S1 Figure: Predicted metabolite pools and flux trajectories


a – Plasma metabolite pools

b – Hepatic metabolite pools

c – Peripheral metabolite pools
d – Metabolite pools in the intestinal lumen

- Intestinal triglycerides [μmol]
- Intestinal cholesterol [μmol]
- Intestinal bile acids [μmol]

e – Dietary intake in terms of macronutrients

- Carbohydrate intake [μmol/day]
- Triglyceride intake [μmol/day]
- Cholesterol intake [μmol/day]
- Amino acid intake [μmol/day]

f – Dietary triglyceride and cholesterol uptake

- Hepatic CM-TG uptake [μmol/day]
- Peripheral CM-TG uptake [μmol/day]
- Hepatic CM-C uptake [μmol/day]

g – Dietary amino acid uptake fluxes

- Hepatic AA uptake [μmol/day]
- Peripheral AA uptake [μmol/day]

h – Amino acid uptake via the glucogenic (50%) and ketogenic (50%) pathway in liver and periphery
i – Dietary carbohydrate uptake fluxes

j – Carbohydrate metabolic fluxes

k – Lipoprotein formation fluxes

l – Lipoprotein (remnant) uptake fluxes

m – Lipoprotein metabolism fluxes
n – Fatty acid uptake flux

o – Hepatic metabolic fluxes

p – Peripheral metabolic fluxes

q – Hepatic cholesterol storage and release fluxes

r – Bile acid fluxes
s – Intestinal metabolic fluxes

![Graphs showing intestinal metabolic fluxes.](image)

**t – Respiratory fluxes**

![Graphs showing respiratory fluxes.](image)

**S1 Fig.: Predicted metabolite pools and flux trajectories.**

Panels a-b display the dynamics in metabolite pools over time and panels e-t display the corresponding flux trajectories. We selected the n=100 best trajectories (top 10% based on WSSE). The 10% range around the median trajectory is depicted by the shaded area and the median trajectory for each model component is depicted by the solid line for the low-fat diet group (light blue), high-fat diet group (dark blue), non-dyslipidemic Metabolic Syndrome phenotype (gray) and the dyslipidemic Metabolic Syndrome phenotype (red) respectively. Experimental data is represented by the black error bars (mean ± standard deviation).