001)

Model 1: Unconditional mean
Level 1: $FPG_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $FPG_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $FPG_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Quadratic growth model with the intercept and slope variability
Level 1: $FPG_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$

Final Model: Was obtained with adding following error structure into Model 4:
RCS: Was not adjusted for residual correlation structure
RH: $\sigma^2 \times e^{2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 4 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{2\delta \times Age}$: variance proportional to the exponential of Age multiplied by a constant

Table S7. Characteristics of different submodels and final growth model for systolic blood pressure (SBP) in men

	Notation	Value (Standard Error), P value					
		Model 1	Model 2	Model 3	Model 4	Model 5	Final model
Intercept	β_0	118.69 (0.25), <0.001	118.55 (0.22), <0.001	117.60 (0.25), <0.001	117.33 (0.25), <0.001	117.32 (0.24), <0.001	117.26 (0.24), <0.001
Age	β_1		0.37 (0.01), <0.001	0.36 (0.01), <0.001	0.51 (0.01), <0.001	0.53 (0.01), <0.001	0.51 (0.02), <0.001
Age ^{2}	β_2			0.04 (0.005), <0.001	0.08 (0.005), <0.001	0.07 (0.006), <0.001	0.08 (0.006), <0.001
Age ^{3}	β_3				-0.006 (0.0005), <0.001	-0.007 (0.0005), <0.001	-0.006 (0.0006), <0.001
Variance of random intercept	$\sigma^2\,u_0$	171.65 (4.99)	137.06 (4.11)	134.71 (4.04)	134.30 (4.02)	119.56 (3.91)	111.82 (3.99)
Variance of random Age term	$\sigma^2\,u_1$					0.10 (0.01)	0.09 (0.01)
AIC		114402	113437.6	113362.5	113225.7	112871.2	111807.3
Log Likelihood (P value for LR test)		-57197.98	-56714.80 (<0.001)	-56676.24 (<0.001)	-56606.84 (<0.001)	-56427.58 (<0.001)	-55893.63 (<0.001)

Model 1: Unconditional mean
Level 1: SBP$_{ij}$= b$_{oi}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$

Model 2: Unconditional growth model
Level 1: SBP$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1

Model 3: Quadratic unconditional growth model
Level 1: SBP$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ +e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1
Level 2: b$_{2i}$ = β_2

Model 4: Cubic unconditional growth model
Level 1: SBP$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ + b$_3$Age$^3_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1
Level 2: b$_{2i}$ = β_2
Level 2: b$_{3i}$ = β_3

Model 5: Cubic growth model with the intercept and slope variability
Level 1: SBP$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ + b$_3$Age$^3_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1 + u$_{1i}$
Level 2: b$_{2i}$ = β_2
Level 2: b$_{3i}$ = β_3

Final Model: Was obtained with adding following error structure into Model 5:
RCS: First-Order Autoregressive
RH: $\sigma^2\times e^{\,2\delta\times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 5 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2\times e^{\,2\delta\times Age}$: variance proportional to the exponential of Age multiplied by a constant

Table S8. Characteristics of different submodels and final growth model for systolic blood pressure (SBP) in women

	Notation	Value (Standard Error), P value					
		Model 1	**Model 2**	**Model 3**	**Model 4**	**Model 5**	**Final model**
Intercept	β_0	114.10 (0.23), <0.001	114.75 (0.19), <0.001	113.6 (0.21), <0.001	113.56 (0.21), <0.001	113.57 (0.21), <0.001	113.29 (0.21), <0.001
Age	β_1		0.44 (0.01), <0.001	0.45 (0.01), <0.001	0.64 (0.02), <0.001	0.65 (0.02), <0.001	0.65 (0.01), <0.001
Age ^{2}	β_2			0.06 (0.005), <0.001	0.08 (0.005), <0.001	0.05 (0.005), <0.001	0.07 (0.006), <0.001
Age ^{3}	β_3				-0.008 (0.0005), <0.001	-0.008 (0.0005), <0.001	-0.008 (0.0006), <0.001
Variance of random intercept	$\sigma^2\,u_0$	203.22 (5.07)	132.75 (3.68)	129.73 (3.59)	127.56 (3.51)	124.52 (3.70)	116.12 (3.75)
Variance of random Age term	$\sigma^2\,u_1$					0.07 (0.01)	0.09 (0.01)
AIC			161219.3	159815.5	159670.3	159468.4	158874.2	157076.2
Log Likelihood (P value for LR test)		-80606.63	-79903.75 (<0.001)	-79830.14 (<0.001)	-79728.22 (<0.001)	-79429.09 (<0.001)	-78528.1 (<0.001)

Model 1: Unconditional mean
Level 1: $SBP_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $SBP_{ij} = b_{oi} + b_1Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $SBP_{ij} = b_{oi} + b_1Age_{ij} + b_2Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Cubic unconditional growth model
Level 1: $SBP_{ij} = b_{oi} + b_1Age_{ij} + b_2Age^2_{ij} + b_3Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Model 5: Cubic growth model with the intercept and slope variability
Level 1: $SBP_{ij} = b_{oi} + b_1Age_{ij} + b_2Age^2_{ij} + b_3Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Final Model: Was obtained with adding following error structure into Model 5:
RCS: First-Order Autoregressive
RH: $\sigma^2 \times e^{2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 5 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{2\delta \times Age}$: variance proportional to the exponential of Age multiplied by a constant

Table S9. Characteristics of different submodels and final growth model for diastolic blood pressure (DBP) in men

	Notation	Value (Standard Error), P value					
		Model 1	**Model 2**	**Model 3**	**Model 4**	**Model 5**	**Final model**
Intercept	β_0	77.81 (0.14), <0.001	77.75 (0.15), <0.001	79.47 (0.16), <0.001	79.42 (0.16), <0.001	79.44 (0.16), <0.001	79.45 (0.16), <0.001
Age	β_1		0.16 (0.01), <0.001	0.19 (0.01), <0.001	0.21 (0.01), <0.001	0.22 (0.01), <0.001	0.22 (0.01), <0.001
Age ^{2}	β_2			-0.08 (0.003), <0.001	-0.08 (0.004), <0.001	-0.08 (0.004), <0.001	-0.08 (0.004), <0.001
Age ^{3}	β_3				-0.001 (0.0003), 0.003	-0.001 (0.0004), 0.004	-0.001 (0.0004), <0.001
Variance of random intercept	$\sigma^2\, u_0$	54.38 (1.71)	56.99 (1.79)	55.05 (1.72)	55.25 (1.73)	52.28 (1.76)	52.25 (1.77)
Variance of random Age term	$\sigma^2\, u_1$					0.02 (0.005)	0.02 (0.005)
AIC		103769.1	103387.8	102867.2	102860.4	102809.7	102778.1
Log Likelihood (P value for LR test)		-51881.53	-51689.89 (<0001)	-51428.62 (<0001)	-51424.20 (0.002)	-51396.86 (<0001)	-51380.04 (<0001)

Model 1: Unconditional mean
Level 1: DBP$_{ij}$= b$_{oi}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$

Model 2: Unconditional growth model
Level 1: DBP$_{ij}$ = b$_{oi}$ + b$_1$Age$_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1

Model 3: Quadratic unconditional growth model
Level 1: DBP$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ +e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1
Level 2: b$_{2i}$ = β_2

Model 4: Cubic unconditional growth model
Level 1: DBP$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ + b$_3$Age$^3_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1
Level 2: b$_{2i}$ = β_2
Level 2: b$_{3i}$ = β_3

Model 5: Cubic growth model with the intercept and slope variability
Level 1: DBP$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ + b$_3$Age$^3_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1 + u$_{1i}$
Level 2: b$_{2i}$ = β_2
Level 2: b$_{3i}$ = β_3

Final Model: Was obtained with adding following error structure into Model 5:
RCS: Was not adjusted for residual correlation structure
RH: $\sigma^2 \times e^{\,2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 5 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{\,2\delta \times Age}$: variance proportional to the exponential of Age multiplied by a constant

Table S10. Characteristics of different submodels and final growth model for diastolic blood pressure (DBP) in women

		Value (Standard Error), P value					
	Notation	**Model 1**	**Model 2**	**Model 3**	**Model 4**	**Model 5**	**Final model**
Intercept	β_0	75.10 (0.12), <0.001	75.36 (0.11), <0.001	76.14 (0.13), <0.001	76.12 (0.13), <0.001	76.14 (0.13), <0.001	76.13 (0.13), <0.001
Age	β_1		0.17 (0.006), <0.001	0.17 (0.006), <0.001	0.24 (0.01), <0.001	0.26 (0.01), <0.001	0.26 (0.01), <0.001
Age ^{2}	β_2			-0.04 (0.003), <0.001	-0.04 (0.01), <0.001	-0.04 (0.003), <0.001	-0.04 (0.003), <0.001
Age ^{3}	β_3				-0.003 (0.0004), <0.001	-0.003 (0.0004), <0.001	-0.004 (0.0004), <0.001
Variance of random intercept	$\sigma^2 u_0$	53.77 (1.45)	46.51 (1.29)	45.82 (1.28)	45.56 (1.27)	44.62 (1.36)	44.45 (1.37)
Variance of random Age term	$\sigma^2 u_1$					0.02 (0.004)	0.02 (0.004)
AIC		143780.1	143154.4	142991.5	142919.4	142809.6	142651.2
Log Likelihood (P value for LR test)		-71887.06	-71573.22 (<0.001)	-71490.75 (<0.001)	-71453.7 (<0.001)	-71396.8 (<0.001)	-71316.63 (<0.001)

Model 1: Unconditional mean
Level 1: $DBP_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $DBP_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $DBP_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Cubic unconditional growth model
Level 1: $DBP_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Model 5: Cubic growth model with the intercept and slope variability
Level 1: $DBP_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Final Model: Was obtained with adding following error structure into Model 5:
RCS: Was not adjusted for residual correlation structure
RH: $\sigma^2 \times e^{2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 5 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{2\delta \times Age}$: Variance proportional to the exponential of Age multiplied by a constant

Table S11. Characteristics of different submodels and final growth model for high density lipoprotein cholesterol (HDL-C) in men

	Notation	Value (Standard Error), P value				
		Model 1	Model 2	Model 3	Model 4	Final model
Intercept	β_0	1.03 (0.004), <0.001	1.03 (0.003), <0.001	1.02 (0.004), <0.001	1.02 (0.004), <0.001	1.02 (0.004), <0.001
Age	β_1		0.007 (0.0001), <0.001	0.01 (0.0001), <0.001	0.01 (0.0002), <0.001	0.01 (0.0002), <0.001
Age ^{2}	β_2			0.001(0.0001), <0.001	0.001(0.0001), <0.001	0.001(0.0001), <0.001
Variance of random intercept	$\sigma^2 u_0$	0.04 (0.001)	0.04 (0.001)	0.04 (0.001)	0.04 (0.001)	0.03 (0.001)
Variance of random Age term	$\sigma^2 u_1$				0.00002 (0.000003)	0.000004(0.000003)
AIC		-4891.253	-6431.502	-6489.027	-6626.129	-6823.337
Log Likelihood (P value for LR test)		2448.627	3219.751 <0.001	3249.513 <0.001	3320.065 <0.001	3420.668 <0.001

Model 1: Unconditional mean
Level 1: $HDL_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $HDL_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $DBP_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Quadratic unconditional growth model
Level 1: $DBP_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$

Final Model: Was obtained with adding following error structure into Model 4:
RCS: First-Order Autoregressive
RH: $\sigma^2 \times |Age|^{2\delta}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 4 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (LR) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times |Age|^{2\delta}$: Variance proportional to the absolute value of Age raised to a constant power

Table S12. Characteristics of different submodels and final growth model for high density lipoprotein cholesterol (HDL-C) in women

	Notation	Value (Standard Error), P value				
		Model 1	Model 2	Model 3	Model 4	Final model
Intercept	β_0	1.24 (0.004), <0.001	1.25 (0.004), <0.001	1.25 (0.004), <0.001	1.26 (0.004), <0.001	1.26 (0.005), <0.001
Age	β_1		0.009 (0.0002), <0.001	0.009 (0.0002), <0.001	0.01 (0.0002), <0.001	0.01 (0.0002), <0.001
Age^2	β_2			0.00006 (0.00009), 0.516	0.0005 (0.0001), <0.001	0.0005 (0.0001), <0.001
Variance of random intercept	$\sigma^2\,u_0$	0.05 (0.001)	0.07 (0.001)	0.07 (0.001)	0.07 (0.002)	0.07 (0.002)
Variance of random Age term	$\sigma^2\,u_1$				0.00003 (0.000004)	0.00003 (0.000005)
AIC		1814.589	-86.87082	-109.4839	-203.3837	-210.0115
Log Likelihood (P value for LR test)		-904.2946	47.43541 (<0.001)	59.74194 (<0.001)	108.69188 (<0.001)	113.0058 (0.003)

Model 1: Unconditional mean
Level 1: HDL-C$_{ij}$= b$_{oi}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$

Model 2: Unconditional growth model
Level 1: HDL-C$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1

Model 3: Quadratic unconditional growth model
Level 1: HDL-C$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ +e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1
Level 2: b$_{2i}$ = β_2

Model 4: Quadratic unconditional growth model
Level 1: HDL-C$_{ij}$= b$_{oi}$ + b$_1$Age$_{ij}$ + b$_2$Age$^2_{ij}$ + e$_{ij}$
Level 2: b$_{oi}$ = β_0 + u$_{0i}$
Level 2: b$_{1i}$ = β_1 + u$_{1i}$
Level 2: b$_{2i}$ = β_2

Final Model: Was obtained with adding following error structure into Model 4:
RCS: Was not adjusted for residual correlation structure
RH: $\sigma^2 \times |Age|^{2\delta}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; **b$_{ki}$** represent individual component or random effects; **u$_{ki}$** represents the deviation of **b$_{ki}$** from the value of **β_k** in the population for individual ***i***.

Models 1 to 4 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; **$\sigma^2 \times |Age|^{2\delta}$:** Variance proportional to the absolute value of Age raised to a constant power

Table S13. Characteristics of different submodels and final growth model for total cholesterol (TC) in men

	Notation	Value (Standard Error), P value				
		Model 1	Model 2	Model 3	Model 4	Final model
Intercept	β_0	4.98 (0.01), <0.001	4.98 (0.01), <0.001	5.14 (0.02), <0.001	5.15 (0.02), <0.001	5.17 (0.02), <0.001
Age	β_1		-0.003 (0.0007), <0.001	-0.0005(0.0007), 0.476	-0.004 (0.001), <0.001	-0.003 (0.001), 0.036
Age ^{2}	β_2			-0.008 (0.0003), <0.001	-0.008 (0.0004), <0.001	-0.008 (0.0004), <0.001
Age ^{3}	β_3				0.0001 (0.00003), <0.001	0.0001 (0.00004), <0.001
Variance of random intercept	$\sigma^2 u_0$	0.62 (0.02)	0.63 (0.02)	0.64 (0.02)	0.64 (0.02)	0.62 (0.02)
AIC		33991.55	33974.32	33454.35	33405.58	32981.21
Log Likelihood (P value for LR test)		-16992.77	-16983.16 (<0.001)	-16722.17 (<0.001)	-16696.79 (<0.001)	-16469.61 (<0.001)

Model 1: Unconditional mean
Level 1: $TC_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Cubic unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Final Model: Was obtained with adding following error structure into Model 4:
RCS: General correlation structure
RH: Was not adjusted for variance structure

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual *i*.

Models 1 to 4 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity

Table S14. Characteristics of different submodels and final growth model for total cholesterol (TC) in women

	Notation	Value (Standard Error), P value					
		Model 1	**Model 2**	**Model 3**	**Model 4**	**Model 5**	**Final model**
Intercept	β_0	5.11 (0.01), <0.001	5.13 (0.01), <0.001	5.27 (0.01), <0.001	5.27 (0.01), <0.001	5.27 (0.01), <0.001	5.26 (0.01), <0.001
Age	β_1		0.01 (0.001), <0.001	0.01 (0.001), <0.001	0.03 (0.001), <0.001	0.03 (0.001), <0.001	0.03 (0.001), <0.001
Age^2	β_2			-0.01 (0.0003), <0.001	-0.01 (0.0003), <0.001	-0.01 (0.0003), <0.001	-0.005 (0.0004), <0.001
Age^3	β_3				-0.001 (0.00003), <0.001	-0.001 (0.00003), <0.001	-0.001(0.00004), <0.001
Variance of random intercept	$\sigma^2\,u_0$	0.66 (0.02)	0.55 (0.01)	0.57 (0.01)	0.56 (0.01)	0.51 (0.01)	0.46 (0.01)
Variance of random Age term	$\sigma^2\,u_1$					0.0007(0.00006)	0.0003 (0.00006)
AIC		49834.05	49513.67	48964.68	48623.72	48434.96	47594.15
Log Likelihood (P value for LR test)		-24914.03	-24752.84 (<0.001)	-24477.34 (<0.001)	-24305.86 (<0.001)	-24209.48 (<0.001)	-23787.08 (<0.001)

Model 1: Unconditional mean
Level 1: $TC_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Cubic unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Model 5: Cubic growth model with the intercept and slope variability
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Final Model: Was obtained with adding following error structure into Model 5:
RCS: First-Order Autoregressive
RH: $\sigma^2 \times e^{\,2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 5 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{\,2\delta \times Age}$: Variance proportional to the exponential of Age multiplied by a constant

Table S15. Characteristics of different submodels and final growth model natural logarithm of triglyceride (Ln-TG) in men

	Notation	Value (Standard Error), P value					
		Model 1	Model 2	Model 3	Model 4	Model 5	Final model
Intercept	β_0	0.48 (0.01), <0.001	0.47 (0.01), <0.001	0.57 (0.01), <0.001	0.57 (0.01), <0.001	0.57 (0.01), <0.001	0.57 (0.01), <0.001
Age	β_1		-0.002 (0.0004), <0.001	-0.001 (0.0004), <0.01	-0.005 (0.0005), <0.001	-0.004 (0.0006), <0.001	-0.004 (0.0006), <0.001
Age ^{2}	β_2			-0.004 (0.0002), <0.001	-0.004 (0.0002), <0.001	-0.004 (0.0002), <0.001	-0.005 (0.0002), <0.001
Age ^{3}	β_3				0.0001 (0.00002), <0.001	0.0001 (0.00002), <0.001	0.0001 (0.00002), <0.001
Variance of random intercept	$\sigma^2\,u_0$	0.17 (0.005)	0.17 (0.005)	0.17 (0.005)	0.17 (0.005)	0.17 (0.005)	0.16 (0.005)
Variance of random Age term	$\sigma^2\,u_1$					0.00009 (0.00001)	0.00002 (0.00001)
AIC		13657.48	13619.7	13007.22	12938.91	12840.78	12600.77
Log Likelihood (P value for LR test)		-6825.74	-6805.85 (<0.001)	-6498.609 (<0.001)	-6463.453 (<0.001)	-6412.392 (<0.001)	-6290.387 (<0.001)

Model 1: Unconditional mean
Level 1: $TC_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Cubic unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Model 5: Cubic growth model with the intercept and slope variability
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Final Model: Was obtained with adding following error structure into Model 5:
RCS: First-Order Autoregressive
RH: $\sigma^2 \times e^{\,2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 5 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{\,2\delta \times Age}$: Variance proportional to the exponential of Age multiplied by a constant

Table S16. Characteristics of different submodels and final growth model natural logarithm of triglyceride (Ln-TG) in women

	Notation	Value (Standard Error), P value					
		Model 1	**Model 2**	**Model 3**	**Model 4**	**Model 5**	**Final model**
Intercept	β_0	0.32 (0.01), <0.001	0.33 (0.01), <0.001	0.38 (0.01), <0.001	0.38 (0.01), <0.001	0.38 (0.01), <0.001	0.39 (0.01), <0.001
Age	β_1		0.003 (0.0003), <0.001	0.004 (0.0003), <0.001	0.01 (0.0004), <0.001	0.01 (0.0004), <0.001	0.01 (0.0005), <0.001
Age^2	β_2			-0.003 (0.0001), <0.001	-0.003 (0.0001), <0.001	-0.002 (0.0001), <0.001	-0.003 (0.0001), <0.001
Age^3	β_3				-0.0001 (0.00001), <0.001	-0.0001 (0.00001), <0.001	-0.0001 (0.00001), <0.001
Variance of random intercept	$\sigma^2 u_0$	0.16 (0.004)	0.15 (0.003)	0.15 (0.004)	0.15 (0.004)	0.15 (0.004)	0.14 (0.003)
Variance of random Age term	$\sigma^2 u_1$					0.00005 (0.00001)	0.00005 (0.00001)
AIC		17363.1	17143.56	16738.47	16666.37	16627.17	16474.67
Log Likelihood (P value for LR test)		-8678.548	-8567.78 (<0.001)	-8364.235 (<0.001)	-8327.183 (<0.001)	-8305.587 (<0.001)	-8228.335 (<0.001)

Model 1: Unconditional mean
Level 1: $TC_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Model 3: Quadratic unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$

Model 4: Cubic unconditional growth model
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Model 5: Cubic growth model with the intercept and slope variability
Level 1: $TC_{ij} = b_{oi} + b_1 Age_{ij} + b_2 Age^2_{ij} + b_3 Age^3_{ij} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1 + u_{1i}$
Level 2: $b_{2i} = \beta_2$
Level 2: $b_{3i} = \beta_3$

Final Model: Was obtained with adding following error structure into Model 5:
RCS: Was not adjusted for residual correlation structure
RH: $\sigma^2 \times e^{2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 to 5 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{2\delta \times Age}$: Variance proportional to the exponential of Age multiplied by a constant

Table S17. Characteristics of different submodels and final growth model for 2-h post-load plasma (2-hPG) in men

	Notation	Value (Standard Error), P value		
		Model 1	**Model 2**	**Final model**
Intercept	β_0	5.80 (0.02), <0.001	5.78 (0.02), <0.001	5.81 (0.02), <0.001
Age	β_1		0.05 (0.001), <0.001	0.04 (0.001), <0.001
Variance of random intercept	$\sigma^2 u_0$	1.12 (0.05)	1.02 (0.04)	0.96 (0.02)
AIC		50587.49	49337.88	49220.22
Log Likelihood (P value for LR test)		-25290.74	-24664.94 (<0.001)	-24591.11 (<0.001)

Model 1: Unconditional mean
Level 1: $BMI_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $BMI_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$

Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Final Model: Was obtained with adding following error structure into Model 2:
RCS: General correlation structure
RH: Was not adjusted for variance structure

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.

Models 1 and 2 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{2\delta \times Age}$**:** Variance proportional to the exponential of Age multiplied by a constant

Table S18. Characteristics of different submodels and final growth model for 2-h post-load plasma (2-hPG) in women

	Notation	Value (Standard Error), P value		
		Model 1	Model 2	Final model
Intercept	β_0	6.05 (0.02), <0.001	6.12 (0.02), <0.001	6.13 (0.02), <0.001
Age	β_1		0.04 (0.001), <0.001	0.04 (0.001), <0.001
Variance of random intercept	$\sigma^2 u_0$	1.02 (0.04)	0.84 (0.03)	0.74 (0.03)
AIC		63983.61	62302.42	62002.42
Log Likelihood (P value for LR test)		-31988.81	-31147.21 (<0.001)	-30995.21 (<0.001)

Model 1: Unconditional mean
Level 1: $BMI_{ij} = b_{oi} + e_{ij}$
Level 2: $b_{oi} = \beta_0 + u_{0i}$

Model 2: Unconditional growth model
Level 1: $BMI_{ij} = b_{oi} + b_1 Age_{ij} + e_{ij}$

Level 2: $b_{oi} = \beta_0 + u_{0i}$
Level 2: $b_{1i} = \beta_1$

Final Model: Was obtained with adding following error structure into Model 2:
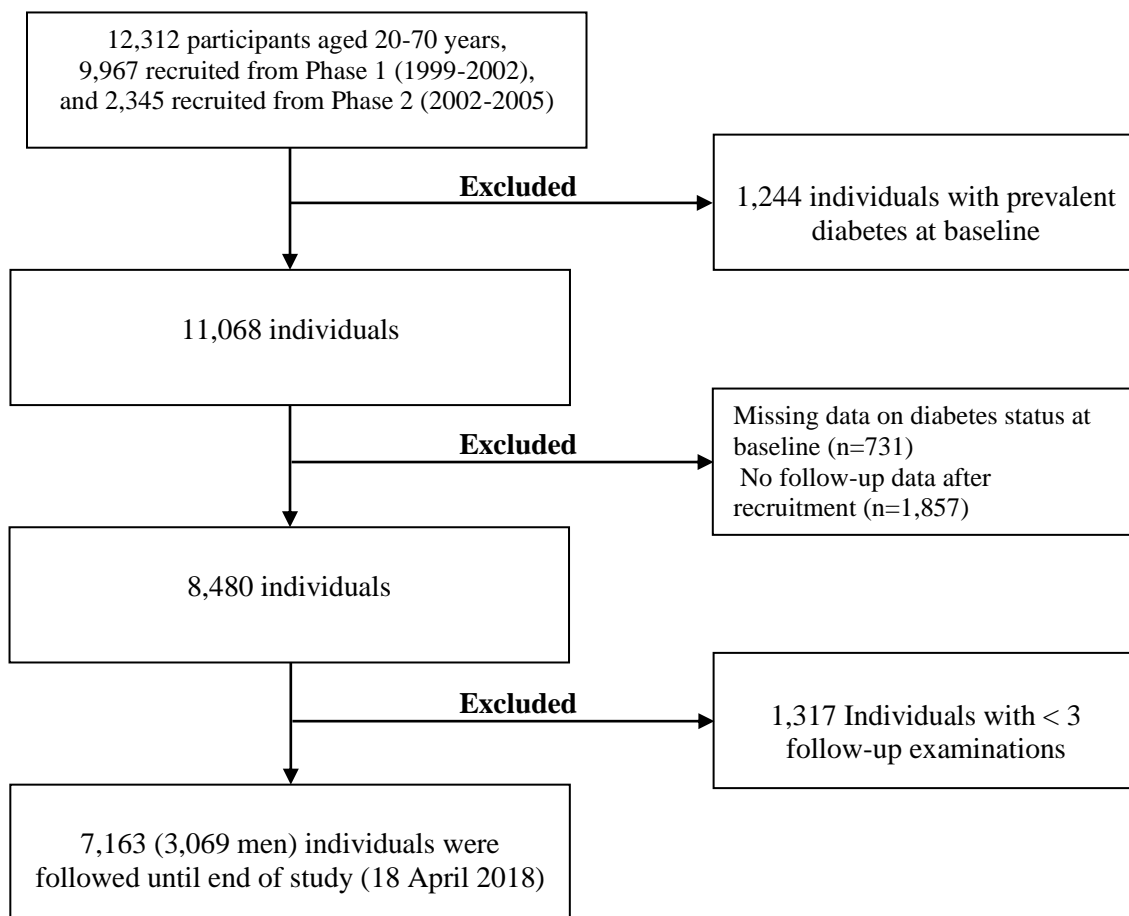**RCS:** First-Order Autoregressive
RH: $\sigma^2 \times e^{2\delta \times Age}$

In level 1 of growth models, change over time is modelled at individual-level, and in level 2, it is modelled at group-level.

β_k represent population parameter or fixed effect; b_{ki} represent individual component or random effects; u_{ki} represents the deviation of b_{ki} from the value of β_k in the population for individual i.
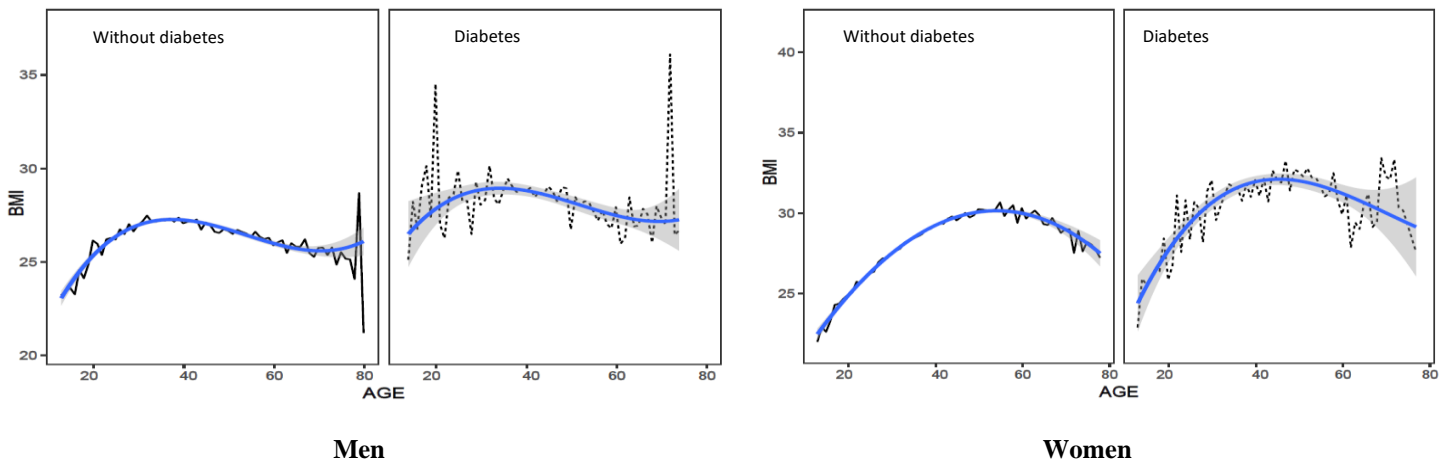
Models 1 and 2 were developed without testing residual correlation structure and residual heteroscedasticity, and after reaching the optimal function, three commonly examined types of correlation and variance structure were tested to select the optimal error structure (**Final model**).

AIC: Akaike Information Criterion; **Log Likelihood** represents the maximum likelihood estimator of the parameter, and P value is a test of this difference using a likelihood ratio (**LR**) test; **RCS:** Residual correlation structure; **RH:** Residual heteroscedasticity; $\sigma^2 \times e^{2\delta \times Age}$: Variance proportional to the exponential of Age multiplied by a constant
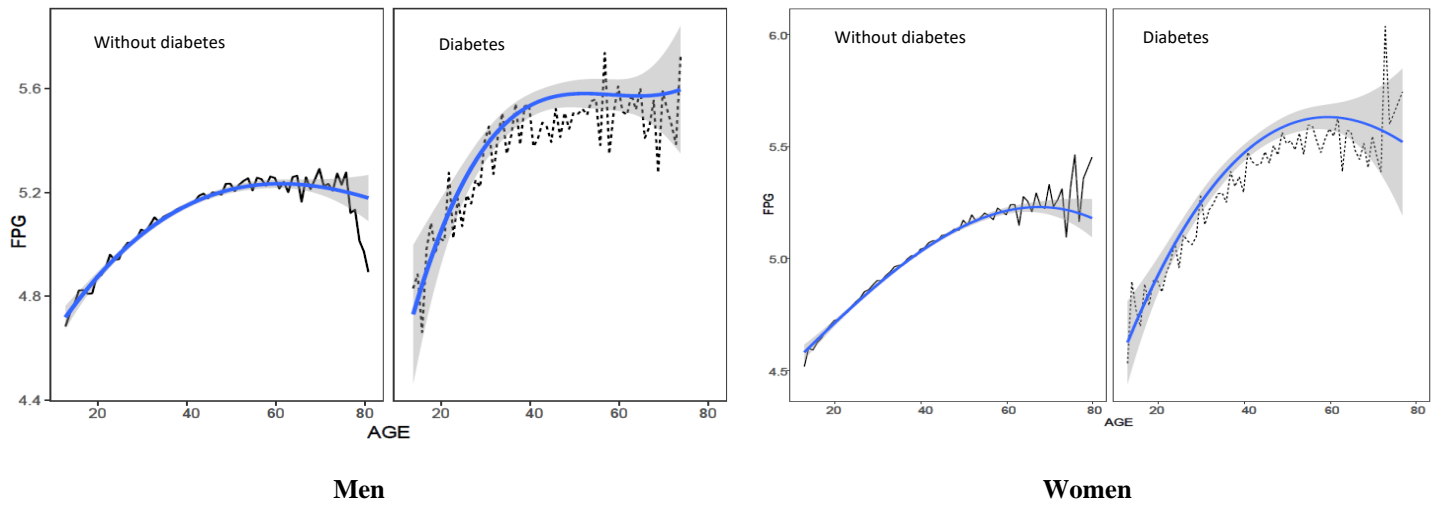
```
┌─────────────────────────────────────────┐
│  12,312 participants aged 20-70 years,   │
│  9,967 recruited from Phase 1 (1999-2002),│
│  and 2,345 recruited from Phase 2 (2002-2005)│
└─────────────────────────────────────────┘
                │
       Excluded │──────────────►  ┌──────────────────────────────┐
                │                  │ 1,244 individuals with prevalent│
                ▼                  │ diabetes at baseline          │
                                   └──────────────────────────────┘
┌─────────────────────────────────────────┐
│  11,068 individuals                      │
└─────────────────────────────────────────┘
                │
       Excluded │──────────────►  ┌──────────────────────────────┐
                │                  │ Missing data on diabetes status at│
                ▼                  │ baseline (n=731)              │
                                   │ No follow-up data after       │
                                   │ recruitment (n=1,857)         │
                                   └──────────────────────────────┘
┌─────────────────────────────────────────┐
│  8,480 individuals                       │
└─────────────────────────────────────────┘
                │
       Excluded │──────────────►  ┌──────────────────────────────┐
                │                  │ 1,317 Individuals with < 3    │
                ▼                  │ follow-up examinations        │
                                   └──────────────────────────────┘
┌─────────────────────────────────────────┐
│  7,163 (3,069 men) individuals were      │
│  followed until end of study (18 April 2018)│
└─────────────────────────────────────────┘
```

Supplementary Figure 1: Study sample selection flow chart, Tehran Lipid and Glucose Study

BMI
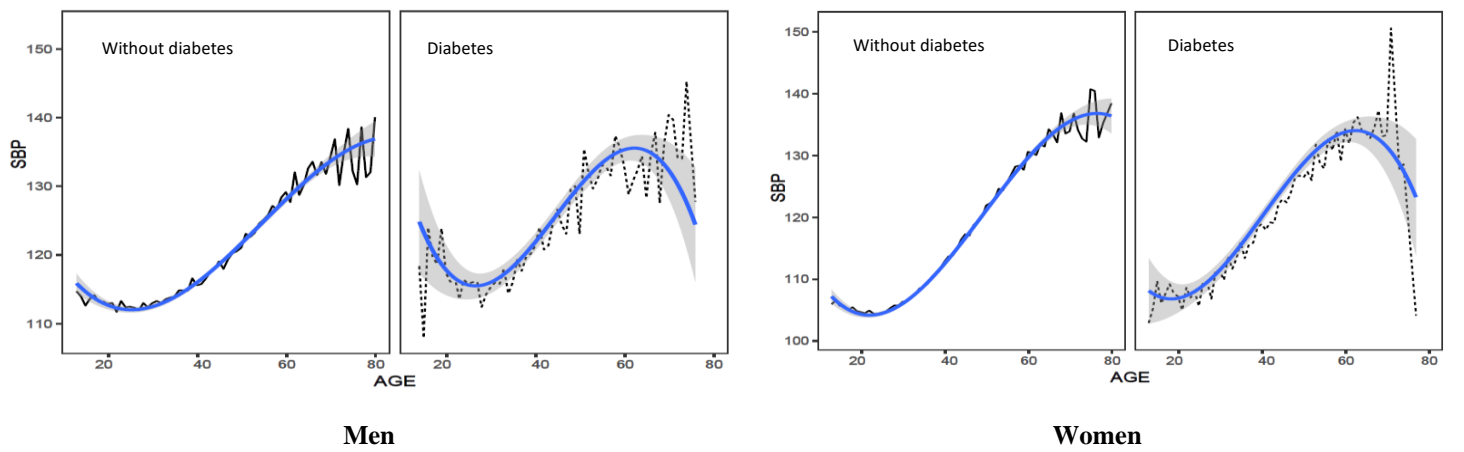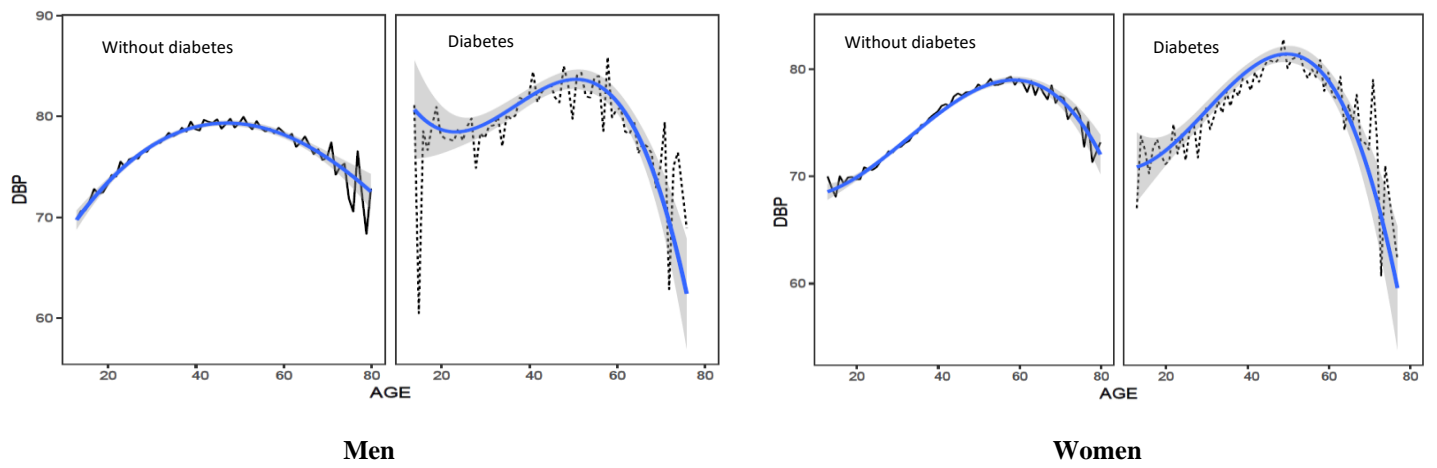
Men   **Women**
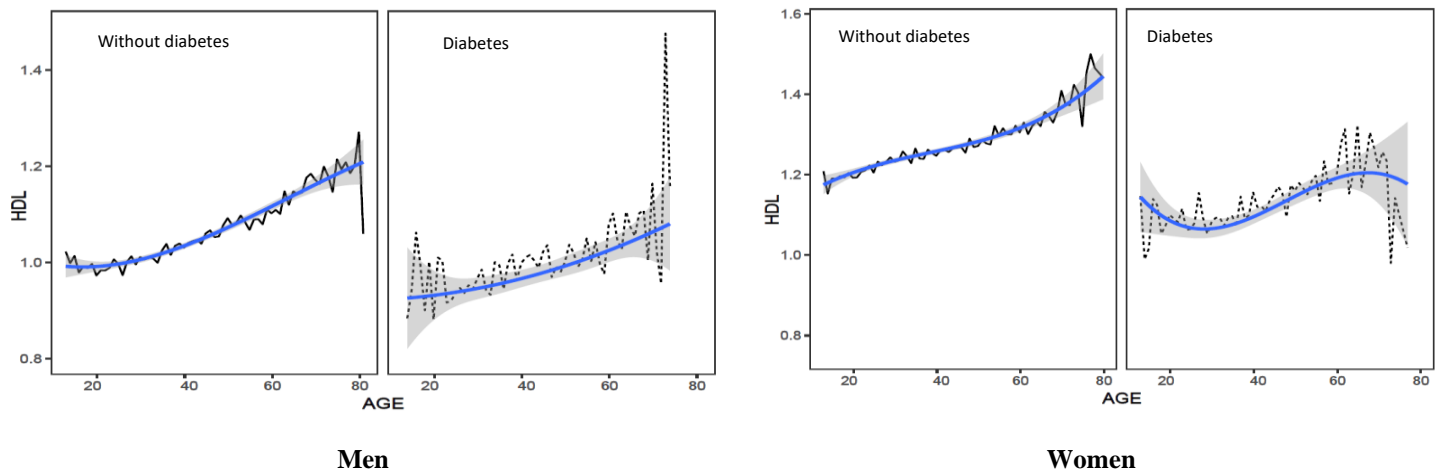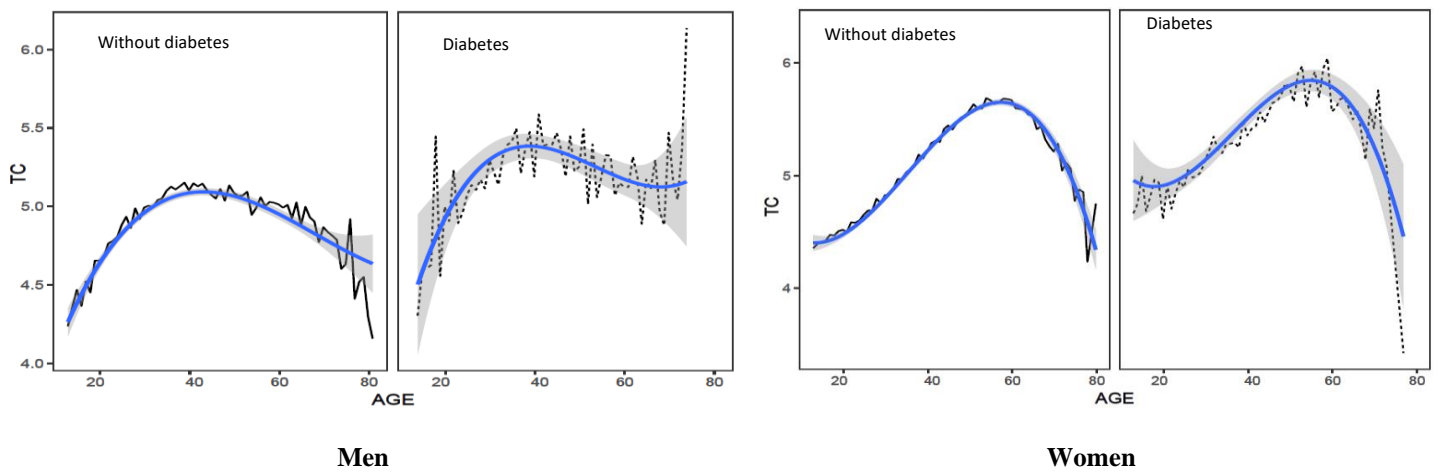
FPG

Men   **Women**

SBP

Men   **Women**

DBP

Men   **Women**

HDL-C

Men   **Women**

TC

Men   **Women**
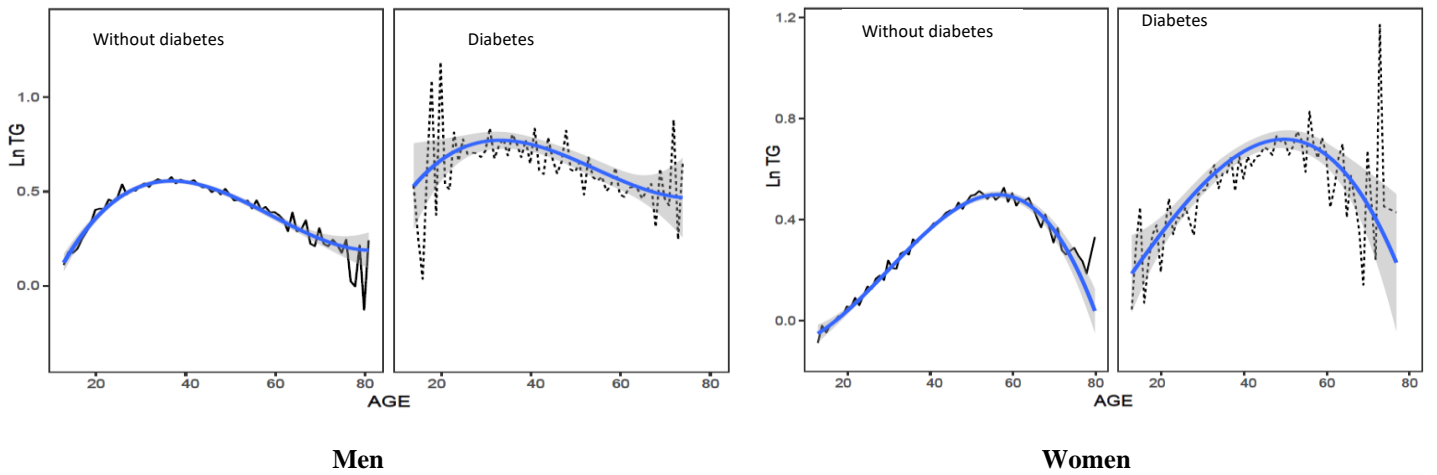
Ln-TG

Men **Women**

2-hPG

Men **Women**

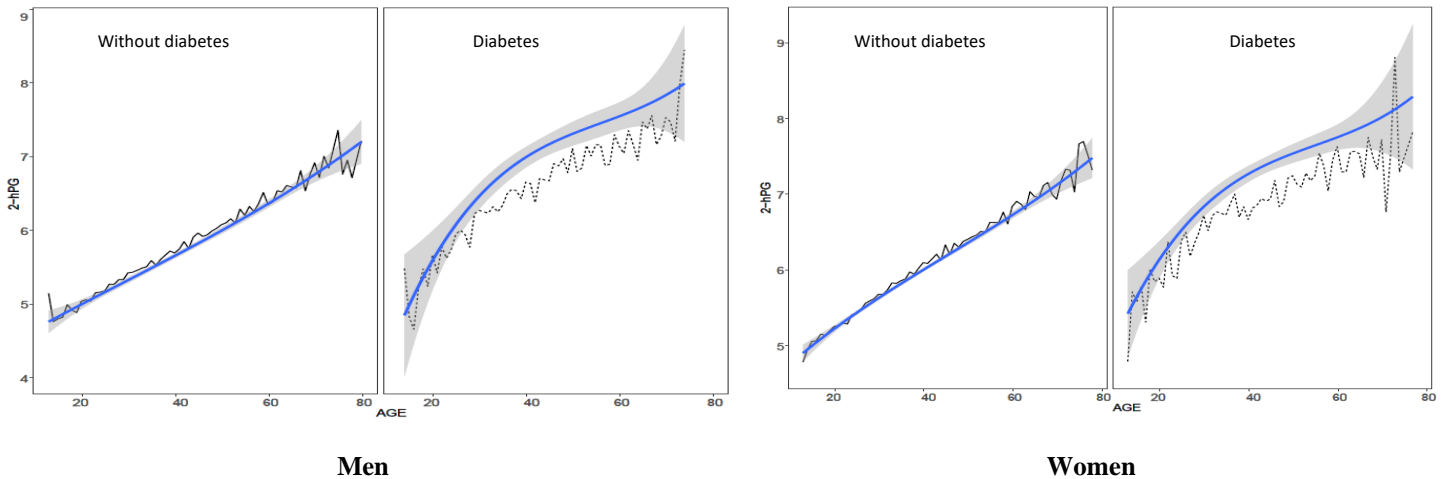**Supplementary Figure 2:** Mean predicted value for metabolic risk factors from mixed effects models by gender.

The solid and dotted black lines are predictions based on combined fixed and random effects, and the smooth lines were computed using generalized additive model (GAM) with polynomial function. Grey shading indicates ± SE

BMI: body mass index; **FPG:** fasting plasma glucose; **TC:** total cholesterol; **SBP:** systolic blood pressure; **DBP:** diastolic blood pressure; **HDL-C:** high-density lipoprotein cholesterol; **2-hPG:** 2-h post-load plasma; **Ln-TG:** natural logarithm of triglyceride; **SE:** standard error